

THE GENOMICS REVOLUTION AND ITS MARKETING IMPLICATIONS

by

Layne McGuire

A dissertation submitted to the faculty of
The University of North Carolina at Charlotte
In partial fulfillment of the requirements
for the Degree of Doctor of Business Administration

Charlotte

2023

Approved by:

Dr. Sunil Erevelles, Chair

Dr. Mason Jenkins

Dr. Jennifer Ames Stuart

Dr. Pinku Mukerjee

ABSTRACT

LAYNE MCGUIRE. The Genomics Revolution and Its Marketing Implications.
(Under the direction of DR. SUNIL EREVELLES)

Genetic characteristics drive around 50% of human behavioral traits. The capacity of genes to help predict consumer behavioral traits may far exceed that of current behavioral and Big Data paradigms. Genomic data thus represents a seminal paradigm shift likely to radically transform marketing in the future. To date, this potentially enormous role of genomics in marketing and consumer behavior has barely been considered. The purpose of this research is to help fill this gap. Using Hunt's indigenous theory development, inductive realist methodology, this research presents an initial theoretical framework for using gene-centric logic in marketing. This theoretical foundation, ideal for relatively new research areas, could help accelerate future academic research on genomics in marketing and help practitioners better utilize genomic data in marketing activities. Following the creation of this framework, an exploratory empirical analysis involving textual analytical procedures was conducted with a "Cultivated Pool" knowledgeable about both genomics and marketing. Textual analysis of survey responses and a cognitive map were then created to identify the relationships between themes. Theoretical, managerial and methodological contributions and an agenda for future research are then presented. Finally, limitations and most importantly, ethical considerations will be addressed. It is envisioned that this research could provide a foundation upon which a new body of knowledge in marketing can be built.

Dedication

My college band director gave me an amazing example of patience under pressure, and perhaps the most valuable piece of advice I have ever received. At a critical point in this process, I was able to recall that example and advice. For that reason, I dedicate this to Mr. David Willson, Professor of Music Emeritus, University of Mississippi. Your guidance has meant more than you can ever know.

Acknowledgment

I would like to thank my committee chair, Dr. Sunil Erevelles for encouraging me to take on this project and introducing me to a field that is dynamic and fascinating. You said it would be worth it and you were right. Thank you to Dr. Mason Jenkins for your guidance on the empirical analysis. Thank you to Dr. Jennifer Stuart for your insights that I think will lead to my next project. Finally, thank you to Dr. Pinku Mukerjee for your keen insights. I further acknowledge the faculty in the DBA program. I am incredibly grateful.

There are people who have played an instrumental role behind the scenes. To Diane Adams, thank you for your expert copy editing. Your suggestions raised the quality of my writing. To Camelia Protzol, your deconstruction of Hunt's methodology was a helpful guide. To Aryan Patel, assistance with my references was extremely helpful. I can't say enough about my colleagues in Cohort 4. We started in the middle of a pandemic and still managed to bond. Your support, guidance, and getting to know you as humans has been a high point of this process.

To the St. Thomas Ringers, your support and encouragement have meant more than you know. To the Anna Ethridge, you have been a vital sounding board and source of sanity during this process. Finally, I would like to thank my parents for so many reasons. My father did not live to see the completion of this dissertation but was always one of my biggest supporters. My mother's unfailing and never-ending support is behind everything I do.

TABLE OF CONTENTS

List of Tables	vii
List of Figures	viii
Chapter 1—Introduction.....	1
Chapter 2—Literature Review.....	6
Chapter 3—Methodology.....	26
Chapter 4—Initial Theoretical Framework.....	38
Chapter 5—Empirical Results.....	73
Chapter 6—Discussion.....	91
References.....	101
Appendix: Survey Information.....	129

LIST OF TABLES AND FIGURES

Tables

1. Genomics Timeline.....	8
2. Perceptions of Heritability.....	12
3. Marketing Applications of Genomic Data.....	16
4. Theoretical Gaps.....	19
5. Key Terms and Insights for Marketing.....	25
6. Application of Indigenous Theory Development.....	29
7. Limitations of Methodology.....	31
8. Participant Cultivation Process.....	35
9. Cohen's Kappa.....	36
10. Key Terms and Definitions.....	47
11. Behavioral Genomic Studies on Traits.....	61
12. Behavioral Genomic Studies on Traits and Related Marketing Uses.....	70
13. List of Major Keywords Used in Coding Attributes of Genomic Data.....	74
14. Attributes of Genomic Data.....	75
15. PMI Matrix.....	80
16. List of Major Keywords Used in Coding Themes for Potential Applications.....	81
17. Themes of the Potential Uses for Genomic Data in Marketing.....	82
18. Pointwise Mutual Information Matrix.....	89
19. Theoretical Contributions of Framework.....	94
20. Managerial Contributions.....	95
21. Ethical Considerations.....	99

Figures:

1. Function of a Gene.....	21
2. Top Journal of Marketing Articles and Their Impact.....	32
3. DNA Double Helix.....	41
4. Normal Distribution.....	67
5. Distribution of Polygenic Scores.....	68
6. PMI Relationships for Genomic Attributes.....	79
7. Positive PMI Relationships for Potential Applications.....	87
8. Negative PMI Relationships for Potential Applications.....	88

CHAPTER 1

Introduction

The genomics revolution represents a monumental moment in the understanding of human behavior and traits. At its core is the mapping of the human genome, which is a game-changing step forward in comprehending the building blocks of life and our ability to predict how humans function. DNA sequencing has opened the door to previously unimaginable precision and detail in detecting, predicting, and potentially modifying human traits. The genomics revolution will likely change much of what we know about ourselves and life itself. In this research, we also suggest that the genomics revolution will likely change much of what we do in marketing.

The gene is the fundamental building block of heredity (Mukherjee 2016). The human genome can be thought of as the “software of life” or the “instruction manual” for how our genes work together to make us who we are (Sanjana 2017). Genes are segments of DNA molecules that carry the instructions for physical or behavioral traits (Portin and Wilkins 2017). The genome is the complete DNA sequence for an organism (Venter et al. 2001).

The debate on the relative role of “nature” versus “nurture” (Galton 1875) has raged for almost one hundred and fifty years. The seeds of this revolution began with Mendel’s observations on the transmission of traits in the 1860s (Cold Harbor Springs Laboratory 2022). Watson and Crick’s 1953 discovery of the double helix structure of DNA eventually led to the launch of the Human Genome Project in 1990, which helped identify the “instruction book” (Collins 1999, p 28) for how humans function. This extraordinary trajectory, which is evolving faster than Moore’s law (November 2019, Burke 2012), has led to Nobel prize-winning

technologies such as CRISPR (Douda and Sternberg 2017), opening the possibility of potentially ending disease and dramatically extending or improving human life. We are at an inflection point that likely will usher in a new transformational age of genomics.

A key part of the genomics revolution involves behavioral genomics. Genes are responsible for 40%-50% of all behavioral traits (Plomin 2019). Moreover, all behavioral traits are heritable (Turkheimer 2000). Contrary to traditional behavioral dogma, the body of genomic research for the past several decades unequivocally indicates that genomics (nature) has roughly (around 50%) the same amount of influence as the environment (nurture) in shaping human behavior (e.g., Plomin and Rende 1991; Bouchard 2004). Twin and adoption studies, as well as studies using genome-wide data sets, collectively provide rich and detailed evidence to support this conclusion (Ayorech et al. 2016, Bouchard et al. 1990; Johnson et al. 2000; Ramanan et al. 2012). Strikingly and counterintuitively, the role of genomics may increase, rather than decrease, over a person's lifetime, as had previously been believed (McGue and Christiansen 2013; Plomin, Owen, and McGuffin 1994).

Motivation and Research Gap

Surprisingly, these paradigm- shifting findings have received barely any attention from marketing scholars. Since the advent of the marketing field, approximately one hundred twenty years ago, scholars and practitioners have focused almost exclusively on the approximately 50% of behavioral traits attributable to environmental factors. With two notable exceptions (Simonson and Sela 2011; Daviet, Nave, and Wind 2022), the marketing literature does not consider genomics' role in consumer behavior and other marketing phenomena. (It is possible that the effect of genomics in marketing or consumer behavior may unknowingly have been captured in past marketing studies.) In sum, understanding of the role of genomics in marketing or consumer

behavior is practically nonexistent. In other words, the vast body of marketing literature may explain only around half the variance in consumption behavior and other marketing phenomena and is largely blind to the other half. Thus, it can reasonably be argued that we are missing much of our understanding of consumers in marketing scenarios. This represents a substantial gap in the marketing literature. This research aims to help narrow that gap.

Research Goals

To narrow the research gap identified above, we first advance a set of foundational premises (FPs) to patch together an initial theoretical framework for genomics in marketing. This framework, lacking in the current literature, could help us better understand and predict consumer behavior and other marketing phenomena. This initial theoretical advance could provide a foundation for future research and practice for genomics in marketing. We use Hunt's (2014, 2015, 2020) indigenous theory building, inductive realist approach to advance a set of foundational premises. Hunt (2020) argues that theory is more relevant if it is developed indigenously in the field in which it will be used. Hunt's methodology is a rigorous and relevant methodology that previously has been used in the first and fourth most impactful articles in the history of the *Journal of Marketing* (Zeithaml 2020).

The second research goal is to conduct an exploratory empirical analysis to add further insight to the initial theoretical framework. Like the theoretical methodology, the empirical methodology was selected for its ability to address new or novel research. Textual analytics will be used to identify key themes related to genomics in marketing. This, in turn, was used to build cognitive maps associated with the key themes and include the strength of associations between identified themes. Both manual coding and semantic mapping techniques were used to assess associations between identified themes. The exploratory empirical analysis will finally be used to

fine-tune assumptions in the foundational premises, advance foundational premises that have previously not been specified, or modify previously specified foundational premises.

Potentially Seminal Nature of This Research

This research is unique in that it is *non-linear* research (in the field of marketing) as opposed to *linear* (incremental) research. Changes in business occur non-linearly, and yet most academic research is incremental. This creates a disconnect related to academic research not reflecting what is needed in the business world. Genomics in marketing is one such non-linear area. While there is a rich literature on genomics outside the marketing field that we build upon, it is still a new, non-linear area in marketing. Genomics is one of the technologies (along with blockchain, energy storage and distribution, artificial intelligence (AI), and robotics) poised for significant transformative growth (Barnett and Urman 2022) in the foreseeable future. Despite this, hardly any genomics research exists in marketing. Transformative growth calls for transformative research. The goal of this research is to help move marketing in that direction.

Ethical Considerations

The positive potential for the transformative power of genomics must be balanced with important ethical considerations. The pace of change and what is possible is moving much faster than the ethical guide rails, frameworks, and regulations (Doudna and Sternberg 2017). The complexity of the genome means that medical and technological innovations will carry consequences both intended and unintended (Isaacson 2021; Plomin 2019). In addition, genomic data contains our most personal information. Critical security, privacy, and consent issues will have to be addressed at an individual and Big Data level (Mathaiyan, Chandrasekaran, and Davis

2013; Shabani and Borry 2018; Shabani 2019). While the power of genomics is evident, considerable care should be taken to use this power responsibly.

Conclusion

The rest of this dissertation will be structured as follows. Chapter 2 presents the literature review, providing historical context, an overview of twin and adoption studies, physical and behavioral trait studies, and studies involving genome-wide data sets. The literature review concludes by analyzing the limited marketing research currently available. In Chapter 3, the theoretical and empirical methodologies are described in detail. In Chapter 4, we develop the initial theoretical framework. In Chapter 5, we discuss the results of empirical methodology. Finally, the dissertation will include a discussion of findings, limitations, and contributions in Chapter 6.

This research is part of a stream of research that includes genomics and blockchain. As this research has progressed, early iterations have been disseminated in peer-reviewed conference proceedings or invited academic presentations. The stream of research includes, “The Genomics Blockchain” (Erevelles et al. 2022) at the Duke University School of Medicine, and “Genetic Data and the Transformation of Marketing” (Erevelles, McGuire, and Erevelles 2022) in the Society of Marketing Advances Proceedings. It is hoped that this dissertation and the research stream collectively will have an impact in the field of marketing.

CHAPTER 2

Literature Review

Historical Context

Most bodies of literature evolve as their fields develop; this has been especially evident in the progression of genetic research literature. Although the concept of heredity began with Mendel in the mid-nineteenth century, the field of genetics was not a discrete scientific discipline until much later. By 1906 genetics was recognized as a field of study for several reasons: the codification of the word, gene, the work of scientists engaging in theories and research, the emergence of professional academic conferences, and the establishment of a publication source for scholarship (Gayon 2016). The oldest English language journal in the field, *Journal of Genetics*, was founded by W. Bateson and R.C. Punnett in 1910. Although the seminal papers of the early twentieth century are interesting historically, they are less relevant for twenty-first-century literature reviews. For example, key discoveries about biochemical processes' role in genetics (Beadle and Tatum 1941) were soon superseded by those of Watson, Crick, and Franklin in 1953, who discovered the double helix structure of DNA.

From the 1950s through the 2000s, the key theme in genetics literature was an ongoing effort to define and often refine standard definitions (e.g., gene) and the mechanisms by which processes (e.g., gene expression) work. The twentieth century saw an even more remarkable leap in the field with the human genome project (Human Genome Research Institute 2022) and the explosion in gene editing technologies such as CRISPR (Cohen 2020). Exploring the history and evolution of this literature would require a full-length text to explore properly. For this dissertation, it is more relevant to survey the literature on physical and behavioral traits and how

they have been studied over the last fifty years. Table 1 highlights a few of the most critical developments in the field.

Table 1-Genomics Timeline

Year	Event	Major Contribution	Citation
1798	Thomas R. Malthus published <i>An Essay on the Principle of Population</i> .	Introduced the Malthusian Trap, which argued that population growth would outpace food supply. His theories influenced Darwin.	Malthus, 1798. Mukerjee, 2016, p. 36-39.
1859	Charles Darwin published <i>On the Origins of the Species by Means of Natural Selection</i> .	The culmination of Darwin's research on natural selection resulted in Darwin's Theory of Evolution which focused on the survival of the fittest.	Mukerjee, 2016, p.28-40.
1865	Gregor Mendel conducted experiments on pea plants that led to observations on the transmission of traits.	As the "Father of Modern Genetics," Mendel's work laid the foundation for our understanding of heredity.	Cold Harbor Springs Laboratory, 2022.
1883	Francis Galton published <i>Inquiries into Human Faculty and Its Development</i> , which introduced the term eugenics	Galton coined the phrase "nature vs. nurture."	National Human Genome Research Institute, 2022. Galton, 1875.
1953	James Watson and Francis Crick (along with Rosalind Franklin) discovered the double helix structure of DNA and were awarded the Nobel Prize in 1962. (Note: Rosalind Franklin died in 1958 at the age of 37 and therefore did not share the prize.)	The idea of the gene as a messenger was replaced by the idea of as a code to be deciphered.	Mukherjee, 2016, 149-160.
1990	Launch of the Human Genome Project-Initiative led by James Watson with Francis Collins assuming leadership in 1993.	A publicly funded multinational project completed in 2003 mapped the human genome.	Human Genome Research Institute, 2022.
1992	Launch of the J. Craig Venter Institute.	Privately funded efforts were undertaken to map the human genome, with reports published in 2001.	J. Craig Venter Institute, 2022.
1996	Dolly the sheep cloned in Scotland	The first mammal cloned from an adult cell led to the development of personalized stem cells.	Roslin Institute, 2022.
2012	Jennifer Doudna and Emmanuelle Charpentier discovered CRISPR and were awarded the Nobel Prize in 2020.	CRISPR technology enables genome editing.	Cohen, 2020.

While the marketing literature on genomics is in its infancy, an exhaustive review of the literature on behavioral traits is a labor-intensive undertaking that would only skim the surface of the topic. Almost 20,000 academic articles on behavioral genetics were published between 2010 and 2014 (Ayorech et al. 2016). Given this exponential growth, the approach taken by many leading researchers is to attempt to aggregate findings from individual studies (primarily twin methods) and identify common themes.

The gold standard for findings is replicability, which has proven elusive for most scientific studies (Plomin et al. 2016). Evidence suggests that most published research findings are false (Ioannidis 2005). That said, the sheer volume of studies has enabled the identification of several key findings or trends that permeate the literature and provide support for the foundational premises in this study. Perhaps the most important is that while essentially all behavioral traits show significant heritability, it is not the sole driver of any trait (Plomin et al. 2016). In other words, no trait is unaffected by genetics, but no trait is 100% attributable to genetics, as has been noted by other researchers (Turkheimer 2000). Other significant and replicable findings are that heritability for behavioral traits is polygenic, and the effect of any single genetic variation is small (Chabris et al. 2015; Plomin et al. 2016).

Twin and Adoption Studies

The “nature versus nurture” question raised by Galton (1875) is the genesis of the idea that studying twins over the course of their lifetime is an effective method to measure the impact of environmental versus genetic factors on behavior. Though Galton’s “The History of Twins, as a Criterion of the Relative Powers of Nature and Nurture” is a seminal work, it is not the origin of the type of twin studies that have become the cornerstone of behavioral genetics. While there was an understanding that some twins were more alike than others, the discovery of monozygotic

(identical or MZ) and dizygotic (fraternal or DZ) twins was still fifty years away (Rende, Plomin, and Vandenberg 1990). Galton also fell firmly on the side of the ongoing importance of nature throughout the lifespan (Rende, Plomin, and Vandenberg 1990). Though that position was often out of favor for various scientific and social reasons, it eventually returned to favor (Plomin 2019).

Twin studies are valuable for multiple reasons, mainly the ability to examine the behaviors of those who share a common genetic blueprint. While valuable information is gained from studying the parent-child transmission of traits, twins provide an additional control variable. Researchers can study MZ and DZ twins longitudinally, reared separately, or reared together (adoption studies). Therefore, twin, sibling, and adoption studies can test a wide range of evolutionary- based hypotheses (Segal 1993).

The Colorado Adoption Project (CAP) and the Twins Early Development Study (TEDS), both longitudinal studies, continue to provide insights. The CAP, which began in 1975, examines birth parents, children adopted as infants, and adoptive families (Rhea et al. 2012). This method for studying genetic versus environmental factors has allowed researchers to consider the cumulative effects of the environment and the role that genetics plays over the lifespan (Rhea et al. 2012). The TEDS focuses on the cognitive and behavioral development of over 10,000 pairs of twins born in the United Kingdom between 1994 and 1996; its key contribution lies in the ability to glean data as the participants develop into adults.

A third important study is the Minnesota Study of Twins Reared Apart, which covers the span of both the CAP and the TEDS but focuses on MZ and DZ twins reared apart (Bouchard et al. 1990). The volume and richness of the data collected by these three studies enable researchers to consider genetics' role in behavioral traits and how that evolves or remains static over the

lifespan as well as how the environment does or does not play a role and, therefore, what interventions have the potential to change outcomes.

Correlation is not causation, but causation is ultimately what researchers would like to understand about behavioral traits. The proliferation of twin studies on almost any trait (corroborated by adoption and family studies) has left little doubt that behavioral traits are heritable and that, given the preponderance of the evidence, the degree of influence is of less interest than the cause (Johnson et al. 2009). The other primary value of twin studies reinforces the need to understand both the intrinsic and extrinsic drivers of behavior (Johnson et al. 2009). The results may challenge or reinforce what is already understood about consumer behavior.

Physical and Behavioral Trait Studies

By 1994, researchers had firmly established that there is a genetic component to essentially all complex behaviors (Plomin, Owen, and McGuffin 1994). What also emerges from the literature is that until the 1990s, there was no full integration of biological, genetic, and psychological approaches to understanding behavioral genetics. From a scientific perspective, genetic research is interested in the heritability of traits. Behavioral geneticists examine not only heritability but the perception or belief in heritability. For example, those who believe that obesity or alcoholism results from environmental factors or personal choices rather than genetic influence exhibit behaviors or beliefs consistent with that perception. From a marketing perspective, the relationship between perception and reality becomes essential for understanding consumer behavior. Table 2 illustrates the results of a study asking young adults to estimate the heritability of certain traits and then comparing that with the results of genetic studies.

Table 2-Perceptions of Heritability

Trait	Perception of Genetic Influence (Plomin 2019, p.6)	Actual Genetic Influence (Approximate)	Relevant Studies
Personality	38%	40%	Bouchard and McGue 2003
General Intelligence	41%	50%	Plomin and Von Stumm 2018
School Achievement	29%	60%	Rimfeld et al. 2018
Verbal Ability	27%	60%	Trzaskowski, Shakeshaft and Plomin 2015
Spatial Ability	30%	70%	Rimfeld et al. 2017
Reading Disability	38%	60%	Friend, DeFries, and Olson 2008
Remembering Faces	31%	60%	Shakeshaft and Plomin 2015
Breast Cancer	53%	10%	Rowell et al. 1994
Stomach Ulcers	29%	70%	Malaty et al. 2000
Schizophrenia	43%	50%	Plomin et al. 2016
Weight	40%	70%	Grilo and Pogue-Geile 1991
Eye Color	77%	90%	Lin et al. 2016
Height	76%	80%	McEvoy and Visscher 2009

Two key points can be derived from Table 2. First, for any of the traits listed, there are thousands of studies, and none of the attributes are straightforward. Even seemingly simple traits, such as eye color, are far more complicated than the Punnett squares used in elementary school science classes would suggest. Second, several disorders indicate a wide gap between science and popular perception. For example, weight and breast cancer research results are likely surprising to those unfamiliar with the research.

Statistics do not provide enough information to explain the mechanism by which heritability occurs or to address the complex relationship between the genes that drive intelligence. For example, while research indicates that 50% of general intelligence is heritable, that does not explain how or why it occurs. Related traits such as personality and scholastic have also been replicated (Plomin, Owen, and McGuffin 1994). That understanding becomes relevant as researchers try to uncover causation as well as to identify efficacious interventions.

Genomic Datasets

While early genomic studies relied on twin and adoption studies, current and future research will rely on genomic databases for data. GenBank is the registered trademark of a comprehensive database that is accessed through the National Institute of Health (Benson et al. 2012). The next generation of research in genomics will utilize the massive number of genome-wide data sets (Ramanan et al. 2012). This is an enormous step forward for genomics. Correlation is not causation, yet establishing causation for diseases and behaviors is the most effective way to identify appropriate cures and treatments. Furthermore, complex traits and diseases are almost never simple. These data sets and the appropriate tools with which to analyze them have the potential to transform what is possible. While beyond the scope of this dissertation, a comprehensive review of genomic data as a subset of big data would be valuable for future research. In addition to the impact on results of medical and behavioral genomic research, there is an area of literature that has emerged on issues surrounding access, security, privacy, and other concerns related to data (Khan 2011). As both the field and technology continue to grow and evolve, the research on genomic databases will as well. The value of the initial theoretical framework is that it will be enhanced but not replaced by the results of research using genomic datasets.

Marketing

Marketing has existed as a distinct business discipline since the early twentieth century, with the advent of marketing courses at the University of Michigan, The Ohio State University, and the Wharton School of Business at the University of Pennsylvania (Weld, 1941). The founding of the *Journal of Retailing* in 1925, followed by the *Journal of Marketing* in 1936 and the *Journal of Consumer Research* in 1974, provided platforms for academic research with notable theoretical and empirical contributions. While all three tout a multidisciplinary research approach, biology, genetics, and genome research results have been absent. The focus of research has centered almost entirely on environmental drivers of consumer behaviors.

While the genetic and behavioral literature is extensive, the marketing literature is limited to three articles, which is surprising given the field's longevity. The most recent contribution to the marketing literature extends Belk's stimulus-response theory by extending the construct of an organism to include the genome and suggesting a causal relationship to consumer behavior (David, Nave, and Wind 2022). The authors base this extension on the fourth law of behavioral genetics, which suggests that the cumulative effect of slight variations in SNPs is significant (Chabris et al. 2015). The article focuses on the specific yet vital role that the DTC market plays in the genetic data ecosystem. The authors point out that the role of genetic data in marketing has been largely ignored; in fact, the marketing literature was relatively silent on the topic between 2011 and 2022.

Simonson and Sela (2011) explored a different yet equally relevant area: the genetic basis of consumer choice, specifically, the role of genetics on a range of consumer choice and judgment constructs that had already been explored in marketing. Their empirical model for measuring marketing constructs using genetic data represented a 10-year step forward for the

literature. The initial step occurred when the human genome project was still two years from completion. While Hirschman and Stern (2001) provided interesting initial insight into how research in neuropsychology can inform research on novelty-seeking and compulsive consumption, their article reflects the infancy of the field. The primary limitation of the current literature is the topic's novelty; all three articles offer research agendas that could benefit from a theoretical framework.

Genomics plays a significant role in almost all behavioral traits. How that occurs is complex, and our understanding of it continues to evolve. The literature relevant to current research comes from the areas of biology, genetics, and behavior. Each is highly expansive, but common themes emerge and support the foundational premises presented here. The amount of data available, particularly from twin and adoption studies, is an indicator of the exponential growth in the availability of genomic data.

The potential marketing applications of genomic data are extensive. Table 3 contains nine illustrative examples of marketing applications that are currently or potentially in use. In some cases, such as Google, consumers may not consciously provide their data or fully appreciate the extent of the data they are providing. In other cases, such as Ancestry or 23 and Me, consumers do not always fully understand the potential applications of the data they are providing.

Table 3- Marketing Applications of Genomic Data

	Marketing Application	Description	Examples	Citation
1	Market research, predicting consumer behavior	Testing that allows an individual to provide a saliva sample and obtain information for reasons from tracing genealogy to identifying genetic predisposition to disease.	Ancestry 23 and Me	Daviet, Nave, and Wind 2022
2	Predicting consumer behavior	Genetic variants will enable the understanding of factors that will impact downstream behavior	lactose intolerance leads the consumer to seek dairy alternatives	Daviet, Nave, and Wind 2022
3	Targeting and positioning	Can be utilized for targeting and positioning. Consumers with Irish ancestry might be drawn to Irish cultural experiences	Spotify Aeroméxico	Daviet, Nave, and Wind 2022
4	Marketing research	The ability to predict or estimate preferences may enable marketers to do research without large-scale consumer surveys.	Google Calico Google	Daviet, Nave, and Wind 2022
5	Genomic segmentation,	GWAS (Genome-Wide Association Studies) generate genetic data that can predict future behavior before other behavioral measures.	Genetics can predict a propensity for coffee consumption before the consumer demonstrates buying behavior, and therefore there is the potential for advanced targeting.	Daviet, Nave, and Wind 2022
6	Genealogical trait segmentation	Understanding the consumer's inherent preferences for consumer choice can potentially expand segmentation options.	Risk aversion Preference for compromise	Simonson and Sela 2011
7	Genealogical trait targeting	Understanding inherent preference can potentially enable more specific targeting based on personality traits	Choices between hedonic and utilitarian options	Simonson and Sela 2011
8	Genetic behavioral marketing strategies	Understanding the consumer based on how genetics influences behaviors such as novelty seeking, and compulsive consumption can inform marketing strategies.	ADHD and ADD and product choice Smoking cessation programs	Hirschman and Stern 2001
9	Genealogical segmentation	Even if a consumer does not provide their genomic data, it will be available.	Ancestry 23 and Me	Erevelles, Erevelles, and McGuire 2022

Theoretical Background

This dissertation draws on theories from multiple disciplines, including but not limited to biology, genetics, psychology, and marketing. While theories in each of these fields are valuable, no one area alone provides sufficient theoretical background. Interfield theory uses concepts and techniques from more than one field to support indigenous theory development, provides an optimal theoretical basis, and potentially leads to additional interfield theories (Darden and Maull 1977).

Mendel's theory of heredity is that traits are passed from parent to offspring, with each parent contributing traits. (Mendel 1866). It was not until the independent work of Hugo de Vries, William Bateson, and Carl Correns that the theory evolved to identify the gene as the inheritance mechanism (Mukherjee 2016). In 1917, Thomas Hunt Morgan's theory of the gene crystallized the work of Mendel and others. Morgan's work laid the groundwork for subsequent theories of behavioral genetics, the primary theory from which this dissertation will draw.

According to the theory of behavioral genetics, behaviors are based on genetic factors (Plomin and Rende 1991). The driving force is the quest to understand how genetic factors influence human behavior (Bouchard 2003). It is an interfield theory in that it pulls from research in both genetics and psychology. Turkheimer (2000) and Bouchard (2004) have extended theories on genetics to understanding human behavior, culminating in the fourth law of genetics (Chabris et al. 2015). It is, therefore, the degree to which genetics drive or influence behavior that becomes the area of interest. Because genetics always plays a role, however small and often overwhelmingly large (Turkheimer 2000), it is a valuable theory upon which to build a theoretical framework for marketing research.

Genomic data will likely transform the field of consumer behavior and raise the curtain on an area of marketing relatively unexplored. The past one hundred years have primarily been epitomized by a behavioral and quantitative focus on better understanding the macro and micro environmental factors surrounding consumers and the institutions they interact with in the marketplace. Over the past two decades, the richness of Big Data (Erevelles, Fukawa, and Swayne 2016; Hofacker, Malthouse, and Sultan 2016; Wedel and Kannan 2016) has allowed marketers to examine and predict the behaviors of customers to an extent unheard in the past. Despite these fascinating advances, only 50%-60% (Plomin, Owen, and McGuffin 1994) of consumer behavior is understood today. Although we now accept that “all human behavioral traits are heritable” (Turkheimer 2000, p.160), neither behaviorally- based experimentation nor Big Data quantitative modeling has taken us much beyond this 50%-60%.

Each foundational premise was developed to address a theoretical gap in the marketing literature. By addressing these gaps, marketing research has the potential to transform the marketing discipline. Genomic data is the tool that will provide that opportunity. Table 4 lists the theoretical gap for each foundational premise which will be developed in Chapter 4, and highlights the transformative potential of genomic data in marketing if that gap is addressed.

Table 4- Theoretical Gaps

	Genomics foundational premise	Theoretical Gap	The transformational potential of genomic data for marketing
1	The gene is the foundational unit for all behavioral consumer traits.	The gene has been relatively unconsidered as the foundational unit of consumer behavior.	The availability and ability to analyze individual and group genomic data could improve consumer outcomes in a nonlinear way.
2	Consumer behavior is a function of both environmental factors (nurture) and genetic (nature).	An estimated 40%-50% of consumer behavioral influences have not been fully explored (Plomin, Owen, and McGuffin 1994).	Genomic data can provide an improved understanding of the percentage of consumer behavior based on genetic factors.
3	Interactions between genes influence consumer behavior.	Given the lack of research on genetic influences on consumer behavior, there has been little exploration of the interactions among genes.	Genomic data will enable marketers to understand the relationship more fully between genetic factors.
4	Interactions between genes and the environment influence consumer behavior.	Marketing research has focused almost exclusively on environmental factors without considering genetic interactions with the environment.	Genomic data analysis can increase the understanding of the environmental factors that cause gene mutation, amplification, or innovation and how those changes influence behavioral traits.
5	As consumers age, genomic factors increase, rather than decrease in importance over environmental factors in influencing consumer behavior.	Despite the relatively greater impact of genomics, research has focused only on environmental factors.	An increased understanding of the genetic basis of behavioral traits provides the opportunity for more effective research on environmental approaches and interventions.
6	Genomics can probabilistically predict lifetime consumer behavior at birth.	Genomics as a predictor of consumer behavior has not been extensively explored in marketing research.	Genomic data offers the potential to capture and utilize this predictive information fully.
7a	Genomics can help predict and alleviate negative consumption behavior.	The predictive ability of genomics in marketing has not been explored in marketing research.	Genomic data has the potential to enable treatments and interventions at a much earlier point and can perhaps alleviate behavior before it is expressed.
7b	Gene intervention has the potential to mitigate or alleviate negative consumer behavior.	The efficacy of gene editing to alleviate undesirable consumption behavior has not been explored.	The advent of biotech solutions will transform the types of interventions possible.
8	Polygenic Risk Scores (PRS) can probabilistically predict consumer behavior.	PRSs have not been examined in the context of consumer behavior.	PRS scores will enable consumers to make more informed assessments of their risks and possible mitigating factors.

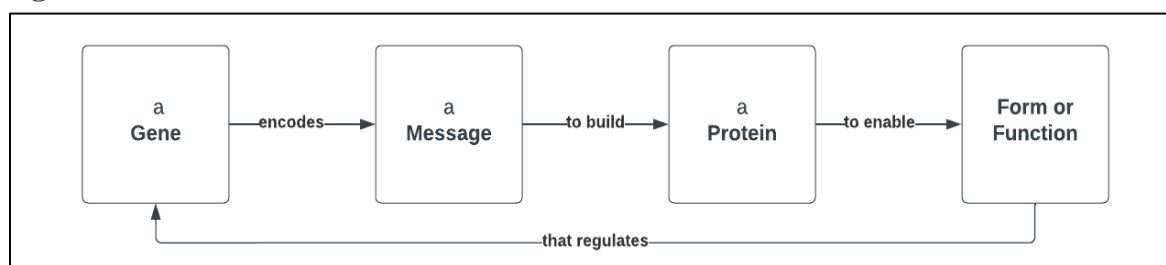
The initial theoretical framework for the use of genomic data in marketing presented here is meant to provide a foundation for future academic research that leads to a better understanding of how genes drive and influence consumer behavior and the relationship of genetics to environmental influences. Science has long maintained that behavioral traits result from complex interactions, but the focus has been on the primacy of environment (Plomin 2019). The emerging understanding of the role that genes play in behavior has the potential to confirm, refute, or modify previous findings.

What is genomic data?

“If you can’t explain a principle simply, then you don’t know it well enough” - Albert Einstein

Genetic data, which is personal information about genetic characteristics (Shabani and Borry 2017), is a subset of genomic data. Understanding what that data is and how it relates to Big Data is helpful. Table 6 provides relevant definitions and insights for marketing.

Genes are segments of DNA (deoxyribonucleic acid) molecules that carry instructions (“messages”) for physical or behavioral traits (e.g., eye color, intelligence, personality) (Francis 2011). mRNA (messenger Ribonucleic acid) is a copy or “transcription” of DNA information that is carried to the part of the cell where the message can be decoded. (Flint, Greenspan, and Kendler, 2020). A gene encodes a message to build a protein to enable a form or function (Mukerjee 2016). See Figure 1.

Figure 1: Function of a Gene

(Mukherjee 2016; Flint, Greenspan and Kendler 2020)

Proteins are the complex molecules of amino acids within our cells that combine to form all the structures and functions in the body (Plomin 2019; National Library of Medicine 2022). Everything about humans is linked to proteins and how those proteins work or fail to work together. The process of decoding the message is called gene expression (Plomin 2019). A SNP (single-nucleotide polymorphism) is a change in a part of DNA that somehow alters how a gene is expressed (Plomin 2019). When we refer to genes, we are referring to gene expression (e.g., eye color, height, personality traits).

While genetics focuses on individual genes, genomics refers to the study of the complete DNA sequence that contains all the genetic information of an organism (Mukherjee 2016), as well as the interactions between genes in the sequence (National Human Genome Research Institute 2022). The human genome, which contains more than 20,000 genes (Flint, Greenspan, and Kendler 2020), can be thought of as an “instruction manual” (Sanjana 2017). Genome wide association studies (GWAS) are a methodological approach used to identify genomic variants associated with complex traits or diseases (National Human Genome Research Institute 2022).

Jennifer Doudna and Emmanuelle Charpentier were awarded the Nobel Prize in 2020 (Nobelprize.org) for their gene-editing technology, CRISPR (clustered regularly interspaced short palindromic repeats), which opened the door for editing genetic sequences (Doudna and

Sternberg 2017). When there are errors (diseases) in the instruction manual (genome), CRISPR works like a pair of molecular scissors to snip out a section of “bad” DNA and replace it with healthy DNA (Kaiser 2016). In other words, it corrects errors in the manual (genome) by targeting the sequence of DNA that causes a particular illness or disorder and then writing a new message or “cure” that can be inserted into the space created when the unhealthy section is removed (Broadfoot 2018). Imagine CRISPR as a word processing application that corrects an error in a document (Doudna 2015).

The precision with which CRISPR works on specific pieces of DNA makes it heavily reliant on genetic data (Doudna 2015). The scissors must know precisely where to cut. For example, CRISPR can identify viral DNA, such as HIV, and destroy or remove and replace that section of the DNA sequence with healthy cells (Doudna 2015). Because CRISPR essentially rewrites the DNA, it can cure the disease in the parent and potentially prevent it from passing to future generations (Ledford 2019). Thus, CRISPR can be both a therapeutic and a preventive technology.

The raw data produced from a DNA sample is a file that contains the location and chemical composition of the genetic variants in the sample (National Library of Medicine 2022); it indicates the chromosome number, location on the chromosome, and genotype (i.e., the base pair combination) (National Library of Medicine 2022). While scientists have mapped the entire human genome, 99.9% of human DNA does not vary from person to person (Flint, Greenspan, and Kendler 2020). The 0.1% that does vary is what is contained in the file and is of interest to researchers, data consolidators, and consumers and drives differences in traits, diseases, and behaviors. (Gene Heritage 2022; Flint, Greenspan, and Kendler 2020).

As technology advances and costs decline, companies and organizations are accumulating massive amounts of human DNA or genetic data that can be used to study links between genes, environmental factors, and disease risk (Doudna 2015). The mapping of the human genome and the ease with which DNA data can be obtained from individuals has resulted in an exponential increase in the amount of raw data with which to conduct research. Genomic data science applies computational and statistical methods to decode the functional information within DNA code (National Human Genome Research Institute, 2022).

Two primary factors drive genomic data science as a separate field. The first is that such data is less structured and not as clean as that often used for data analysis; therefore, preparing the genomic data for analysis requires more advanced tools and methods than other data types (Berkely, 2022). Second is the exponential growth in the volume and complexity of data available for analysis, including both genomic information from experimentation and other sources (National Human Genome Research Institute 2022). Due to its volume, variety, and complexity, genomic data qualifies as “Big Data” (National Human Genome Research Institute, 2022). Thus, many research questions, limitations, and opportunities that fall under Big Data research will also be relevant for genomic data.

Genomic data falls under the umbrella of personal data and encompasses the human genome down to individual genetic variations (Shabani and Borry 2017). From an individual perspective, while genomic data provides opportunities for targeted marketing, products, or health solutions, it also presents challenges around security, consent, and appropriate use (Daviet, Nave, and Wind 2022). Consumers provide genetic data in various ways, most commonly as blood or tissue samples supplied as part of standard medical care or for the explicit purpose of genetic analysis (National Library of Medicine). Direct-to-consumer genetic testing

(DTC-GT) companies (e.g., AncestryDNA, 23andMe) obtain genetic data by providing information to consumers in exchange for the ability to collect information about personal history and habits (e.g., personality, lifestyle) (Daviet, Nave, and Wind 2022). Data consolidators such as Gene Heritage and XCode Life interpret raw data for consumers who have obtained data from DTC companies (XCode Life 2022). The data collected by DTC-GT companies then becomes a product to be sold to other companies for either product development or marketing purposes (Daviet, Nave, and Wind 2022). Genetic data can potentially transform marketing like Big Data has (Erevelles, Fukawa, and Swayne 2016).

Table 5 provides additional key terms and descriptions that are relevant to the understanding of genomic data. Included is also an insight into marketing implications. The goal is to provide enough context for the underlying concepts while focusing on marketing implications.

Table 5-Key Terms and Insights for Marketing

	Term	Description	Insight for Marketing
1	Genetics	Genetics is the study of <i>individual</i> genes and the transmission of genes via heredity (National Institute of General Medical Sciences 2022).	All behavioral traits are genetic; and therefore, genetic research can provide insight into consumer behavior.
2	Genomics	Genomics is the study of the complete set of DNA or genes (National Human Genome Research Institute 2022).	As most behavior is complex, genomics can provide insights into a broader range of behaviors than genetics alone.
3	Gene	The gene is the fundamental unit of heredity that defines traits passed from parent to child (Mukherjee 2016).	Genes account for around half of all behavioral traits.
4	DNA	DNA contains the fundamental building blocks for humans. It carries all genetic information which is comprised of four chemicals: adenine(A), thymine(T), guanine(G), and cytosine(C) (National Library of Medicine 2022).	0.1% of DNA accounts for variances among individuals.
5	mRNA	mRNA carries information from the DNA in a cell's nucleus to a location to be translated into a protein. This protein causes the trait to express itself (National Human Genome Research Institute 2022).	mRNA plays a critical role in gene expression and the efficacy of many vaccines and other treatments.
6	Chromosome	Chromosomes are structures in the nucleus of cells that store our genetic information (DNA) (Mukherjee 2016). They play a vital role in ensuring that DNA has copied accurately from cell to cell (Jax.org 2022)	Some genetic disorders result from chromosome abnormalities; therefore, advances in editing techniques present opportunities for new therapeutic interventions.
7	Genomic/Gene Editing	Intentional changes to genome segments or individual genes (Doudna and Sternberg 2017).	Changes in the genome or an individual's genes potentially alter behavioral traits (Doudna and Charpentier 2014).
8	GWAS	Genome-Wide Association Studies are large-scale studies that test genetic variants across large populations to find statistically significant associations with specific traits or diseases (Uffelmann et al., 2021).	Genomic data becomes genomic information as a result of the analyses in GWAS.
9	PRS	Polygenic Risk Scores (Also called Polygenic Scores) are quantitative measures that indicate an individual's genetic liability for a trait relative to other people (Nguyen and Eisman 2020).	PRS can provide demographic overviews to marketers that enable them to understand average and outlier behaviors.

CHAPTER 3

Methodology

This was one of the first studies on the role of genomic data in marketing; therefore, the first section focused on creating an initial theoretical framework. Though genomics has not been explored in marketing, there was a substantial body of research and data from other disciplines, including behavioral genomics, genetics, and psychology, from which to build. The literature review in Chapter 2 synthesized the research that supports the theoretical framework for marketing. The foundational premises articulated here will eventually lead to testable hypotheses. Hunt's indigenous theory approach was used to build the theoretical framework for the value of achieving the goals in the first section (2020). The second section was an exploratory textual analysis that identified key themes related to the attributes and potential marketing applications of genomic data. The rationale for using these specific methodologies follows below.

Methodology for Theoretical Framework

"In many cases, we are defending the past at the expense of creating the future." (Erevelles 2022)

This research followed an original process based on indigenous theory development to advance core foundational premises on the role of genomics in consumer behavior (Hunt 2020). This methodological contribution, which is necessary given the novelty and potential impact of the field, will provide an agenda or roadmap for future research. Before establishing the rigor of the theoretical approach, the relevance should be considered. This consideration explains why the methodology was selected and why it was the most appropriate, in fact only one, to address the research problem.

For a body of scholarship to develop, the field needs to have a framework for grounding theory. Hunt noted that marketing was a leader in business scholarship for approximately three decades through the mid-twentieth century; the period since was marked by a reliance on theory from other disciplines (2020). This suggests that the field reoriented its perspective and positioned it as a discipline more focused on application than theory (Hunt 2020). Hunt's perspective is not without criticism. One can argue that the purpose of any business research is ultimately about the practical application to real-world business problems. That said, Hunt's argument was that there had been a lack of well-developed processes and procedures. Given that marketing does not appear to have pulled in research from other disciplines to address the current research question, an initial framework grounded in indigenous theory, research can progress rapidly and impact scholarship and managerial practice in the marketing field. This is valuable for new fields that do not yet have a body of research upon which to build or a set of constructs and variables to test.

A non-linear approach was the only one suitable for the current research problem. As there has been no marketing research on genomics, no theories were available to effectively challenge or test. While 50% of consumer behavior is driven to some degree by genetics, consumer research reflects an almost exclusive focus on environmental factors, thus leaving a gap in the body of knowledge. The research gap and motivation section of this dissertation established the need for a theoretical framework to fill the gap. Indigenous theory development offers a way to fill the gap.

Before applying the process, it was important to understand the steps in Hunt's approach. The foundational premises approach to theory development is a seven-step process Participant to feedback loops at specific points. The first step is to identify the current problem. That is,

establish the phenomenon to be explored or explained. The following two steps identify the characteristics, strengths, and weaknesses of extant and alternative theories, models, or frameworks relying on existing literature. This will help identify gaps in theories, models, and frameworks (step two), while alternative literature can provide insight into theories that have not been applied to the problem (step three). These first three steps segue into the development of an initial set of foundational premises (step four), the purpose of which is to concisely facilitate understanding of the problem by explaining aspects of it that could potentially result in theories that lead to solutions. Steps five, six, and seven operate within a feedback loop. In step five, constraints are identified, potentially leading to a revision of the foundational premises. Step six presents the revised premises for publication and demonstrates that they facilitate understanding of the problem, contribute to explaining the problem, and lead to theories that contribute to forming solutions to the problem. Finally, step seven forms a feedback loop with the fourth step. The foundational premises are revised as new constraints are introduced and revisions are proposed. Foundational premises are intended to be organic. They lay the foundation, but at the same time, they evolve to reflect and incorporate new knowledge. Much of that new knowledge is the result of traditional linear research. Ultimately, this methodology forms a symbiotic relationship with traditional linear research. This dissertation executes steps one through five, as shown below.

Table 6- Application of Indigenous Theory Development

Step	Description of Steps in Indigenous Theory Development (Hunt 2020)	The Genomics Revolution and Its Implications for Marketing
1	Identify the current problem.	The role of genomics has not been considered in marketing literature.
2	Identify the factors that cause the problem and how to address it effectively.	The literature review in Chapter 2 addressed this step by providing historical context, an overview of twin and adoption studies, and an overview of physical and behavioral trait studies.
3	Classify elements of other theories that can address the problem but have not been utilized.	The theoretical background in Chapter 2 addressed this step.
4	Develop a set of foundational premises.	8 foundational premises are set forth in Chapter 4.
5	Evaluate the preliminary set of foundational premises.	The 8 foundational premises set forth in Chapter 4 reflect multiple iterations and refinement of the premises throughout the dissertation process.
6	Propose by means of publications the set of foundational premises.	At the time of this writing, these ideas have been presented at two conferences (Erevelles, McGuire, Erevelles 2022; Erevelles et al. 2022)
7	Revise the original set of foundational premises by means of additional publications.	Revisions should be an output of the areas for future research articulated in Chapter 5.

For this dissertation, these foundational premises will result from identifying the attributes that highlight the value proposition of genomics in marketing, an emerging problem because genomics is an evolving field. As scientific research continues to illuminate our understanding of the role that genetics plays in driving consumer behavior, the need for research grows. There is no question that emerging scientific research will result in reconsidering the factors that drive consumer behavior. For marketing research in this area to have both academic and practical value, it must be based on a solid foundation that can change logically and systematically. The methodology presented here will achieve that goal.

Most academic research is linear or incremental. Linear research dates to the 16th century with Copernicus and Galileo with the development of the scientific method. The scientific method is largely responsible for the progress of science over the last five centuries. While it has unquestionable strengths, there are situations where it hinders progress (Firestein 2012). One of those situations is when the research area involves a paradigm shift, or it is a new area where theories from which to develop hypotheses have not been developed. Not only does genomics in marketing represent such a shift, but the field of genomics and the data it creates also changes at a rapid and exponential pace (Schilling 2013). Therefore, in a world where change occurs non-linearly, we need non-linear research to keep up with the pace of change. It requires a strategic balance of knowledge creation.

There are limitations to this theoretical approach that should not be ignored. (See Table 5 below.) The primary challenge in examining genetic data and consumer behavior is the inability to conclude or establish causation or attribution decisively. Consumer traits are challenging to study because it is impossible to completely control the variables involved. The environment can never be completely excluded from consideration, and genetic expression for behavioral traits involves multiple genes interacting in ways that cannot be controlled in a research setting. Therefore, the foundational premises are not reflections of absolute but rather “approximate truth” (Hunt 2011). In essence, marketing theory creates a model. Models are simulations rather than replications of phenomena. Another limitation is that for areas such as genomics, scientific discoveries are ongoing. Therefore, foundational premises are based on the available knowledge at the time of development. They evolve based on both effective challenges and new scientific discoveries in both the fields from which they emerge and on the research in the field for which they are being developed. Finally, as with other theoretical fields (e.g., mathematics), the

application of theory is not always immediately evident. Foundational Premises lead to testable hypotheses. The results of those tests drive the application of the findings. Though there are limitations that should not be dismissed, they do not undermine the relevance of the methodology. Rather they serve to provide valuable boundaries within which research can advance.

Table 7: Limitations of Methodology

#	Limitations
1	Foundational Premises create models. Models simulate but do not replicate actual results (Hunt 2011)
2	Foundational premises are approximations based on available knowledge at the time of development and, therefore, prone to error and necessary revision (Hunt 2011).
3	Foundational premises do not immediately lead to testable hypotheses. Premises evolve and develop through multiple iterations as new information is discovered. The practical managerial application is not always evident at the onset. (Varadarjan 2020)
4	Hunt's methodology is an iterative process that depends upon an effective challenge to create a feedback loop, so Foundational Premises necessarily evolve over time and new premises are added.

The impact of this method offers further support for its rigor. Figure 2 below lists the citation statistics for the top ten articles published in the *Journal of Marketing*. The second most cited and two of the four most cited articles use this approach presented here. In addition, the eighth most cited marketing paper (Erevelles et al. 2016) used the method. Of relevance for the current project is that it also considered a non-linear paradigm-shifting phenomenon, Big Data, and how it will transform marketing.

Figure 2: Top Journal of Marketing Articles and Their Impact

Citations of Top Ten Articles Published in the <i>Journal of Marketing</i>. (Zeithaml et al., 2020)			
Authors	Title	From WOS	From GS
Morgan and Hunt (1994)	The Commitment-Trust Theory of Relationship Marketing	7,213	26,150
Parasuraman, Zeithaml, and Berry (1985)	A Conceptual Model of Service Quality and Its Implications for Future Research	5,779	28,886
Zeithaml (1988)	Consumer Perceptions of Price, Quality, and Value: A Means-End Model and Synthesis of Evidence	4,960	19,926
Vargo and Lusch (2004)	Evolving to a New Dominant Logic for Marketing	4,885	14,721
Keller (1993)	Conceptualizing, Measuring, and Managing Customer-Based Brand Equity	4,099	18,070
Zeithaml, Berry, and Parasuraman (1996)	The Behavioral Consequences of Service Quality	3,732	13,364
Narver and Slater (1990)	The Effect of Market Orientation on Business Profitability	3,304	12,336
Cronin and Taylor (1992)	Measuring Service Quality: A Reexamination and Extension	3,215	16,350
Kohli and Jaworski (1990)	Market Orientation: The Construct, Research Propositions, and Managerial Implications	3,204	11,616
Dwyer, Schurr, and Oh (1987)	Developing Buyer-Seller Relationships	3,150	12,949
Notes: Articles in bold employ an IR approach. WOS ¼ Web of Science Index; GS ¼ Google Scholar.			

Methodology for Empirical Analysis

The empirical methodology for this dissertation was an exploratory textual analysis of data obtained from survey participants selected, as noted earlier, from doctoral students that had been presented with a high-level overview of the topic. This first analysis served as a pilot for the approach. Further analysis was performed with a cultivated participant pool of graduate students. This methodology was selected for several reasons. The primary was that while the field of genomics is relatively mature, genomics in marketing is a new field of study. Therefore, there is no existing body of empirical research upon which to build. This means that exploratory methods are needed to lay the foundation upon which future research can build. The goal of this exploratory textual analysis was to provide insight into the attributes and applications that resonate in a marketing setting. While eventually, it will be valuable to replicate marketing strategy research as well as consumer behavior research studies incorporating genomically derived constructs and variables, the field has not yet developed enough to do that. One way to

develop concepts that lead to constructs and variables is “a continuous dialogue with empirical data” (Corbin and Strauss, 2015, p. 220).

Sample Participants and Research Design

Initial participants were graduate students at the University of North Carolina at Charlotte who had a presentation on genomic data and its potential use in marketing. They were recruited from a Master of Business Administration (MBA) and a Doctor of Business Administration (DBA) class taught by the same professor. The respondents were approximately 50% male and 50% female. All were professionals representing a wide range of industries with anywhere from several years to decades of professional experience. The initial pool of participants had been educated on the topic of genomics. However, as Doctor of Business Administration candidates with a variety of educational backgrounds, they were not necessarily familiar with marketing-specific attributes or applications. While their responses did provide valuable insight for marketing managers on the general understanding of the topic of genomics, they did not provide actionable insight for managers or scholars from a marketing discipline perspective. Therefore, the results from the initial exploratory analysis, though interesting, were deemed less than sufficient to constitute a meaningful contribution. Because a subject pool with a deeper knowledge of both genomics and marketing was available, it was determined that cultivating that population for analysis might yield more meaningful results. We feel that the additional analysis provides a sizable methodological contribution. That said, the initial analysis was an effective pilot for both the coding approach and a test of interrater reliability.

Materials and Design

The participants were asked to complete two open-ended essay-style questions to ascertain their understanding of the attributes of genomic data (Question 1) and the potential use of that data in marketing (Question 2). The participants were given guidelines to maximize the text available for analysis while not constraining responses. The objective was to obtain enough data to identify a range of themes. The survey was conducted online, and participants were nominally compensated. Appendix 1 contains the questions included in the survey and the project overview. It was expected that the participants in the initial pool had limited knowledge outside of the class lecture and limited assigned pre-reading.

The design for the cultivated subject pool was similar but significantly expanded students were enrolled in a graduate-level marketing course of which genomics was one topic. Therefore, the expectation was that they were both familiar and conversant with marketing discipline concepts and applications. Table 9 details the steps in cultivating or educating the pool. The MBA students were enrolled in a graduate-level marketing course. They received both assigned readings and a classroom lecture on genomics. They were assigned a term paper with the requirement to identify an additional twenty resources. The instructions in the term paper were to address the two questions in the survey. 1. What are the attributes of genomic data? And 2. What are the potential applications for genomics in marketing? Two weeks following the lecture, students participated in a facilitated classroom discussion. The students had approximately two months to complete and submit the term paper. The responses to the survey were largely pulled from the term paper content.

Table 8- Participant Cultivation Process

Step #	Date	Process Step	Description
1	1/11/23	Initial Presentation	Professor introduced the topic and assigned readings on genomics.
2	1/18/23	2 ½ hour lecture on “Genomics in Marketing”	
3	3/15/23	Interactive Classroom Discussion (Outline of term paper with at least 20 independent references needed)	Students participated in an instructor-facilitated classroom discussion following classroom lectures and assigned reading on genomics.
4	4/3/23	Term Paper Submitted with at least 20 independent references	Term paper addressing the two questions in the survey according to specified guidelines.
5	4/5/23	Questionnaire made available and data collected – Participation was optional	MBA Students were recruited via a verbal appeal explaining the purpose of the research, the method for the response, and compensation for participation.

Coding Process

Open coding was used to analyze the data. This inductive coding approach is conducive to exploratory studies that aim to understand certain propositions or concepts to facilitate theory development (Mason 2018). The approach was the same for the two questions and is described as follows.

Coding was a two-step process. First, manual open coding identified key themes for each participant's response. Two coders independently identified keywords within each response. Following the initial identification, each coder aggregated their keywords into themes. The coders then consolidated their themes to determine a final list of themes to code responses.

Reliability Analysis. For the pilot, the next step was for each coder to code the responses to each question separately. Cohen’s Kappa was calculated to determine interrater reliability (See

Table 9 below) (Landis and Koch 1977). This methodology was like that used by Fukawa and Erevelles (2014).

Table 9- Cohen's Kappa

Kappa Statistic	Strength of Agreement
<0.00	Poor
0.00-0.20	Slight
0.21-0.40	Fair
0.41-0.60	Moderate
0.61-0.80	Substantial
0.81-1.00	Almost Perfect

(c.f. Landis and Koch 1977)

The final step was to evaluate the relationship between the themes identified in each question. Pointwise Mutual Information (PMI) identifies the strength of the relationships between themes in terms of the likelihood to cooccur together given the overall probability of appearing independently (Aggarwal et al. 2009). PMI is an algorithm that enables the statistical analysis of unstructured data and is grounded in information theory (Balducci and Marinova 2018). Figure 2 is the equation used to calculate PMI.

Pointwise mutual information equation

$$\text{pmi}(x; y) \equiv \log_2 \frac{p(x, y)}{p(x)p(y)} = \log_2 \frac{p(x|y)}{p(x)} = \log_2 \frac{p(y|x)}{p(y)}$$

While the theoretical framework will be the primary theoretical contribution of this research, the empirical study has managerial implications in that it illustrates the attributes and themes around marketing applications. It provided a window into consumer understanding of what, for many, is an unfamiliar topic. As noted throughout the dissertation, there has been very

little research on this topic in the marketing field. The empirical study presented here was intended to be a starting point for empirical consideration. The results of the exploratory analysis are described in detail in Chapter 5.

The approach was not without limitations. The greatest limitation was the lack of research from which to build. A corollary to that limitation is that textual analysis depends on how the questions are framed and what knowledge the participants already possess. While those limitations are acknowledged, the approach was appropriate to meet the objectives outlined in Chapter 1.

CHAPTER 4

Initial Theoretical Framework

Genomics in Marketing

Foundational Premises

FP1: The gene is the foundational unit for all behavioral consumer traits.

*“To create the sum of the parts, we must begin by dividing it into the parts of the sum.”
(Mukherjee 2016, p.485)*

Framing the argument

One must understand genes to understand behavioral traits and their potential impact on consumer behavior. Genes are the foundational and functional unit of inheritance (Mukherjee 2016). They encode the information needed to specify traits that are the distinguishing characteristics of a person (Flint, Greenspan, and Kendler 2020; National Human Genome Research Institute 2022). The first law of behavioral genetics asserts that “all human behavioral traits are heritable” (Turkheimer 2000 p. 160). Behavioral traits are those traits that relate to factors that drive behaviors. The sections of DNA (deoxyribonucleic acid) for which we know the location on the chromosome are called genetic markers. (National Human Genome Research Institute 2023). There are many indications that causal relationships exist between genetic markers and aspects of consumer behavior (Daviet, Nave, and Wind 2022), as well as between some heritable traits that impact decision-making and consumer behavior (Simonson and Sela 2011). As the gene is the mechanism for establishing human traits and traits drive behavior, the gene can reasonably be presumed to be the foundational unit for all consumer behavioral traits.

Background

For offspring to inherit traits from their parents, each parent contributes DNA, a spiraling ladder of sugar and phosphate molecules that form a double helix (Plomin 2019) (See Figure 4.). As noted previously, genes are segments of DNA molecules that carry the instructions for physical or behavioral traits (Portin and Wilkins 2017). The genome is the complete DNA sequence for an organism (Venter et al. 2001). Watson and Crick's Nobel Prize-winning discovery of the double helix structure of DNA was a seminal event in understanding human behavior (Flint, Greenspan, and Kendler 2020). A gene can be considered as the "recipe" for behaviors (Ridley 2003, p.235). To understand the recipe, it is important to understand the key ingredients, how they are mixed, and what happens when they are mixed. While the first and most basic ingredient is DNA alone, it accomplishes little. RNA (ribonucleic acid) is like DNA, as it is also a combination of sugar and phosphate molecules, but its role is to carry the coding information to a place where it can be transformed into a protein (Flint, Greenspan, and Kendler, 2020). That place is the gene (Ridley 2003). The proteins created are vital to how the human body, including the brain, functions and are, therefore, crucial to human behavior (Plomin 2010). The 'Central Dogma' (Crick 1958) is that the DNA on a gene sends information via RNA to create a protein that establishes function or gene expression (Mukerjee 2016).

Genes are the foundational unit of behavior

Many factors determine how genes are expressed and why that expression might differ among individuals. Variances in a single rung on the double helix, referred to as SNPs (single nucleotide polymorphisms, pronounced "snips"), indicate differences in gene expression, including those associated with behavioral traits (Plomin 2019). SNPs are the common source of genetic variations, with over 4 million in a person's genome (National Library of Medicine

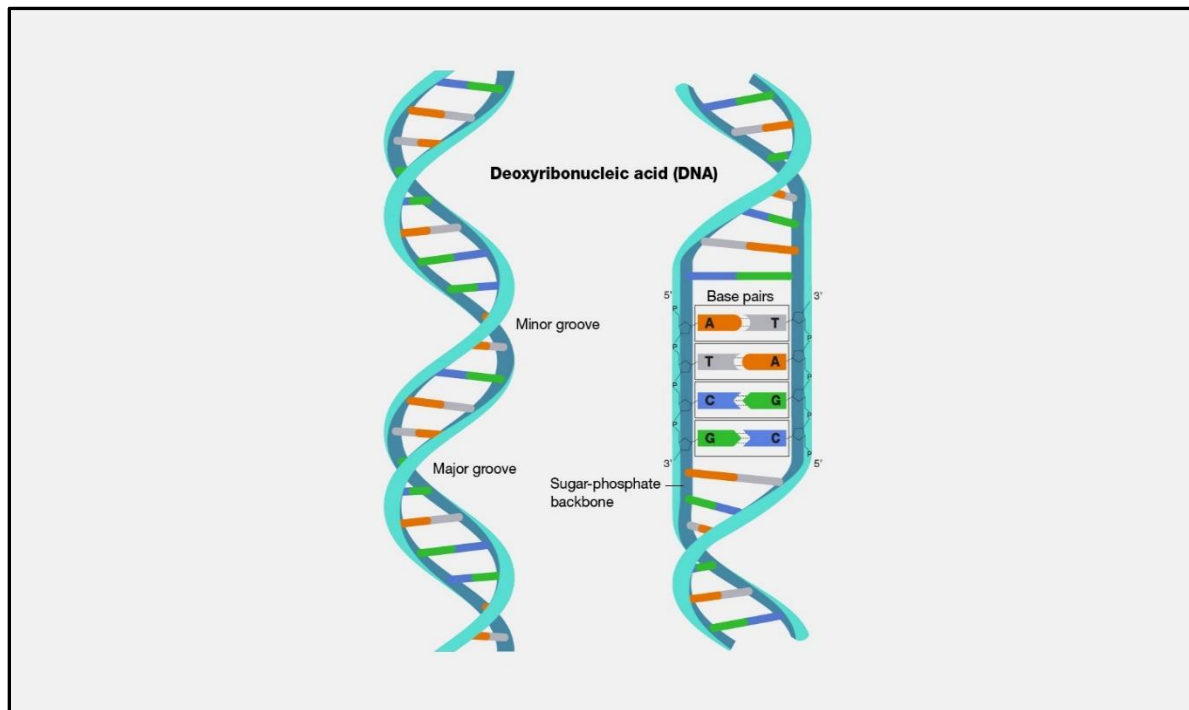
2023). Another potential factor is epigenetic variations, chemical alternations to DNA, which sometimes are heritable (Mukerjee 2016). The human genome, which is the complete DNA sequence for a human, has over 20,000 coding genes. (Flint, Greenspan, and Kendler, 2020). Amid this complexity, studies have found that most behavioral traits have a genetic driver or influence (Plomin and Rende 1991). In other words, all psychological differences among individuals show at least a moderate level of heritability (Bouchard and McGue 2003). For example, the heritability of personality is 40%-50% (Bouchard 2004). Similarly, spatial ability is a strong predictor of academic achievement for science-related fields and is 70% heritable (Rimfeld et al. 2017). In recent years, studies no longer look for heritability but rather the degree of heritability and the mechanism by which it occurs (Bouchard 2004).

Genes are the foundational unit for consumer behavior traits

Given the evidence that genes are the foundational unit for behavioral traits and the fact that all behavioral traits are at least somewhat heritable (Turkheimer 2000), a reasonable inference is that genes are the foundational unit for all consumer behavior traits. Research on twins has shown a heritable influence on consumer preferences and decision making (Simonson and Sela 2011). For example, choices between utilitarian verses hedonistic options indicate that whether some choses a utilitarian option like batteries instead of a hedonistic option like chocolate has a genetic driver. Likewise, studies on consumer outcomes, such as beverage consumption, loneliness, and risk tolerance, show the influence of genes (Daviet, Nave, and Wind 2022). For example, approximately 20% of the variance in financial risk-taking behavior is due to genetics (Cesarini et al., 2009). A GWAS found that that coffee and tea consumption were linked to genetic factors (Taylor, Smith, and Munafò, 2017). While the associations were small, 0.38% and 0.19%, they are relevant because higher risk for consumption correlated with reduced

water consumption (Taylor, Smith, and Munafò, 2017). In sum, we reasonably can conclude that the gene is the foundational unit for all behavioral consumer traits. Thus, the ability to better understand genomic characteristics of consumers could help us to better understand and predict consumer behavior.

Figure 3: DNA Double Helix



(c. f., National Institute of Health National Human Genome Research Institute)

FP2: Consumer Behavior is a function of both environmental factors (nurture) and genomics (nature).

“Nature is the length of the rectangle, nurture the width. There can be no rectangle without both.” (Ridley 1993, p.265)

Framing the argument

There are two factors that can shape behavior: the environment and genomics. Galton coined the phrase “nature versus nurture” to describe these two, at times competing and at times

complementary factors (Galton 1875). Behavioral geneticists have known for over thirty years that the percentage of variance in a population due to genetic influences (heritability) is estimated to account for close to half of some behavioral characteristics. “Heritabilities range from about 40 to 50% for personality, vocation interests, scholastic achievement, and general intelligence.” (Plomin, Owen, and McGuffin 1994, p. 1734). Meta-analyses have confirmed that “across all traits the reported heritability is 49%” (Polderman 2015, et.al, p. 702). The implication is that environmental factors account for the remainder. The consistent finding resulting from behavioral genetic research is the importance of both the environment and genetics in the prediction of behavior (Plomin 2023). Almost all behavioral research, including in marketing, has been focused almost entirely on environmental factors. (It is worth noting that genetic factors may have been unknowingly reflected in these findings.) For example, in consumer behavior literature, parenting, stress, and overall well-being usually assume that environmental factors are the main driver of behavioral outcomes (e.g., de Mooij and Hofstede 2011; Moschis 2007; Nanda and Banerjee 2021).

Evidence from the literature

Biologists have long established that genes influence behavior (Rose 1995; Robinson 2004). Though there is little debate about whether the transfer of genetic traits (with single or multiple genes) from parent to offspring occurs (Cold Springs Harbor Laboratory 2022, Turkheimer 2000), the question is how and to what extent genetic factors account for different human traits. For example, biologists have found a genetic link for most investigated behavioral disorders, such as violence, hyperactivity, and reading disability (Plomin, Owen, and McGuffin 1994). However, heritability does not suggest that the environment is unimportant in influencing behavior or preferences. For example, studies of twins reared found that while attributes such as

religiosity are heritable, religious affiliation may be influenced by the environment (Bouchard and McGue 2003). The evidence in the literature led to Turkheimer's (2000) seminal work suggesting three fundamental "laws" of genetics. The second law is that "the effect of being raised in the same family is smaller than the effect of genes" (Turkheimer 2000 p.160). In other words, Turkheimer (2000) suggests that both genes and the environment play an important role in the formation of behavioral traits. (It should be noted that environmental influences outside the family should not be ignored.) The results of studies using twins, families, and adoption support these conclusions (Plomin, Owen, and McGuffin 1994). For example, studies indicating that psychopathology runs in families is not the result of just the environment as previously believed, but a manifestation also of genetic influences (Plomin, Owen and McGuffin, 1994).

Behavior is a function of both genomic and environmental factors: While the first law of behavioral genetics is that all traits are heritable, no trait has been found to be 100% heritable (Turkheimer 2000). In an analysis of the top ten replicated findings from behavioral genetics, it was noted that while all psychological traits show genetic influence, none show 100% heritability (Plomin et al. 2016). As noted in Table 2, the percentage of heritability has been measured for multiple traits and disorders. None of those percentages was 100%. The overwhelming conclusion of the last 100 years of genetic research has repeatedly found that both genetics and the environment influence behavior (Plomin 2023). For example, if the heritability of personality, school achievement, and breast cancer are 40%, 60% and 10% respectively, then the approximate environmental influence is 60% for personality, 40% for school achievement and 90% for breast cancer.

Consumer Behavior is a function of both environmental factors and genomics: Behaviors that appear to be driven by the environment likely have a direct genetic link or at least a connection to a genetic predisposition (Turkheimer 2000). However, there is evidence that environment can serve as a mediating or moderating factor. For example, a study on the decision to own versus rent a home is influenced by a genetic predisposition, yet is moderated by environmental factors such as family wealth (Cronqvist, Munkel, and Siegel 2014). A nutritional study found that eating behaviors play a mediating role in body weight for those with a genetic susceptibility to obesity (Jacob, et al 2018). Caregiver communication was found to be both a moderator and a mediator for language development in children (Onnis, 2017). The interesting findings are not that the environment does not matter, but that genomics also plays a role in behavior. In sum, while considerably more research is needed in consumption situations, the preponderance of evidence in the behavioral genomics literature suggests that consumer behavior is a function of both the environment and genomics.

FP3: Interactions between genes influence consumer behavior.

“Life is [found]...in organization, not in symbiosis but in synthesis.” (Conklin, 1940).

Framing the argument

Genes do not act in isolation. They interact with other genes (Phillips 1998). Observable behavior (a person’s phenotype) is the expression of multiple genes interacting with each other or with the environment (Mahner and Kary 1996). Also, important to note is that there is no single gene responsible for any behavioral trait; all behavioral traits are complex (Chabris et al. 2015). One of the most effective methods of studying behavioral traits is with GWAS (Genome-Wide Association Studies). GWAS test genetic variants across large populations to find statistically significant associations with specific traits or diseases (Uffelmann, et al., 2021). One

of the advantages of GWAS is that it allows researchers to study interactions between genes and their effects. (Begum et al. 2012). For example, a GWAS was conducted with over 100,000 individuals to understand the genomic drivers of educational attainment and found three genetic variations or SNPs that were statistically significant and they were in the region of the genome that had also been associated with health, cognition levels, and aspects of the central nervous system (Rietveld et al. 2013). Genome Wide Association Studies indicate that most behavioral traits are polygenic, with some having as many as 200,000 causal genetic markers (Harbin & Koellinger 2020). The sections of DNA (deoxyribonucleic acid) for which we know the location on the chromosome are called genetic markers. (National Human Genome Research Institute 2023). In other words, researchers are coming closer to being able to establish not only correlation, but a causation between genetic markers and behavioral traits. (National Human Genome Research Institute 2023).

Background

At this stage, it is helpful to understand a few technical terms that are germane to the discussion (See Table 11). In simple terms, a person's genotype refers to the complete set of genes for an individual, as well as the location on the chromosome where each sit (Mahner and Kary 1996). Chromosomes are structures in the nucleus of cells that store our genetic information (DNA) (Mukherjee 2016). They play a vital role in ensuring that DNA has been copied accurately from cell to cell (Jax.org 2022). When we describe an individual's physical characteristics or behavior, we are talking about their phenotype. While a person's genotype is defined by the nature and location of their genes, a person's phenotype is the observable expression of their genes (Wojczynski and Tiwari 2008). For example, height, eye color, hair color and lifetime achievement are observable traits. Two other relevant concepts are alleles and

loci. Alleles are forms that a gene can take (e.g., for eye color or blood type) (Turner 2013). A person's eye color or phenotype that is observable is a function of the dominant or recessive nature of the gene and what specific allele each parent provides. Loci is simply the location on a chromosome where a particular gene is located (National Human Genome Research Institute 2023). Simply put location matters. The proximity of genetic markers can impact the probability of inheritance as the closer they are, the more likely they are to be inherited together and thus may be expressed differently (National Human Genome Research Institute 2023). The sections of DNA (deoxyribonucleic acid) for which we know the location on the chromosome are called genetic markers. (National Human Genome Research Institute 2023). Mapping the human genome includes identifying genes, alleles, and loci.

Finally, perhaps the most crucial gene-gene interaction for behavioral and complex disease research is epistasis. Epistasis is the interaction of non-allelic partner genes (Nagel 2005). In other words, epistasis is the interaction of genes that do not share the same loci (Nagel 2005). The distance between genes may alter how the gene is expressed (National Human Genome Institute). For example, the propensity for a person to be highly anxious may be related to the loci of other personality traits (Cloninger, et. al 1998). The terms and definitions in Table 10 are important for understanding the interactions among genes.

Table 10- Key Terms and Definitions

Term	Brief Definition	Citation
Allele	Alleles are forms of a gene, and every gene has at least one allele.	(Darker, Gellman, and Turner 2013)
Loci	Plural of locus which refers to the physical location of a gene on a chromosome.	(National Human Genome Research Institute 2023)
Genotype	All the genes or alleles for an individual as well as the loci for those genes.	(Mahner and Kary 1997)
Phenotype	The observable expression of a gene.	(Wojczynski and Tiwari 2008)
Epistasis	The expression of a gene is modified by the expression of another gene.	(National Human Genome Research Institute 2023)

Interactions between genes influence gene expression

The challenge of genomics and the power of genomic data is the ability to better understand epistasis, as it is the driver of the genetic factors that drive behavioral traits and complex diseases. Even single-gene diseases such as sickle cell anemia are influenced by the expression of other genes (Nagel 2005). In other words, while the disease is traceable to a single gene, not every person with the disease has an identical experience. Of the fifteen potential complications of sickle cell, most patients exhibit 3-5 of them, and even then, the intensity of the symptoms can vary (Nagel 2005). Nowhere is the importance of gene interaction more notable than with disease studies. Most disorders involve gene interactions. For example, the interactions among multiple genes are responsible for the onset of schizophrenia, autism, and essentially all mental disabilities (Plomin 2019). Similarly, physical disorders, such as Type 1 Diabetes (Redondo, Steck, and Pugliese 2017) and stomach ulcers (Malaty et al. 2000), are influenced by the interactions of multiple genes.

Interactions between genes influence all behavior and hence consumer behavior

Studies have found evidence that gene interactions can be strong predictors of behavioral problems in children based on genetic drivers of behaviors that are evident during development (e.g., Schmidt, Fox, and Hamer 2007). For example, genetic interactions influence personality traits related to reward dependence, which is a measure of response to verbal signals of social approval (Schmidt, Fox, and Hamer 2007). Furthermore, studies suggest that genetic interaction can predict criminal and anti-social behavior (Boutwell et al. 2014). Finally, research indicates that gene interactions are associated with both smoking behaviors as well as difficulty with concentration (Vandenberg et al. 2007). While there is almost no research directly examining the influence of genomics on consumer behavior, it would be reasonable to conclude that if gene interactions influence all types of behavior, they also will influence all types of consumer behavior.

FP4: Interactions between genes and the environment influence consumer behavior.

“In the real world, there is no nature vs. nurture argument, only an infinitely complex and moment-by-moment interaction between genetic and environmental effects.” (Maté, 2010, p.213)

Framing the argument

The dichotomous paradigm of “nature” (genes) versus “nurture” (environment) has given way to one that looks at the relationship between the two (Robinson 2004). Neither genes nor the environment act in isolation. Neither do they act in predictable consort. For almost any trait of interest, there will be some unique balance of genetic and environmental influence. Those interactions influence behavior. Variability in individual behavior is, in part, a consequence of

interactions between genes and the environment (Chabris et al. 2015). The question is the extent each plays in the expression of a trait and how the relationship influences behavior. No traits have been found to be 100% heritable, and therefore environment always plays a role in behavior (Plomin et al. 2016).

Evidence from the literature

One central theme from the literature is that these relationships are simultaneously simple and complex (Kendler and Baker 2007). One of the top ten replicated findings from behavioral genetics is that most measurements of environmental influences for behavior show a statistically significant level of genetic influence, and genetics often serves as a mediator in measuring the environmental drivers of traits. (Plomin et. al 2016). For example, studies on parenting show behavioral outcomes in children are the result of genetics, but also parenting and life events (Plomin et al. 2016).

Genes do not only interact with the environment. They are sometimes changed by it. Some of the most compelling evidence for the profound impact that environmental factors can have on genes comes from epigenetic research, which indicates that environmental triggers can permanently alter a person's genes (Carey 2012). Epigenetics is different than gene-environment interaction. It is not the modification of gene expression. It is a temporary or permanent alteration of the genetic code (Carey 2012). While different from gene-environment interactions that do not change the genetic code, it is nonetheless an important manifestation of the interaction between the two.

Interactions between genes and the environment matter

Studies on personality and coping with professional demands offer an illustrative example of the interactions between genes and the environment. Researchers found moderate correlations between personality and coping with professional demands (Maas and Spinath 2012). In other words, there was an interaction between genetic factors (personality) and coping with professional demands (environmental triggers).

There are also relevant examples of epigenetic changes. Research on the impact of malnutrition during extreme famine provides evidence of genetic changes passed on to subsequent generations (Francis 2011; Moore 2015). Even after the environmental stimulus (malnutrition) had been removed, the impact on those who were not malnourished indicates that the environment somehow changed the genes that were then passed on to the next generation. When environmental factors interact with genes in a way that changes behavior, the interaction is more crucial than the degree of influence of either nature or nurture. In other words, nurture can alter nature.

Interactions between genes and the environment influence consumer behavior.

This point reinforces the frequently replicated finding that genomic factors mediate the role of the environment in influencing consumer behavior (Plomin et al. 2016). Studies also indicate that behavioral traits such as personality, social attitudes, and personal interests are largely a function of environmental influences that are mediated by genetics (Bouchard and McGue 2003). Interestingly, when environmental measures such as parenting or various life events serve as dependent variables in genetic studies, they have reinforced the importance of both genetics and environment on outcomes (Plomin et al. 2016). Finally, there are multiple

studies that support the premise that genes and the environment work together for a variety of behavioral traits, including visual processing, comprehensive knowledge, and short-term memory (Bouchard and McGue 2003). The logical inference is that interaction between genes and the environment also influences consumer behavior.

FP5: As consumers age, genomic factors increase, rather than decrease in importance over environmental factors in influencing consumer behavior.

“DNA matters more as time goes by” (Plomin 2019, p. 52)

Framing the argument

Although it is counterintuitive, research evidence indicates that the importance of DNA increases, rather than decreases, over time (Plomin 2019). Logically, one would assume the opposite to be true, as one would reasonably assume that as people interact more with their environment, the influence of their environment on their behavior will increase while the influence of genomics will decrease. For example, as a child grows older and interacts more and more with their environment (e.g., family life, education, socialization), the impact of those interactions increasingly shapes behavior. One could reasonably presume that nurture would overtake nature in explaining the variance in behavior among people. Much behavioral research is based on this premise when the opposite may be true.

Evidence from the Literature

Studies on language development in young children have found a strong correlation between the vocabulary of the parent and that of the child and have suggested a causal relationship based on the environment rather than on inherited aptitude (Bouchard and McGue 2003). However, making the leap from correlation to causation is challenging. The challenge is

determining what the underlying driver is. It may be that highly verbal parents provide their children with more verbal stimulation, or they provide a higher predisposition for language skills. “What is unrecognized in this interpretation, however, is the possibility that bright parents provide their children not only with a verbally stimulating environment but also a genetic potential for intellectual achievement. Without unconfounding the two sources of parental influence, we are unable to unambiguously infer the existence of either effect” (Bouchard and McGue 2003 p. 6). Policymakers and researchers frequently cite the critical role of nurturing environments primarily based on the premise that the environment plays a more significant role in behavioral outcomes (Biglin et al. 2012). However, genetic research suggests that the causal relationship is inverted and that it is genetics rather than environmental that drives language outcomes (Plomin et al. 2016). Studies on depression symptoms found that based on a sample of more than 2000 pairs of identical and same gender fraternal twins, measures of symptoms changed over the course of the lifespan but were consistent between the pairs of twins studied (McGue and Christensen 2013). Similarly, a meta-analysis of longitudinal twin and adoption studies has found increasing heritability of cognitive ability despite environmental factors (Briley and Tucker-Drob 2013).

As a person becomes older, genetic factors outweigh environmental factors

Longitudinal studies provide the best method for measuring behavioral traits over the course of a lifetime. A meta-analysis of longitudinal twin studies found that although measures such as cognitive ability and depression symptoms correlate with age, the similarity between twins did not decrease (McGue and Christensen 2013). In other words, the cognitive ability of a child and an adult is different over the course of their lifetime, but the cognitive difference between two identical twins does not. The influence of genomics increases while the influence of

the environment decreases. Another found that the heritability of verbal IQ (intelligence quotient) increased from 48% to 84% from ages 5 to 18, and nonverbal increased by ten percentage points (64%-74%) over the same period (Hoekstra, Bartels, and Boomsma 2007). Once again, the increasing role of genomics implies a decreasing role of the environment.

As a person becomes older, genetic factors become more important in influencing consumer behavior.

However, the discussion is more than a debate on ratios. It is also, more importantly, about how the genes act or are acted upon. Genetic effects are not static; some genes only manifest after adolescence as the brain develops or hormones are released (Plomin 2019). For example, people with schizophrenia do not typically show any symptoms until early adulthood, indicating that genes that contribute to the disorder's symptoms are not activated until other cognitive developments have occurred (Plomin 2019). Similarly, baldness is heritable but is not evident until adulthood (Plomin 2019). These examples do not diminish the role of the environment as much as they suggest that the impact of genes does not wane as much as previously thought (Plomin, Owen, and McGuffin 1994). As the evidence from the literature showed, the findings are similar for behavioral traits. The inference is that if these findings are replicated for behavioral traits, they also hold true for consumer behavior.

FP 6: Genomics can probabilistically predict lifetime consumer behavior at birth.

Framing the argument

The predictive nature of genomic data has been well documented in past literature (e.g., Plomin, Owen, McGuffin 1994; Rutter and Plomin 1997; Plomin et al. 2016), making it a

powerful tool for forecasting future behavior. For example, quantitative genetic research utilized in family, twin, and adoption studies all provided evidence that schizophrenia and autism were far more influenced by genetic factors than the environment, which had always been assumed (Plomin, Owen, McGuffin 1994). Similarly, studies showing the heritability of traits such as religiosity and food preferences have been replicated, as have those related to achievement (Plomin et al. 2016).

This is because a person's genomic sequence is essentially the "program" that probabilistically influences their behavior (Venter et al. 2001). Moreover, this information is available at birth and remains virtually unchanged over a person's lifetime. In other words, the genome contains the foundational building blocks for behavior later in life. While genetics is not destiny, it does suggest that behavior can be probabilistically predicted at birth.

Evidence from the Literature

The rise of quantitative genetic research and its impact on molecular genetics has enabled researchers to not only identify genetic influences of complex behaviors but to track trait expression for behaviors as they develop (e.g., Alzheimer's disease onset age, alcoholism sexual orientation) (Plomin, Owen, McGuffin, 1994). This predictive power of genomics was a major part of the motivation for the Human Genome Project (Venter et al. 2001). The hope from the beginning was that it would eventually lead to a better understanding not only of the causation of disease but a better understanding of human complexity (Venter et al. 2001). The twin studies discussed in Chapter 2 have resulted in a large number of replicable findings, many of which are related to the predictive power of genes (Plomin, Owen, McGuffin, 1994). At the same time, there has been strong caution not to conflate probabilistic with deterministic predictions (Rutter and Plomin 1997; Plomin and Rutter 1998).

Genomics can probabilistically predict behavior at birth.

Genomics can probabilistically predict behavior at birth. Examination of several illustrative traits demonstrates both the complexity and predictive power of genomic data. For example, a twin study found that 56% of the propensity or inclination towards sedentary behavior is genetic by examining the activity levels of 800 sets of MZ (identical) and DZ (fraternal) For (Schutte, et al. 2020). Sedentary behavior involves limited energy expenditure while an individual is sitting, reclining, or lying down and is measured objectively via an activity monitor or participative via self-reporting tools (Schutte et al. 2020). This implies that part of the reason that some individuals seek out opportunities to be physically active in either their professional or leisure activities and others do not is due in part to genetics. That may also be a reason that some individuals find it easier to exercise consistently (or enjoy it) than others. However, 56% is a probabilistic, not deterministic, prediction. In other words, a person with a propensity for sedentary behavior can still seek out physically intensive activities, but the probability of doing so is lower. That is to say that there are multiple reasons that individuals vary in their activity levels, but the role of genetics should not be dismissed.

Similar logic results from consideration of other behavioral traits. For example, the genetic influence of general intelligence is 50% (Plomin and Von Stumm 2018), and school achievement is even higher at 60% (Rimfeld et al. 2018). Addictive behavior has been shown to have a comparable level of genetic influence (50%) (National Institute on Drug Abuse 2023). The findings on these behavioral traits have been replicated in the studies of over 10,000 pairs of twins (Plomin 1986; Plomin and Deary 2015). Even more compelling for the probabilistic power of genomics is that research has also shown that the heritability of some traits (e.g., intelligence) increases rather than diminishes over the course of the lifetime (Plomin et al. 2016). For

example, the heritability of intelligence is 66% in adulthood while only 41% in childhood (Haworth et al. 2010). In fact, increasing heritability of intelligence is one of the top ten replicated findings in genomic research (Plomin et al. 2016). Environmental influences do not overtake genetic factors. These findings suggest that what is observed over the course of a lifetime relative to intelligence, achievement, addictive behavior, or other behavioral traits is the manifestation of what was present at birth.

Genomics can probabilistically predict lifetime consumer behavior at birth.

The implication for consumer behavior is that genomic data offers leading indicators of future behavior. From a health perspective, sedentary behavior is a risk factor for a variety of negative health conditions, such as heart disease (Same et al. 2016). A patient with a high tendency for sedentary behavior may be less likely to follow advice to increase exercise, while a lower score on that trait may indicate that more focus is needed on other reasons (e.g., time, resources, ability) that a person may struggle to increase activity level. From a consumer behavior perspective, it enables marketers to tailor their approach to goods and services to accentuate or downplay the level of activity involved. While environmental factors will obviously play a role in trait expression, genetics will drive prediction.

The primary limitation is that probabilistic is not synonymous with deterministic. No traits come even close to 100% heritability. Behavioral traits are complex, and after birth, it is impossible to completely isolate genetic influences from environmental ones. However, as consumer behavior research expands into new areas of research (e.g., user experiences, mindful consumption, shared consumption), the impact of genomics should not be ignored (Sheth 2021). This is because genomics can probabilistically predict lifetime consumer behavior at birth.

FP 7a: Genomics can help predict and alleviate negative consumption behavior.

Framing the argument

The power of genomics is the ability to understand factors for behavior that may not manifest until adolescence or adulthood. A person's genomic sequence is essentially the "program" that probabilistically influences their behavior (Venter et al. 2001). Negative consumption behaviors are the result of complex networks among multiple genomic and environmental factors (Cloninger 1987). The impact of negative consumption has been studied extensively on a wide range of behaviors, including alcohol misuse, impulse buying, and drug addiction (Cloninger 1987; DW Rook 1987; Turel and Bechara 2021). Such behaviors have potentially catastrophic effects. For example, alcohol overconsumption is one of the leading causes of preventable deaths in the United States (Bierut et al. 2010).

Evidence from the Literature

Early studies on alcoholism recognized it as an umbrella term for a collection of behaviors, including dependence, loss of control, and other social problems that, while not mutually exclusive, were only slightly correlated (Cloninger 1987). Alcohol Use Disorders (AUD) include both alcohol misuse as well as alcohol dependence (alcoholism) (Edenberg and Foroud 2013). Alcoholism is a complex disorder that has its roots in both genomics and the environment (Edenberg and Foroud 2006). An estimated 12%-14% of alcohol consumers meet the criteria for alcohol dependence (Farris et al. 2015; Bierut et al. 2010). The variants for dependence are not the same as those for consumption; only those for dependence show a strong

correlation with other negative consumption behaviors, such as depression (Edenberg, Gelernter, and Agrawal 2019).

AUD is multifaceted. The risk of developing an AUD result from the interactions of genetics, environment, and epigenetic changes that alter the way in which the body metabolizes proteins that occur due to the onset and severity of the disorder (Farris et al. 2015). Not only are AUDs problematic on their own, but they are also risk factors for other behaviors (e.g., addictions) and worsen outcomes of other diseases (e.g., heart disease, breast cancer, diabetes) (Edenberg and Foroud 2013). Despite researchers consistently finding a high level of heritability for alcoholism, there is no single alcoholism gene (Enoch 2013). Estimates vary, with the degree of heritability ranging from 50%-80% (Bierut et al. 2010). The genetic risk is due to variations in multiple genes acting in consort (Costas 2015). Mutations in certain genes have been shown to negatively impact alcohol metabolism (Edenberg and Foroud 2013), while other genes appear to provide a level of protection against the disorder (Vasiliou et al. 2006).

Genomics is absent from the marketing literature.

Though a voluminous amount of research has been published in marketing literature about maladaptive and negative consumption behaviors, genetic or genomic factors are virtually absent. This is surprising, given that a genetic link to alcoholism was identified over 30 years ago and considered relevant for developing a theory of compulsive consumption (e.g., Hirschman 1992). Concurrently, there was an awareness that maladaptive behaviors were frequently comorbid (Faber, Christenson, and De Zwaan 1995). For example, a research study suggested clinical screening for compulsive behaviors as an environmental intervention (Faber and O'Guinn 1992). While it appeared that consumer research needed to evolve (Petty and Cacioppo 1996), the body of knowledge in genomics was ignored in marketing.

Even with the mapping of the human genome and the exponential increase in available data, research on behaviors such as alcoholism continues to focus exclusively on environmental correlations, causation, and intervention strategies. Research on the behavior continuum from adaptive or non-problematic to negative or maladaptive focuses on harm and consumer choice and ignores underlying genetic drivers of behavior (Martin et al. 2013; Boland, Martin, and Mason 2021). A primary limitation of these studies is that by ignoring the role of genetics, a key component of behavior is ignored; therefore, recommended interventions are far less likely to be effective and, thus, have limited value.

Genomics can help predict behavior.

The complexity of behavioral traits makes them both challenging to address and a valuable use of genomic science. Genomic technologies have enabled GWAS (Genome Wide Association Studies) to be performed on an increasing number of complex diseases where disease expression is dependent on many SNPs (Single Nucleotide Polymorphism) operating together (Costas 2015). For example, researchers have used genome-wide linkages to identify multiple SNPs that appear to correlate with rates of alcoholism (Edenberg and Foroud 2006). The genetic risk for alcoholism is the result of common variants in multiple genes, with most having very small effects and a few rare variants having much larger ones (Enoch 2013). This risk can be identified from birth even when the degree of genetic influence is unclear or varies considerably based on behavior (Bouchard and McGue 2003). Additionally, quantitative genetic research indicates that complex behavioral traits, including consumption behavior, have a high level of heritability (Plomin, Owen, and McGuffin 1994); that is, they are present at birth though they have not been expressed. Therein lies the ability of genomics to predict negative behavior.

Genomics can help predict and alleviate negative consumption behavior.

The power of genomics to predict negative consumer behavior offers the opportunity to improve treatment options, reduce stigma surrounding the behavior, and develop proactive prevention measures. It might be possible to segment age groups based on risk or target testing or intervention based on risk. For example, an environmental predictor of adult AUDs is childhood trauma in individuals with a higher risk of developing negative alcohol consumption behavior (Enoch 2013). For some, neither trauma nor genetic predisposition individually would drive the behavior, but the combination or interaction of factors triggers the AUD. Studies have also found a correlation and potentially causal interactions between AUD risk and stress response behaviors (Enoch 2013). The various groupings that have been used to study AUDs could potentially be used to segment consumers and, by inference, target interventions (Cloninger 1987).

AUDs often have comorbidities such as drug dependency (e.g., cocaine, marijuana) and nicotine dependence (Bierut et al. 2010). Understanding an individual's or group's genetic risk for alcoholism might also provide insight into the risk for other negative consumption behavior. For example, research on the role that alcohol metabolism plays in risk for AUDs has indicated that race, gender, and ethnicity play a moderating role, as some groups appear to have genetic protection via the presence of proteins that offset certain metabolic processes (Beirut et al. 2010). The Collaborative Study on the Genetics of Alcoholism (COGA) relied on family-based data collected from families with multiple alcoholics (Edenberg and Foroud 2006). While there are challenges and limitations given the complexity and challenge of isolating risk factors, the study provided evidence that has moved research from gene-centered to pathway-centered (Beirut et al.

2010) and has advanced understanding of the genetic predictors of alcoholism and other related negative consumer behaviors.

Table 11 includes illustrative examples of additional traits that have been studied in both the behavioral genomics and marketing fields. Marketing research has focused exclusively on environmental factors and correlation analysis without acknowledging the limitations inherent in excluding consideration of genomic factors. Therefore, the marketing perspective is incomplete and could benefit from consideration of the power of genomics to predict and alleviate negative consumption behavior.

Table 11: Behavioral Genomic Studies on Traits

	Trait		Description	Related Marketing Constructs/Uses	
1	AUD	(Bierut et al. 2010)	Includes misuse and addiction to alcohol and is approximately 50% heritable.	Alcohol Consumption	(Gregory-Smith and Manika 2017)
2	Nicotine Dependence	(Li 2006)	Primarily smoking and smoking behavior is approximately 50% heritable.	Smoking and Anti-Smoking Marketing and Advertising	(Manyiwa and Brennan 2012)
3	Depression	(Dunn et al. 2015)	Depression describes a collection of symptoms (e.g., sadness, loss of interest, physical reactions) that vary in duration, severity, and impact. Studies indicate 40% heritability.	Mood, Mental Health, Depression	(Gomes Alcoforado and Melo 2012)

FP 7b: Gene intervention has the potential to mitigate or alleviate negative consumer behavior.

Framing the argument

The gene is present from the moment of fertilization (Mukherjee 2016). While gene expression often occurs later in life (Plomin 2019) and is subject to epigenetic changes (Mukherjee 2016), the genome is essentially stable unless some type of genetic intervention or therapy occurs; that is, the replacement, removal, or correction of a genetic malfunction (Goncalves and Paiva 2017). The mapping of the human genome results from the analysis of genomic data, which has advanced the field to the point that gene intervention is not only possible but feasible and effective for a growing number of diseases (e.g., cancer, sickle cell anemia, eye disorders) (Dunbar et al. 2018).

Similarly, gene (or genome) editing, a group of technologies that enable genes to be modified by adding, removing, or altering DNA (National Library of Science 2022), shows the potential to theoretically eliminate or change certain consumption behaviors. While the gap between possibility and feasibility is still wide for many behavioral applications, the development of technologies such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) narrows that gap considerably. CRISPR targets sections of malfunctioning DNA so they can be cut out and replaced with healthy DNA (Kaiser 2016); by permanently altering DNA and, therefore, heritability, it potentially mitigates or alleviates the edited trait (Ledford 2019).

Evidence from the Literature

Studies showing that heritability is responsible for a large range of behavioral traits (Chabris et al. 2015) have consistently been replicated (Plomin et al. 2016). Over 50 different

studies involving approximately 800,000 pairs of twins (twin studies) (Johnson et al. 2009) compared traits for identical and fraternal twins, reared together and separately. As many of those studies are longitudinal, traits are examined at multiple points over the life span to compare similarities and differences over time (Tucker-Drob and Briley 2014).

GWAS identifies genetic markers across the genome and looks for variations associated with a particular trait (Plomin 2019). Results from twin studies (Bouchard et al. 1990), GWAS (Plomin 2019), and longitudinal studies (Tucker-Drob and Briley 2014) have consistently found that genetic factors are crucial to behavioral traits and that their importance only strengthens over the course of life span. Another consistent theme is that behavioral traits are complex. Very few traits are the result of a single gene, and the polygenetic basis of behavior traits makes gene intervention difficult or, at least at the present time, impossible (Plomin 2019).

Gene intervention can potentially mitigate or alleviate some diseases.

Despite the complexity of behavioral traits, advances in CRISPR technology and other genomic editing techniques have shown the potential to eliminate or alleviate some diseases. CRISPR acts like a pair of scissors that essentially cuts out unhealthy segments of DNA and replaces them with healthy ones (Doudna and Charpentier 2014); it also allows more complex editing beyond just removing and replacing DNA (Doudna and Sternberg 2017). In addition to editing single genes, CRISPR can edit large gene sequences, which makes it a genomic engineering as well as a gene editing technology (Mukerjee 2016).

Gene intervention can potentially mitigate or alleviate some negative behavior.

In addition to the potential of gene editing to mitigate or alleviate disease is the potential to do the same for some negative behaviors. For example, as more is understood about the underlying causal mechanisms for how alcohol is metabolized (Beirut et al. 2010), it might be possible to eventually find a way to edit or remove those mechanisms for individuals with a high

risk for alcoholism. In addition, alcoholism is frequently comorbid with other psychiatric disorders, including drug dependency, anxiety disorders, and personality disorders (Enoch and Goldman 2001), as well as complex diseases such as depression, heart disease, and dementia.

There are risks and limitations, given that the unintended consequences of interventions are not known (Douda and Sternberg 2017). However, the complexity of behavioral traits is no longer in question, nor is the ability to employ gene therapy and gene editing. In fact, over 33 published studies have successfully replicated the use of CRISPR for eye, liver, and lung diseases in mice and are serving as proof-of-concept studies for human application (Lau and Suh 2017). While currently futuristic, it appears that some interventions will have positive impacts beyond their original intent. It is, therefore, reasonable to believe that there will eventually be the ability to mitigate or alleviate some negative consumer behavior.

FP 8: Polygenic scores can probabilistically predict consumer behavior.

Framing the argument

The terms polygenic score and polygenic risk score (PRS) are used somewhat interchangeably depending on the context (e.g., risk usually implies a disease or disorder). A polygenic score is a quantitative measure that indicates an individual's genetic liability for a trait relative to other people (Nguyen and Eisman 2020). An individual's polygenic score is a single number that aggregates all the genetic factors that may help predict the propensity to display a physical or behavioral trait or to develop a disease relative to the population (Lambert et al. 2021). The number is a weighted measure of multiple genetic factors that contribute to the trait (Torkamani, Wineinger, and Topol 2018) and includes genetic factors that may help contribute

to moderating that trait (Edenberg, Gelernter, and Agrawal 2019). Simply put, it is a robust indicator of the probability of displaying a behavior or condition in the future. Results from multiple GWAS have enabled the development of polygenic scores for a variety of behavioral traits (e.g., depression, shyness) or physical disorders (e.g., coronary artery disease, Type 2 diabetes) (Inouye et al. 2018; Khera et al. 2018, Plomin 2019).

The likelihood of developing a particular trait or disorder is generally the result of three factors: genetic predisposition, environmental factors, and lifestyle choices (Torkamani, Wineinger, and Topol 2018). So, while polygenic scores are key predictive variables, they are only one component of a complex equation with multiple variables. Furthermore, a polygenic score is probabilistic and does not address causation.

Evidence from the Literature

Twin studies and adoption studies have consistently found that variations in behavior are driven in large part by genetic factors (Bouchard et al. 1990). What has also been consistently noted is that the inherent complexity of behavioral traits means that, generally, no single gene is responsible for a behavioral trait. Variations in behavior are the result of tens of thousands of extremely small variations that only impact trait expression when aggregated in some way (Plomin 2019; Flint, Greenspan, and Kendler 2020). In part, the development of PRSs was meant to address the fact that the number of SNPs involved in most disorders was simply too large to be analyzed using traditional statistical methods (Penders and Janssens 2022).

Additionally, gene interactions or non-genetic factors (i.e., environment and lifestyle) are often neither clear nor consistent (Dudbridge 2013). Whether a person develops a disease is a function of genetic predisposition as well as environmental or lifestyle factors such as sleep, diet, and stress management (Torkamani, Wineinger, and Topol 2018). For example, in people with

coronary artery disease (CAD), researchers have identified approximately 60 genomic variants that are spread throughout the genome (National Human Genome Research Institute 2022). By comparing samples of those with CAD and those without it, it is possible to assess an individual person's risk of developing the disease (Dudbridge 2013) while identifying its genomic and non-genomic causes and contributing factors.

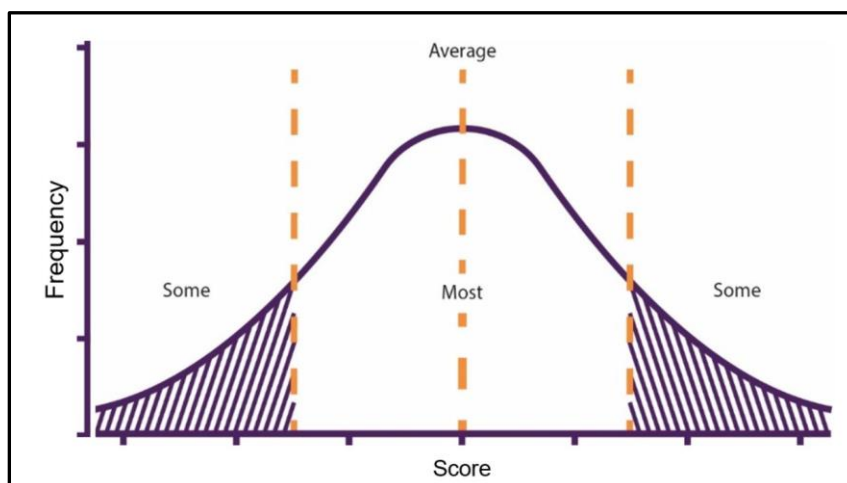
The literature addresses both current and potential uses for PRSs (Euesden, Lewis, and O'Reilly 2015; Newcombe et al. 2019; Uddin et al. 2022). For example, studies have a high genetic correlation between the Big Five personality traits (openness, conscientiousness, extraversion, agreeableness, and neuroticism) and depressive disorders (Amare et al. 2018) and have also found that personality traits influence responses to antidepressants, which suggests that genetics possibly has a mediating effect on drug efficacy (Amare et al. 2018). The implication is that knowing an individual's PRS score for depressive episodes not only helps identify increased risk but also plays a role in determining certain aspects of care.

PRSs can predict relative behavior.

PRSs are normally distributed and therefore enable the identification of outliers that indicate a higher or lower-than-average probability of having a particular trait (Plomin 2019). As Figure 4 illustrates, an individual's polygenic score for any trait will fall somewhere within the normal distribution with a 95% confidence interval. The curve represents the average risk of having the trait (de Villiers, Kroese, and Moorthie 2020). In other words, 95% of the population measured will fall under the "most" area of the curve, with an average risk or likelihood of having a particular disorder or trait. For example, those with an average risk of heart disease or depression can mitigate that risk by following standard guidelines for prevention. On the other hand, those with a score in the higher than normal range have an increased risk; therefore,

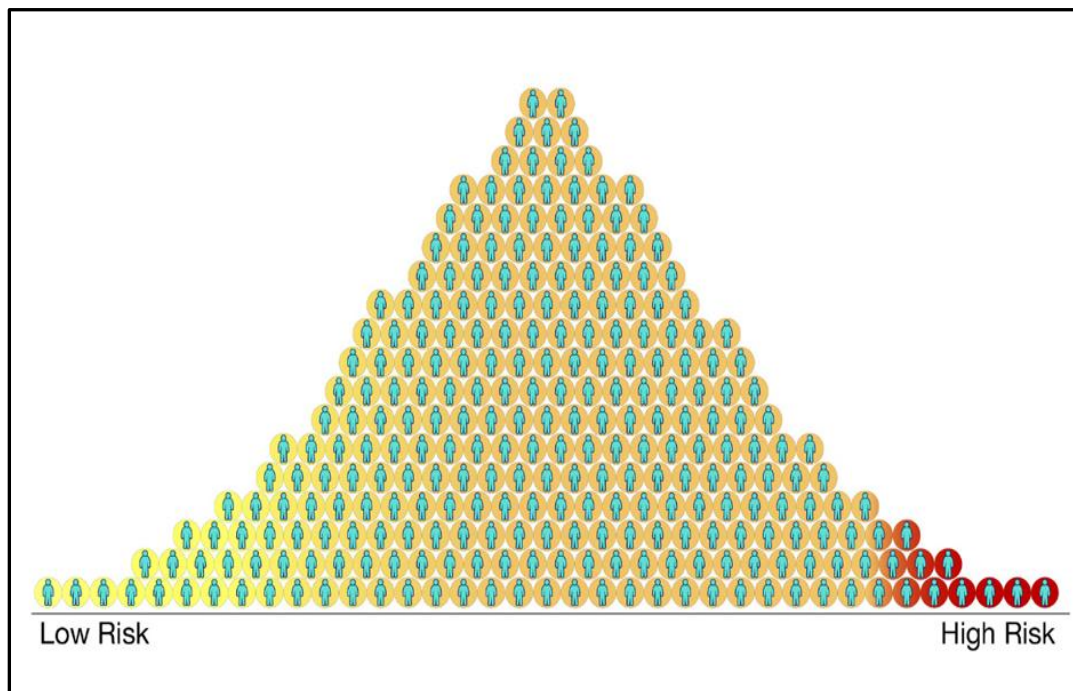
additional environmental, lifestyle, or preventative measures may be necessary in order to mitigate that risk (de Villiers, Kroese, and Moorthie 2020). Figure 5 offers a pictorial representation of the same phenomenon. Each person falls somewhere under the curve. The question is whether one's risk is significantly more or less than the population at large; that is, does it take more or less intervention than is suggested for those with average risk. Therein lies the predictive value of the PRS.

Figure 4 Normal Distribution



(c.f. de Villiers, Kroese, and Moorthie 2020)

Figure 5: Distribution of Polygenic Scores



(c.f. Polygenic Risk Scores (genome.gov))

The value of a PRS is not that it suggests absolute risk or likelihood but relative risk. It is a norm-referenced rather than a criterion-based construct or variable that is analogous to a test score that is based on a defined rubric versus being graded on a curve. PRSs essentially are probabilistic fortune telling devices that function like crystal balls at birth, given that genes do not change (Plomin 2019).

Because most complex diseases manifest over time and with the influence of environmental factors, the score enables a person who is at higher risk for a particular disease to make lifestyle or environmental adjustments (National Human Genome Research Institute 2022). The scores also enable healthcare providers to more closely monitor or utilize preventative measures such as prescribing medications to prevent or delay the onset of disease (Torkamani, Wineinger, and Topol 2018). Because genes are consistent over the life span (Doudna and

Stenberg 2019), PRSs are potentially valuable variables of interest that provide a relative baseline against which predictions can be made.

Polygenic scores can serve as critical probabilistic predictors of variance in consumer behavior.

Behavior involves both the weighing of alternatives and making choices (Valkenburg and Cantor 2001). Research indicates that environmental factors and lifestyle choices impact outcomes for many complex conditions (e.g., depression, heart disease, obesity). Polygenic scores can identify those individuals or populations who might benefit from proactive or more aggressive preventative interventions (Khera et al. 2016). Studies on polygenic scores focus not only on individual traits but on potential associations among traits, which increases their usefulness. For example, meta-analyses of general intelligence have predicted behaviors associated with health and achievement (Savage et al. 2018). Similarly, predictions around externalizing behavior have been made based on the polygenic scores emerging from GWAS (Linnér et al. 2021), which have also been used to develop predictive models for general cognitive scores and academic achievement (Allegrini et al. 2019).

Although behavioral genomic studies are relevant to consumer behavior research, they have not been considered. The combination of the exponential availability of genomic data combined with genomic research on polygenic traits creates a powerful tool for probabilistic prediction of consumer behavior that marketing should not ignore. Market research focused on identifying constructs such as consumer preferences for product identification, cheaters and frauds, risk or thrill-seeking behavior, influencers, or consumer ideologies can be strengthened by considering applicable relevant research from genomics. While these areas have been

examined in genomics research (see Table 7), the results are absent from the marketing literature. This has produced an incomplete and possibly inaccurate understanding of the drivers of consumer behavior.

Table 12- Behavioral Genomic Studies on Traits and Related Marketing Uses

	Trait		Description	Related Marketing Constructs/Uses	
1	Spatial Ability	(Rimfeld et al. 2017)	The capacity to understand visual objects and relationships among objects is 70% heritable.	Geographical Information Systems	(Ozimec, Natter, and Reutterer 2010)
2	Cheating	(Garcia et al. 2010)	Infidelity is 50% heritable? for the 25% of the population with the genetic variant.	Self-Control failure Fraudulent Behavior by Consumers	(Zemack-Rugar, Corus, and Brinberg 2012) (Wilkes 1978)
3	Risk-seeking	(Rao et al. 2018)	Willingness to accept more uncertainty or engage in thrill-seeking endeavors is 41% heritable.	Role of risk in consumer Behavior Risk Reduction Models	(Taylor 1974) (Roselius 1971)
4	Attitudes towards leadership	(Olson et al. 2001)	Attitudes toward leadership roles are 41% heritable.	Political branding Influencers	(Speed, Butler, and Collins 2015) (Feick and Price 1987)
5	Conservatism	(Bouchard 2004)	Resistance to change is 65% heritable in males and 45% heritable in females.	Bodily Marketing Political Branding Market segmentation	(Goenka and Osselaer 2023) (Pich, Dean, and Punjaisri 2016) (Allred, Smith, and Swinyard 2006)

There is a 50-year body of research in behavior genomics on how genetics impacts the development of social attitudes (Eaves and Eysenck 1994). To illustrate, conservative is a relative term that changes over time; survey questions on social attitudes reflect the issues relevant at the time the studies are performed to gauge where an individual falls on a spectrum (Bouchard 2004). While specific studies will define these terms in a variety of ways,

conservative and conservatism generally indicate more traditional attitudes. Studies of twins reared apart indicate that after the age of nineteen, the heritability of conservatism is 0.65 for males and 0.45 for females (Bouchard 2004). Those studies also found an even stronger correlation between conservatism and right-wing authoritarianism (Bouchard 2004). Although marketing literature on conservatives is both extensive and current (Allred, Smith, and Swinyard 2006; Pich, Dean, and Punjaisri 2016; Goenka and Osselaer 2023), research has not addressed the heritability of this social attitude. Because it is not part of the background, literature review, or limitation section of marketing research, a value perspective that should at least be acknowledged is missing.

A similar case can be made for attitudes toward leadership roles and those who occupy them. Studies that have examined the heritability of various dimensions of the construct, including attitudes toward being a leader, public speaking, assertiveness, and being the center of attention, have found significant heritability levels of 0.40 among monozygotic (identical) twins (Olson et al. 2001). Research on political branding considers leaders as brands (Speed, Butler, and Collins 2015). Political branding intersects not only with attitudes toward leadership but also with conservatism research (Pich, Dean, and Punjaisri 2016). Again, the genomic influence of traits that relate to marketing phenomena has not been considered. Perhaps we can better understand how consumers react to these phenomena by considering genomic predispositions.

Finally, genomic research has found a significant level of heritability for risk-seeking behavior (Rao et al. 2018). Risk-seeking behavior has a long history in the marketing literature (e.g., Taylor 1974; Roselius 1971), including research on the level of anxiety that consumers feel when making choices (Taylor 1974) and ways in which they respond to those feelings (Roselius 1971). However, studies have not considered the genetic factors that drive a desire for risk-

seeking behavior or the fact that the bar for risk is relative. It is a reasonable leap to conclude that supplementing environmental factors with genetic factors is a crucial next step in consumer behavior research.

Behavioral traits may not always align with consumer behavior constructs, so it is important to reconcile the constructs and variables under consideration. In addition, empirical research presents challenges for marketers in that only environmental factors can be altered; therefore, understanding the mediating or moderating role of a particular genetic factor is difficult. Finally, the inherent difficulty in studying the genomic drivers of complex traits and behaviors presents challenges to market researchers, a complexity that only increases the importance and value of polygenic scores as a key tool in marketing research.

CHAPTER 5

Empirical Analysis

As described in Chapter 3, two exploratory textual analyses were performed to identify thematic attributes and applications of genomic data for the field of marketing. The results are presented separately for each of the two survey questions. For each question, two coders worked to identify themes and code their presence across participant responses. We identified the themes, provided illustrative examples, and explored the relationships between the themes. The next step was to capture relevant insights gained from the analysis. Furthermore, as noted in Chapter 3, Cohen's Kappa was calculated. With a Kappa Statistic of 0.84 for Question 2 of the cultivated participant pool, the interrater reliability was considered "almost perfect" (Landis and Koch 1977).

Results for Question 1: *Please describe, in detail, at least three key aspects or attributes of genomic data.*

Question 1 was used to first assess participants' understanding of the basics of genomics. Some participants focused on the attributes from a personal perspective. In other words, the attributes of a single person's genomic data. Other participants noted the attributes of genomic data as a subset of big data. In other words, the attributes genomic data as an aggregation of the data from millions of individuals for which genomic data is known. The results are presented in the following tables.

Identified Attributes of Genomic Data

Table 13 provides examples of the keywords associated with each theme.

Table 13 List of Major Keywords Used in Coding Attributes of Genomic Data

	Attribute	Examples of keywords
1	Genomic Data contains all information about human traits	DNA, complete, traits, all information, DNA sequence, specifications, gene expression
2	Genomic Data is predictive	Predictive, forecast, future, risk factors
3	Genomic Data enables comparisons between individuals	Comparable, comparison, variations
4	Genomic Data is heritable	Heritable, parents, ancestors, inherited
5	Genomic Data has large volume	Large, dataset,
6	Genomic Data is highly complex	Complex
7	Genomic Data is immutable	Immutable, no change
8	Genomic Data is individualized and private	Individual, individualized, private, personal, SNPs
9	Most genomic data is the same for everybody (homogeneous)	Identical, same
10	Genomic Data is evolving	Discoveries, evolving, new tools

Table 14 shows the attributes of genomic data. For the 10 attributes, a brief description followed by an illustrative response is presented. In addition, the number of participants who addressed the attribute in their answers is shown. Associations are evaluated later by examining pointwise mutual information.

Table 14- Attributes of Genomic Data

	Attribute	Description	Illustrative Response	Participant #
1	Genomic Data contains all information about human traits	Refers to the complete DNA sequence for an individual that contains all information about a person's traits.	"Analysis of Genomic data has been found to be able to identify human traits by studying the specific genes that have been shown to contribute to the development of that trait. Through genome-wide association studies (GWAS), it is possible to identify specific genes responsible for the development of diseases or phenotypic traits. Furthermore, advances in sequencing technologies have enabled researchers to identify novel genes and genetic variants associated with the development of various physical and behavioral traits." (Participant 33)	21,22,24,26,28, 30,31,33,35,36, 37,38,
2	Genomic Data is predictive	Refers to the ability of genomic data to predict future gene expression for physical and behavioral traits as well as risk factors for diseases and disorders.	"Genomic data can also be used to predict human traits, including disease risk and drug response by providing information on the inheritance pattern of specific genes. This is particularly useful in determining the risk of developing health problems." (Participant 33)	21,22,23,24,26, 28,31,33,34,36, 37
3	Genomic Data enables comparisons between individuals	Refers to the ability to use genetic data to compare traits and risk factors between individuals and among various groups.	"Comparing genomic data from different individuals or populations can provide insights into evolutionary history, genetic diversity, and disease susceptibility. Certain studies have revealed that genomic variation between different populations can be used to trace human migration patterns and ancestry. This information has been used to create genetic ancestry testing services and has improved our understanding of the history of humanity. Moreover, these comparisons allow scientists to trace the history of different disease variants and link them to genetics." (Participant 33)	28,31,33,37

Table 14- Attributes of Genomic Data (continued)

	Attribute	Description	Illustrative Response	Participant #
4	Genomic Data is heritable	Refers to the inheritance of genomic attributes from parents.	“The genetic attribute of individual specifications refers to the characteristics of an individual such as height and weight, as well as eye, hair, and skin color for example. Height and weight are both highly heritable traits, meaning that they are largely determined by an individual’s genes. Studies have shown that a large proportion of the variation in height and weight among individuals is due to genetic factors. For example, height is influenced by multiple genes, and variations in these genes can affect an individual’s final height. Similarly, genetic factors can influence an individual’s weight by affecting factors such as metabolism, appetite, and the distribution of body fat” (Participant 21)	21,22,26,28,30,31,36,37
5	Genomic Data has large volume	Refers to size and volume of genomic data and that it has the attributes of Big Data.	“Genomic data is characterized by its large volume. With the advancement of sequencing technologies, it has become possible to generate massive amounts of genomic data in a relatively short amount of time. For instance, a single human genome contains over three billion base pairs, and sequencing technologies can produce billions of reads in a single experiment.” (Participant 38)	26,28,30,38
6	Genomic Data is highly complex	Refers to the understanding that genomic data is a complex combination of factors.	“Genomic data is highly complex and heterogeneous. It includes not only the DNA sequence itself, but also other genomic features such as gene expression levels, epigenetic modifications, and protein interactions. Moreover, genomic data is dynamic, with changes occurring over time, in different tissues, and in response to different environmental stimuli. As a result, genomic data analysis requires sophisticated bioinformatics tools and algorithms to integrate, visualize, and interpret these diverse data types.” (Participant 38)	26,30,34,38
7	Genomic Data is immutable	Genomic Data does not change over the course of the lifespan.	“(1) Individualistic and personally identifiable, (2) Immutable, (3) Heritable, (4) Variability, (5) Large and Complex” (Participant 30)	30
8	Genomic Data is individualized and private	Each person’s genomic data is unique and individual to them and is private.	“Genomic data is inherently personal, containing information about an individual’s genetic makeup, traits, and potential health risks. As such, there are important ethical and privacy considerations associated with the collection, storage, and use of genomic data.” (Participant 38)	30,32,38

Table 14- Attributes of Genomic Data (continued)

	Attribute	Description	Illustrative Response	Participant #
9	Most genomic data is the same for everybody. (homogenous)	Refers to the understanding that most genomic attributes are the same within and across species.	“Genomic data is highly identical among species. Studies have shown that genomic data have a high degree of identity among species. Researchers who sequenced the chimpanzee genome in 2005 found that humans share about 98.8 percent of their DNA with chimpanzees. Another study sequenced the bonobo genome and confirmed that it shares about 99.6 percent of its DNA with chimpanzees and about 98.7 percent of its DNA with humans—roughly the same amount that chimpanzees share with us. In other words, the genomic data of humans and chimpanzees or bonobos are "almost identical", with only around a 1 percent difference. Even though a later study questioned the rationality of the 1 percent theory and cited the comparison results after the publication of the chimpanzee sequence's first draft, it showed a 6.4 percent difference between the human and chimpanzee genomes. This doesn't change the fact that most of our genomic data are highly identical.” (Participant 29)	
10	Genomic Data is evolving	Research continues to discover both correlations and causal mechanisms for genomic phenomena and the power of analytical tools to interpret these results continues to increase.	“Our understanding of the human genome and the potential applications of genomic data is rapidly evolving, and discoveries and technologies are constantly emerging. This means that companies using genomic data in marketing must stay up to date with the latest research and developments to ensure that their strategies are effective and ethical.” (Participant 24)	24,26

Identifying Associations Between Themes on the Attributes of Genomic Data with Pointwise Mutual Information.

We were interested in understanding the strength of the relationships between attributes to gain insights into understanding of genomic data. Pointwise Mutual Information (PMI) statistics were calculated to show the strength of relationships between themes. Higher PMI values reflect higher cooccurrence relative to expected base rates.

Figure 6 below maps the relationships between the attributes. The highest PMI values were between Attribute 1: Human Traits and each of the other 9 attributes. This result was expected as this is the most fundamental attribute for genomic data as was supported by the first foundational premise. The second strongest were between Attribute 2: Predictive and each of the others. While again, this result was expected, it confirms the attribute that has the greatest implications for marketing.

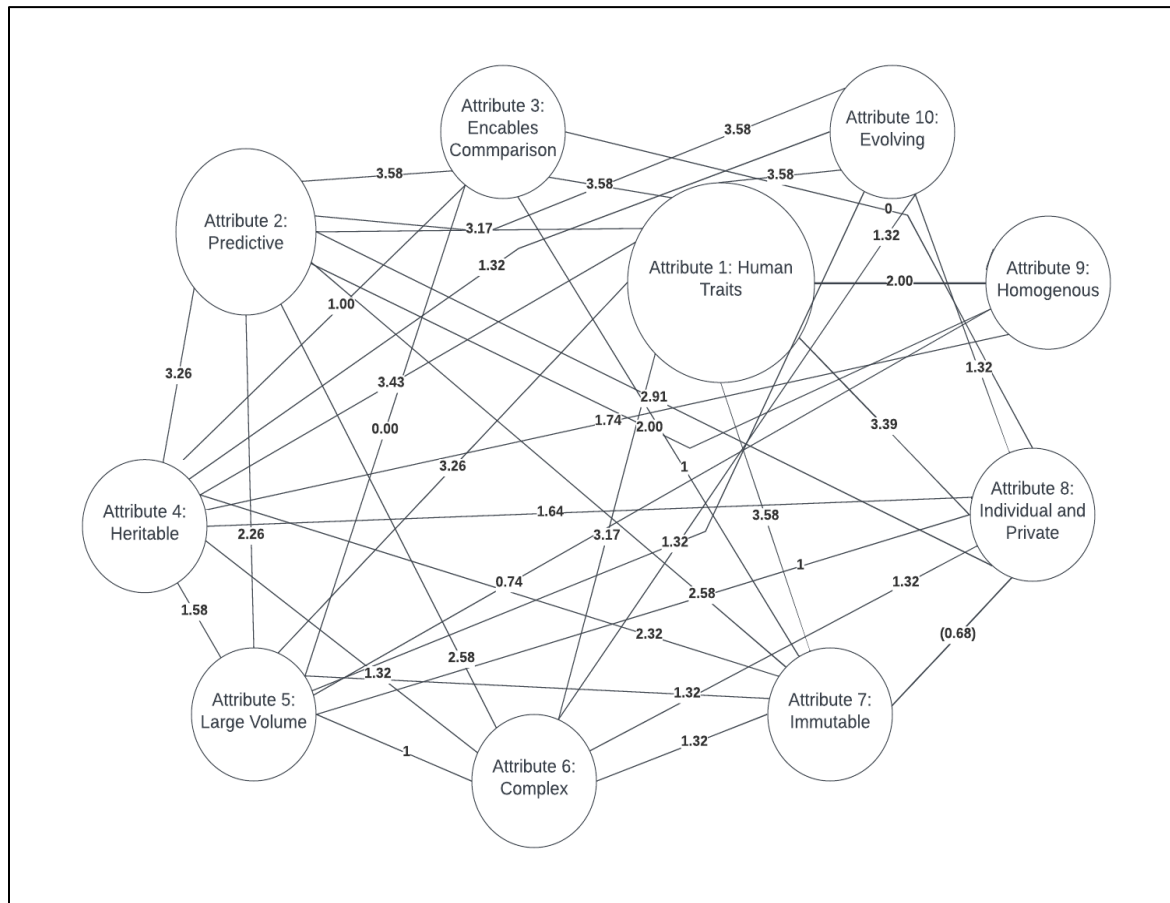
Figure 6: PMI for Genomic Attributes

Table 15 presents the results of the PMI analysis and the concept map for Q1 in matrix form. As noted in the figure the attributes with the strongest relationship are Attributes 1 and 2. These results were expected. The fundamental concept in this dissertation is that genomic data tells us about a human's traits and that there is predictive power in that knowledge.

There were some results that were surprising. The primary one was the low PMI for Attributes 5 and 6. Participant responses did not show a strong relationship between the volume of genomic data and its complexity. There could be methodological drives for this result such as the cultivation process (e.g., lecture and class discussion) where the focus was on other attributes.

Q1 shows that participants understand that the most important attribute of genomic data is that it contains information about human traits and that the data has predictive power. Q1 also showed that participants understand other key attributes of the genomic data. To answer the question about how genomic data can be used in marketing, it was important to ascertain that the participants had a baseline understanding of genomic data.

Table 15- PMI Matrix

		1	2	3	4	5	6	7	8	9	10
1	Human Traits										
2	Predictive	3.17									
3	Enables Comparison	3.58	3.58								
4	Heritable	3.43	3.26	1.00							
5	Large Volume	3.26	2.26	0.00	1.58						
6	Complex	3.17	2.58	N/A	1.32	1.91					
7	Immutable	3.58	2.58	1.32	2.32	1.32	1.32				
8	Individual and Private	3.39	2.91	0.32	1.64	1.32	1.32	-0.68			
9	Homogeneous	2.00	2.00	N/A	1.74	0.74	N/A	N/A	N/A		
10	Evolving	3.58	3.58	N/A	1.32	1.32	1.32	N/A	1.32	N/A	

Results for Question 2: *Please explain how genomic data can potentially be used to understand consumer behavior better and be used in marketing strategy. Describe, in detail, at least three key potential ways that genomic data can be used to understand consumer behavior.*

The second question asked participants to list three potential uses for genomic data in marketing.

Identified Themes of the Potential for Genomic Data in Marketing

Table 16 provides examples of the topics associated with each theme.

Table 16 List of Major Keywords Used in Coding

	Theme	Examples of topics
1	Product Customization	Personalization, customization
2	Communication Preferences	Personalized marketing, personalized advertising
3	Pricing	Value, Price, Cost
4	Channel/Sales Preferences	Channel, Preferences, Content Economy
5	Segmentation	Segmentation, segments, markets, groups
6	Targeting	Targeting, targeted marketing
7	Positioning	Position, placement, positioning
8	New Product Development/Innovation	New products, innovation
9	Branding Loyalty/Relationship Marketing	Brand loyalty, personalization, relationship
10	Branding	Branding, brand identification
11	Consumer Research	Consumer research, understanding, information,
12	Cultural Heritage Marketing	Culture, identity, history,

Table 17 shows the results of the coding. For the 12 themes, a brief description followed by an illustrative response is presented. In addition, the number of participants who addressed the theme in their answers is shown.

Table 17- Themes of the Potential Uses for Genomic Data in Marketing

	Theme	Description	Illustrative Response	Participant #
1	Product Customization	Refers to products that are changed in order to appeal to a specific individual consumer or group of consumers.	“Given that many people decide to get their genome sequenced, whether through a direct-to-consumer company or another way, in order to learn more about their health conditions, it should seem obvious that one key potential use of genomic data in marketing strategy or consumer behavior would be to offer customized medical treatment. As it was mentioned earlier, the Genetic Information Non-discrimination Act (GINA) was passed, and it is supposed to prevent discrimination against people based on their genomic data, but that does not mean that if a patient shares their genomic data with their healthcare provider, that that information could not be used to help customize their medical treatment.” (Participant 7)	1,2,4,5,6,7,8,9, 12,14,15, 17,18
2	Communication Preferences	Refers to how consumers like for companies to communicate with them.	“Genomic data can be used to create tailored marketing messages that resonate with individual consumers based on their genetic makeup. For example, a skincare brand may target customers with genomic data that suggests they have a higher propensity for developing fine lines and wrinkles, offering them targeted anti-aging products and messaging that speaks to their specific concerns.” (Participant 18)	5,7,12,18
3	Pricing	Refers to the price a consumer is willing to pay for a good or service.	“Price is one of the most critical factors that influence consumers' purchasing decisions. Consumers are always seeking the best value for their money, and pricing is a key factor in determining whether a product is worth purchasing or not.” (Participant 4)	4,5,16,17
4	Channel/Sales Preferences	Refers to the manner in which consumers wish for communication about products and services to occur.	“Marketers could match the consumer's identified traits with the common behavioral factors influencing a consumer's purchase, and then align their sales and service channels, including partners and third parties, to meet the consumer's requirements.” (Participant 6)	2,6,18

Table 17- Themes of the Potential Uses for Genomic Data in Marketing (continued)

	Theme	Description	Illustrative Response	Participant #
5	Segmentation	Refers to dividing or subdividing a consumer market into groups with similar characteristics.	“Currently, most marketers segment through physical or mental attributes, such as dividing a group by age, gender, personal interests, lifestyle choices, etc. However, with the growing amount of genomic data that we have at play, the potential of using genomics in the future of market segmentation could be on the horizon.” (Participant 12)	1,2,3,4,8,9,11, 12,13,14, 15,16,17
6	Targeting	Refers to identifying potential consumers and tailoring messaging to them.	“We are stepping into what could be considered a controversial take on genomic data and its potential use in targeting. Assuming the goal is to identify markets that are found to be most profitable, genomic data could be used to determine several highly profitable segments. According to a GWAS conducted by a team of researchers from Duke University, educational achievement can be predicted by an individual’s genes via education-linked genes. Educational achievement typically leads to career success, and career success leads to financial success. If businesses could use this, or similar, genomic data to identify financially successful segments, they may be able to maximize profits based on those segments of people who are financially well off.” (Participant 11)	1,2,3,4,5,6,7,8, 9, 10,11,12,13,14 ,15,16,17
7	Positioning	Refers to the placement of a product or service.	“Consumers have different levels of dopamine based on their DNA, and marketers can use this to their advantage. Some who have lower levels seek external rewards by stimulating the pleasure-responding areas of their brains. Other sense-seeking consumers prioritize experience. Positioning a product the right way can be a competitive advantage, especially for products that have a strong sense associated with it.” (Participant 5)	3,5,6,8,11

Table 17- Themes of the Potential Uses for Genomic Data in Marketing (continued)

	Theme	Description	Illustrative Response	Participant #
8	New Product Development/ Innovation	Refers to the creation of products or services based on genomic data or improvements or changes to existing goods and services.	“Genomic data can be used to inform product development decisions, helping marketers create products that are tailored to specific consumer needs and preferences. For example, a food and beverage brand may use genomic data to identify ingredients that are particularly well-suited to certain genetic profiles, developing products that are optimized for the unique nutritional needs of their target consumers.” (Participant #18)	1,3,4,5,6,8, 15,16,17,18
9	Brand Loyalty/ Relationship Marketing	Refers to the effort to increase customer loyalty to products or services.	“With a strategic approach to using genomic data and targeting, we can get to a point where we can utilize the predictive nature of genomics to gain clientele before a consumer is locked in and showing loyalty with a brand – as is common, for example, in the coffee industry (Daviet et al., 2022). This type of strategy would help to build a strong pipeline of consumers, much faster than the more traditional advertising methods that are currently employed.” (Participant 3)	2,3,5, 10,11,12,15,17 ,
10	Branding	Refers to applications that connect a particular good or service to a specific brand.	“Having access to individual consumer insights could allow for marketing strategists to pivot and create an impactful brand promise and marketing campaign based on data that is directly compelling and motivational to the consumer.” (Participant 6)	1,2,6, 13,17

Table 17- Themes of the Potential Uses for Genomic Data in Marketing (continued)

	Theme	Description	Illustrative Response	Participant #
11	Consumer Research	Refers to the use of genomic data to understand consumers better.	“It is possible to ascertain the individual consumers who, what, where, why, and how, providing for a more useful, customized, and authentic form of consumer profile data and insight than any of the conventional marketing strategies used widely today (such as demographics, psychographics, geographics, beliefs and values, life stages, surveys, interviewing, and consumer feedback). Marketers are oftentimes using multiple data sources together to create the big picture of the individual consumer, but because genomic data provides a more customized consumer blueprint, the application of science in marketing is the next major consumer market (Brooke, 2018). A consumer’s genomic data may be more informative about their needs than demographics and more valuable about their preferences than responses to survey questions (Wharton Staff, 2020). From the research, the application of genomic data in marketing strategies has many implications.” (Participant 6)	1,2,6,8,8,11,12,15,16,17
12	Cultural Heritage Marketing	Refers to marketing that uses cultural attributes of the consumer.	“The use of genetic data to create an intangible relationship with consumers around their ancestral heritage is a relatively new area of interest for many companies. By analyzing an individual’s genetic makeup, companies can provide insights into their ancestry and help individuals learn more about their family history and cultural roots. Travel and tourism companies like Airbnb are using genetic data to create personalized travel experiences that are tailored to an individual’s ancestral heritage. Companies could also use genetic data to create cultural events and experiences that celebrate an individual’s ancestral heritage. For example, a company might host a cultural festival that is tailored to the ancestral heritage of the attendees based on their genetic data. By tapping into the intangible nature of our ancestral heritage, companies can strike the core of who their customers are and form incredible emotional bonds.” (Participant 1)	1,3,6,7,8,9,11

Identifying Associations Between Themes on the Potential for Genomic Data in Marketing with Pointwise Mutual Information.

The PMI for each relationship association. As noted earlier, PMI is a relative rather than an absolute statistic. The two figures below graphically depict the PMI for the themes. Given the number of themes and the number of relationships, two figures are presented. Figure 7 shows the positive PMI relationships. These are relationships where the association was stronger than expected.

Figure 7 Positive PMI Relationships for Potential Applications

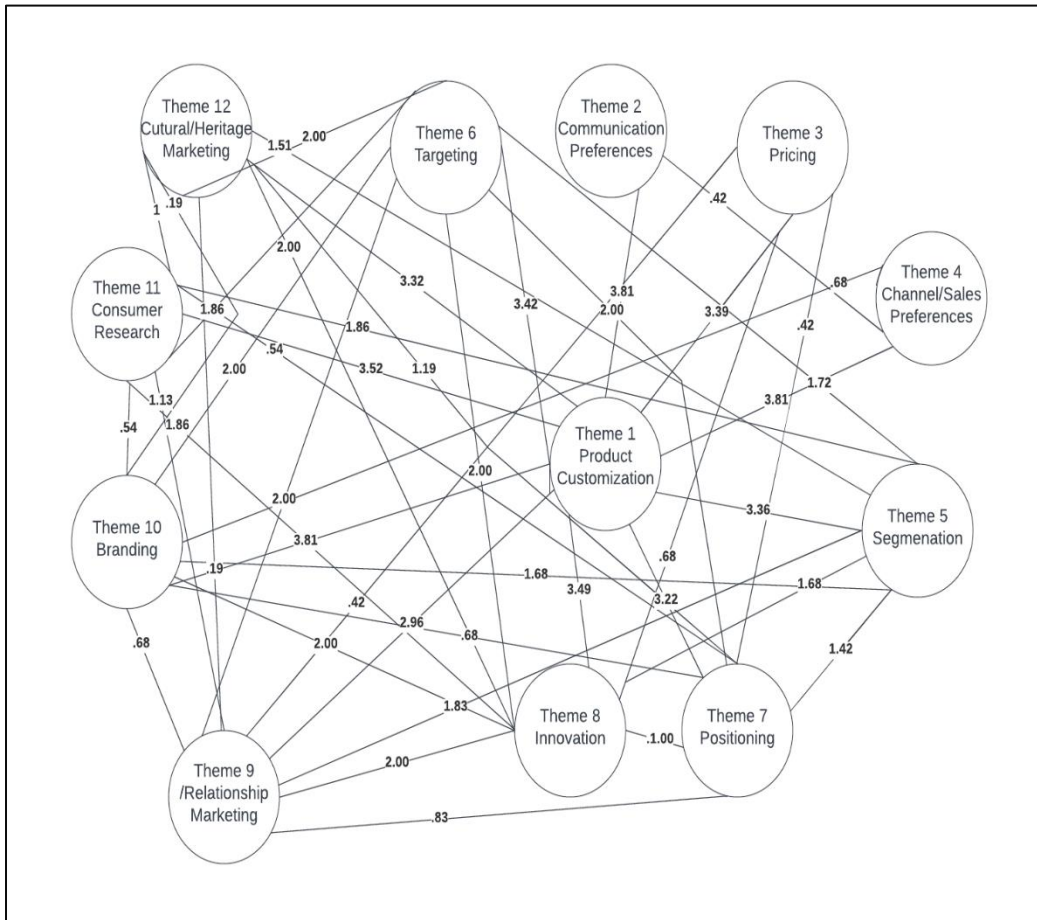


Figure 8 shows negative PMI relationships. For these relationships, the themes cooccurred less frequently than expected. Both Communication Preferences (Theme 2) and Channel/Sales Preferences (Theme 4) had multiple negative relationships. The implications of these results warrant further investigation as both would appear to be ways that genomic data could be used to enhance the consumer experience.

Figure 8- Negative PMI Relationships for Potential Applications

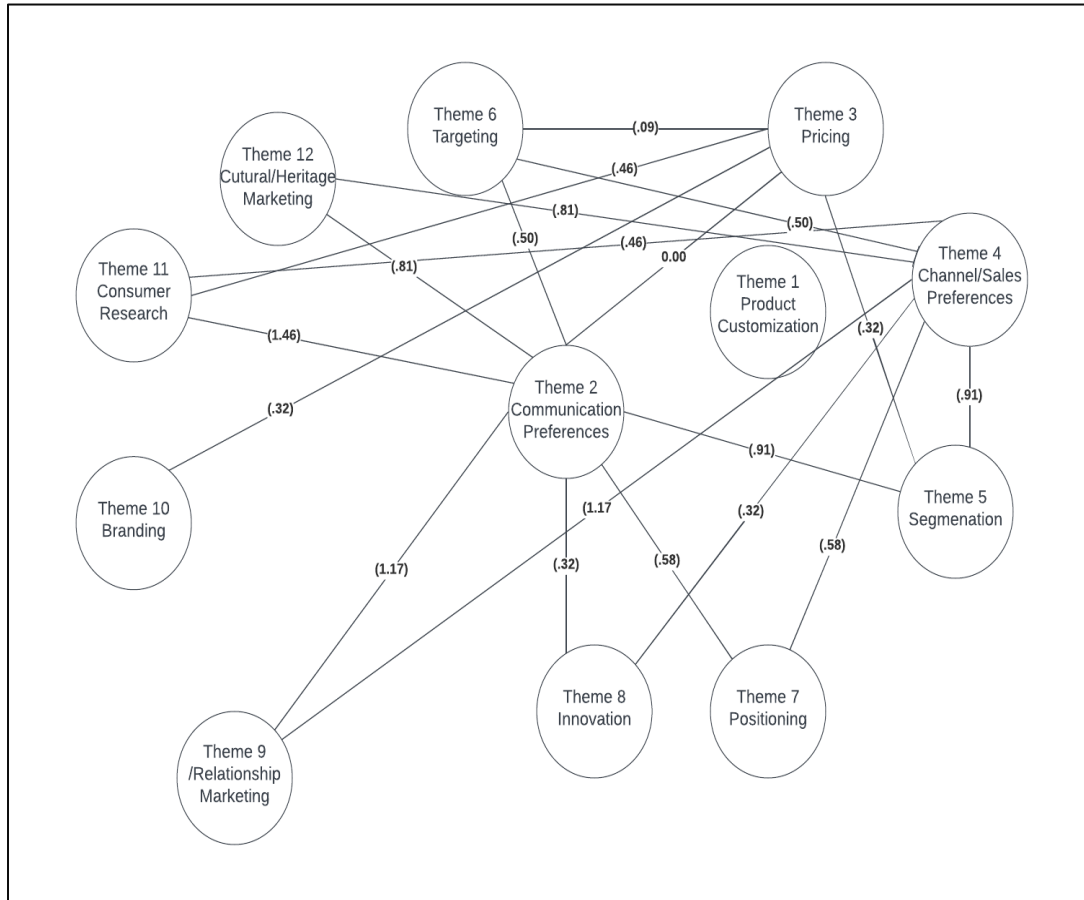


Table 18 is the PMI matrix which shows the 28 relationships for which PMI was calculated. The purpose of the matrix is to show the relative cooccurrence for each theme according to its PMI. The results contained both expected and somewhat insightful results, which are discussed below.

Table 18- Pointwise Mutual Information Matrix

Themes													
	Theme	1	2	3	4	5	6	7	8	9	10	11	12
Product Customization	1												
Communication Preferences	2	3.81											
Pricing	3	3.39	0.00										
Channel/Sales Preferences	4	3.81	0.42	N/A									
Segmentation	5	3.36	-0.91	-0.32	-0.91								
Targeting	6	3.42	-0.50	-0.09	-0.50	1.72							
Positioning	7	3.33	-0.52	0.42	-0.58	1.42	2.00						
New Product Development/Innovation	8	3.49	-0.32	0.68	-0.32	1.68	2.00	1.00					
Brand Loyalty and Relationship Marketing	9	2.96	-1.17	0.42	-1.17	1.83	2.00	0.83	2.00				
Branding	10	3.81	N/A	-0.32	0.68	1.68	2.00	0.68	2.00	0.68			
Consumer Research	11	3.52	-1.46	-0.46	-0.46	1.86	1.86	0.54	1.86	1.13	0.5		
Cultural/Heritage Marketing (tours, etc.)	12	3.32	-0.81	N/A	-0.81	1.51	2.00	1.19	2.00	0.19	0.2	1.5	

Product Customization (Theme 1) had the highest PMI with every other theme. This supports the foundational premises that one of the major implications of genomic data for marketing will be the ability to customize products for both individuals and groups of consumers. Except for Brand Loyalty and Relationship Marketing (Theme 4), the PMI was above 3.00 for every relationship.

Though not as strong as Product Customization, Targeting (Theme 6) had a strong PMI with several themes, including Positioning (Theme 7), New Product Development (Theme 8), Brand Loyalty (Theme 9), and Branding (Theme 10), and Cultural Marketing (Theme 12). The relationship with Consumer Research (Theme 11) was only slightly lower. This indicates that marketers can potentially use genomic data to target more effectively.

Communication Preferences (Theme 2) had the lowest PMI relationship with every other theme, with a positive PMI only with Channels and Sales Preferences (Theme 4). The other notable result was Communication Preferences (Theme 2), and Branding (Theme 10) had no cooccurrence. This result might be due to how the pool was cultivated.

Finally, there was no PMI between Pricing (Theme 3), and Channel and Sales Preferences (Theme 4), and Cultural and Heritage Marketing (Theme 12). These two results were interesting and indicates that participants have a vision of the future where pricing and channel decisions are consequences of genomics rather than constraints. That is, advances in genomic marketing may disentangle entrenched market assumptions about the relationship between price and channel.

The exploratory analysis indicated that participants recognized opportunities for genomic data to enable increased customization of products and services. It also supported the idea that it opens the door to new types of segmentation. The PMI relationships warrant further research.

Both analyses were exploratory. Q1 showed that a cultivated pool of participants understands the attributes of genomic data and Q2 showed that they could envision applications of genomic data for marketing strategy. The results of the exploratory analyses support the marketing applications considered in the foundational premises. They also present opportunities for further research on the relationships between attributes and among potential applications. As an initial exploratory analysis, the objective was to raise additional questions for future consideration.

CHAPTER 6

Discussion

The primary goal of this dissertation was to develop an initial theoretical framework for genomics in marketing. A related objective was to suggest its implications for marketing research and marketing practice. The larger agenda of this research is to provide a foundation for future academic research. Using Hunt's methodology for indigenous theory development, this dissertation has presented the initial theoretical framework and suggested implications for both marketing research and managerial practice.

This is a theoretical contribution. Researchers have developed a framework within consumer behavior theory by extending the stimulus response model developed by Belk in 1975, (Daviet, Nave, and Wind 2022). However, to our knowledge, this is the first effort to develop a theory on the uses of genomic data which is indigenous to marketing. The initial theoretical framework may support a larger agenda by serving as foundational support for future academic research. This potentially could lead to an even better understanding of the implications for marketing.

To achieve these objectives, a set of foundational premises were formulated and supported with research from other disciplines to support a framework for marketing. To establish the practical relevance, the potential for practical managerial applications for both firms and consumers was considered. Table 20 summarizes the highlights of the initial theoretical framework, while Table 21 summarizes potential marketing implications from the perspective of both the firm and the consumer.

An exploratory textual analysis supported the foundational premises. The purpose of the analysis was to identify and understand themes around the potential practical applications of genomic data. The genomics revolution is already transforming other fields and will transform marketing. The current research may help lay the foundation for marketing and service as a starting point for future research.

Both the theoretical and empirical work in this dissertation have limitations that should be acknowledged and considered. The limitations of both were addressed in the Chapters 3 and 5. The overall limitation of the current research is that it is an initial framework. As with any initial attempt, it reflects the limitations of the researchers as well as the field of study. Because the objective was to develop an initial framework, we do not consider the limitations to reduce the significance of the contribution but rather see them as an inherent feature of work in a quickly evolving discipline.

This overall limitation is even more evident in the empirical study. Determining appropriate research designs and methodologies to challenge an initial framework of this nature has inherent limitations. Genomics and marketing are two fields that have not traditionally overlapped, and therefore finding a population to use for research is challenging. There is also no prior research on which to build. While acknowledging these limitations, we still argue that the empirical analysis does make a methodological contribution.

We believe that the initial theoretical framework, supported by the empirical analysis, makes both a theoretical and a managerial contribution and lays the groundwork for future research. Table 20 lists one of the major challenges for marketing related to each of the foundational premises and then presents a theoretical contribution of the premise. Following the

theoretical contributions, Table 21 lists the potential implications for both firms and consumers based on each of the foundational premises.

Table 19- Theoretical Contributions of Framework

	Genomics Foundational Premise	Major Challenges for Marketing	Theoretical Contribution of Premise
FP1	Foundational Unit	Lack of understanding of genomics.	Establishes the starting point from which all other premises emerge.
FP2	Nurture AND Nature	Identifying the primary drivers of behavior.	Both nature and nurture must be considered to understand consumer behavior fully.
FP3	Gene-Gene Interactions	Limited study in marketing and consumer behavior.	Consumer behavior is the result of complex traits that involve genes working in some sort of relationship with each other.
FP4	Genes- Environment Interactions	Epigenetic changes are still being studied, and understanding is evolving.	Epigenetic changes show genes and environment are not mutually exclusive but often lead to a synthesis that is crucial for the expression of behavioral traits.
FP5	Genetic Influence Increases	The premise is counterintuitive and challenges long-held beliefs and practices.	The fact that genes become more and not less important in variances in consumer behavior is both counterintuitive and reflective of the importance of genetics for understanding consumer behavior.
FP6	Predictive Ability	The mechanism by which some behaviors manifest is still unknown.	Given that all traits are, to some extent, heritable, genomics can predict consumer behavior from birth.
FP7a	Alleviation of negative consumption behavior	The interrelationships between traits are still unknown.	By understanding the genomic factors underlying complex traits, negative consumption behavior can be predicted and potentially alleviated.
FP7b	Potential of genomic intervention	The moral, ethical, legal, and regulatory frameworks have not been developed to address new technologies and data.	Genetic intervention options emerging from genomic data research can potentially alleviate some negative consumption behavior.
FP8	Polygenic Scores	Probabilistic is not synonymous with deterministic.	Polygenic Scores provide the best quantitative measure of relative behavior.

Table 20- Managerial Contributions of the Initial Framework

	Genetics foundational premise	Key potential implications for firms	Key potential implications for consumers
FP1	Foundational Unit	The ability to collect, analyze, and monetize genetic data creates new revenue streams for firms.	Consumers can have products and services targeted to their wants and needs.
FP2	Nurture AND Nature	Information gleaned from the 40%-50% (Plomin 2019) of behavioral traits related to genetics can improve marketing results.	Genomic data can increase the efficacy of treatment options or product offerings by considering both genetic and environmental factors.
FP3	Gene-Gene Interactions	An enhanced understanding of the impact of gene interactions will improve the understanding of consumer behavior.	Genomic data will enable the customization of prevention and treatment options for genetically based conditions.
FP4	Genes- Environment Interactions	By understanding the mechanisms by which genes interact with the environment, firms can improve products and services to drive outcomes.	Genomic data can increase the efficacy of treatment options or product offerings by considering genetics as well as environmental factors.
FP5	Genetic Influence Increases	Genetic data will improve marketers' understanding of consumer behavior.	Solutions to common conditions may be improved as options are based on genetic factors instead of focusing exclusively on consumer choices.
FP6	Predictive Ability	The ability to predict consumer needs will enable more customized and targeted solutions.	Consumers can be more proactive in the choices they make.
FP7a	Alleviation of negative consumption behavior	As causal mechanisms are discovered, firms can develop more effective interventions.	Data will enable consumers to be proactive in avoiding negative outcomes.
FP7b	Potential of genomic intervention	The potential market for biotech firms specializing in gene editing technologies is significant.	Gene editing will enable consumers to alleviate problematic behaviors in new ways.
FP8	Polygenic Scores	By understanding PRS, biotech, and other healthcare firms can target solutions.	PRS will enable consumers to understand better the risks they face.

There are marketing implications for both marketing strategy and consumer behavior research. The overall implication is very simple. Behavior is a combination of genomic and non-genomic factors, and most marketing strategy and consumer behavior research has focused on the non-genomic factors. Integrating research on genomic data may or may not change strategy or outcomes, but to ignore it, is to potentially limit the efficaciousness of strategy and the complete of research.

Finally, the moral, ethical, and legal implications of the use of genomic data will provide a rich agenda for research as well as challenging dilemmas for marketing practice. Genomic data can be used in ways that are gimmicky, but it can also be used in ways that may have profound impact on the lives of people. The speed with which both the volume of data as well as the technology to use it in some way make moral, ethical, and legal frameworks imperative. That creates rich opportunities for researchers to do innovative research that can have an almost immediate impact on practice.

The ethical issues around genomics fall into three categories. First will be issues or considerations around both emerging technologies and medical innovations. The scientific discoveries and innovations that arise will create bioethical issues. The second will be issues related to genomic data on both a personal and firm level. Finally, there will be public policy issues around the ethical, legal, and social implications (ESLI) (Neimiec and Howard 2016). Each of these categories will have a plethora of subcategories, any of which will likely warrant extensive research. There is a growing body of literature that addresses these areas, and there is considerable overlap in the discussion. A full-length study of ethical considerations would be a valuable addition to the literature on genomics and its marketing implications. However, a brief

overview of a sample of topics supports the assertion that ethical issues are going to be a key factor in the genomics revolution and these issues will have implications for marketing.

Genomic technologies such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeat), must be considered from the perspective of both the intended and unintended consequences of their application. For example, in China, twin girls were born from edited embryos to prevent the transmission of HIV from the infected father to the unborn children (Hirsh, Iphofen, and Koporc 2019). While the ability to prevent HIV transmission is a positive use of the technology, it has not been around long enough for there to be any consideration of how the editing impacts the human. Doudna (Doudna and Sternberg, 2017, p. 200) has repeatedly cautioned that the power of CRISPR must be balanced with the risks that arise from not having a full understanding of some genetic mechanisms and the fact that some genes are only expressed later in life (Bosely et. al, 2015). In other words, there can be a time lag that makes it difficult to have a complete picture of the impact of some gene editing. Thus, appropriate applications of technology will need frameworks and guidelines within which to assess the risks and benefits of technology.

Similar ethical issues surround research on infectious diseases when they are being studied outside of an emergency response (Boyce and Garibaldi 2018). The ethical guardrails are in place when research is being performed as a crisis response, but not when the research is being performed to anticipate and find ways to mitigate the impact of infectious diseases that have highly negative consequences (Boyce and Garibaldi 2018). The possibility of determining who will get a disease, who will have highly negative outcomes, and what therapies will be effective for both prevention and treatment have obvious value, but there are ethical considerations that have to be considered.

While the two previous areas have tangential marketing implications, there are other areas where the implications are more direct. One of the most applicable is Direct to Consumer Genomic Testing (DTC GT) market. The ability to provide information directly to consumers opens new markets. The ethical challenge will be distinguishing product that have legitimate value from those that are not based on scientific research (Daviet, Nave, and Wind 2022). Additionally, there are considerations around the transparency of research activities and the parameters within which research occurs (Niemic and Howard 2016). The question is what type of consumer protections are needed so that consumers can make informed decisions knowing whether a DTC GT product is based on sound research.

Public perception will also seriously impact the use or misuse of both the technology and the data upon which it relies and therefore there will be ethical issues to address. In a society that appears to have an eroding trust in science and authority, the role of public perception becomes even more critical (Middleton et. al 2022). Genomics is a complex topic and the failure to accurately understand what genomic data does and does not tell us about a phenomenon becomes important and how to address inaccuracies is in part an ethical issue.

Finally, there will be a myriad of issues around security, privacy, and ownership of genomic data at both the individual and firm level. Many of these issues will be the same ethical issues that plague any other type of data (Grishin, Obbad, and Church 2019). Table 21 summarizes a few of the key considerations around these concerns. The list is in no way exhaustive, nor are the areas mutually exclusive. They are provided as an illustration of the complexity of ethical considerations that are emerging in the field.

Table 21: Ethical Considerations

	Areas of Ethical Concern	Key Considerations	Citation
1	Genomic technologies	Appropriate use. The unintended impact of new technologies or innovations.	(Bosely et. al, 2015) (Hirsh, Iphofen, and Koporc 2019)
2	Anticipatory Ethics	Forecasting potential issues during the early stages of research.	(Boyce and Garibaldi 2018)
3	Ownership and Use of Data	Efficacy, misinformation, transparency, privacy, data ownership, informed consent around DTC GT products and data	(Niemiec and Howard 2016) (Daviet Nave and Wind 2022)
4	Public perceptions	Understanding of genomics and genomic data	(Middleton et al. 2020)
5	Privacy and Security of Data	Privacy and security issues at the individual level as well as those same issues at the firm level.	(Malin 2005) (Grishin, Obbad and Church 2019)
6	Public Policy	Legal and regulatory frameworks as well as public health priorities	(Brand, Brand, and Schulte 2008)

The pace of change and what is possible is moving much faster than the ethical guiderails, frameworks, and regulations (Doudna and Sternberg 2017). The complexity of the genome means that medical and technological innovations will carry consequences both intended and unintended (Isaacson 2021; Plomin 2019). In addition, genomic data contains our most personal information. Critical security, privacy, and consent issues will have to be addressed at an individual and Big Data level (Mathaiyan, Chandrasekaran, and Davis 2013; Shabani and Borry 2018; Shabani 2019). While the power of genomics is evident, considerable care should be taken to use this power responsibly.

Public policy will need to consider how to address the myriad of ethical considerations resulting from the genomics revolution. There will likely be significant public policy suggestions that lead to new laws and regulations for extensions of existing rules. Genomics will need to integrate into current public health policy (Brand, Brand, and Schulte 2008). There will also be

public policy considerations around personal genomic data. In some cases, that may involve extension of current laws and regulations to include data (Malin 2005). Finally, other new and disruptive technologies such as blockchain may provide a potential solution for data related issues such as those noted in the table above (Ozercan, et. al 2018).

References

- Adebowale Adeyemo, Mary K. Balaconis, Deanna R. Darnes, Segun Fatumo, Palmira Granados Moreno, Chani J. Hodonsky, et. al (2021), "Responsible Use of Polygenic Risk Scores in the Clinic: Potential Benefits, Risks and Gaps," *Nature Medicine*, 27(11), 1876-84. <https://doi.org/10.1038/s41591-021-01549-6>.
- Aggarwal, Praveen, Rajiv Vaidyanathan, and Alladi Venkatesh (2009), "Using Lexical Semantic Analysis to Derive Online Brand Positions: An application to Retail Marketing Research," *Journal of Retailing*, 85(2), 145-158. <https://doi.org/10.1016/j.jretai.2009.03.001>.
- Allegrini, Andrea G., Saskia Selzam, Kaili Rimfeld, Sophie von Stumm, Jean-Baptiste Pingault, and Robert Plomin (2019), "Genomic Prediction of Cognitive Traits in Childhood and Adolescence," *Molecular Psychiatry*, 24(6), 819-27 <https://doi.org/10.1038/s41380-019-0394-4>.
- Allen, Garland E. (2003), "Mendel and Modern Genetics: The Legacy for Today," *Endeavour*, 27(2), 63-8. [https://doi.org/10.1016/S0160-9327\(03\)00065-6](https://doi.org/10.1016/S0160-9327(03)00065-6).
- Allred, Chad R., Scott M. Smith, and William R. Swinyard (2006), "E-shopping Lovers and Fearful Conservatives: A Market Segmentation Analysis," *International Journal of Retail & Distribution Management*, 34(4/5), 308-33. <https://doi.org/10.1108/09590550610660251>.
- Amare, Azmeraw T., Klaus Oliver Schubert, Fasil Tekola-Ayele, Yi-Hsiang Hsu, Katrin Sangkuhl, Gregory Jenkins, Ryan M. Whaley et al. (2018), "Association of the Polygenic Scores for Personality Traits and Response to Selective Serotonin Reuptake Inhibitors in Patients with Major Depressive Disorder," *Frontiers in Psychiatry*, 9(65), 1-11. <https://doi.org/10.3389/fpsy.2018.00065>.
- Marketing Association, "What is Marketing?" Accessed June 8, 2022. <https://www.ama.org/the-definition-of-marketing-what-is-marketing/>.
- Applegate, Edd (2008), "The Development of Advertising and Marketing Education: The First 75 Years," *Education Resources Information Center*, Accessed August 31, 2022. <https://files.eric.ed.gov/fulltext/ED502731.pdf>.
- Archak, Nikolay, Anindya Ghose, and Panagiotis G. Ipeirotis (2011). "Deriving the Pricing Power of Product Features by Mining Consumer Reviews," *Management Science*, 57(8), 1485-1509. <https://doi.org/10.1287/mnsc.1110.1370>.
- Ark Invest (2022), "What Are The Major Innovation Platforms Evolving Today?", Accessed December 6, 2022. Invest In The Future Today | ARK Investment Management (ark-invest.com).

- Ayorech, Ziada, Saskia Selzam, Emily Smith-Woolley, Valerie S. Knopik, Jenae M. Neiderhiser, John C. DeFries, and Robert Plomin (2016), "Publication Trends Over 55 Years of Behavioral Genetic Research," *Behavior genetics*, 46(5), 603-7. <https://doi.org/10.1007/s10519-016-9786-2>.
- Balducci, Bitty, and Detelina Marinova (2018), "Unstructured Data in Marketing," *Journal of the Academy of Marketing Science*, 46, 557-90. <https://doi.org/10.1007/s11747-018-0581-x>.
- Baltimore, David, Paul Berg, Michael Botchan, Dana Carroll, R. Alta Charo, George Church, Jacob E. Corn, George Q. Daley, et al., (2015), "A Prudent Path Forward for Genomic Engineering and Germline Gene Modification," *Science*, 348(6230), 36-8. <https://doi.org/10.1126/science.aab1028>.
- Barnett, Simon, and Ali Urman (2022), "The View from ARK Invest" *GEN Biotechnology*, 1(5), 435-9. <https://doi.org/10.1089/genbio.2022.29061.sba>.
- Bates, Gillian (2005), "The Molecular Genetics of Huntington Disease: A History," *Nature Reviews Genetics*, 6, 766-73. <https://doi.org/10.1038/nrg1686>.
- Baumgartner, Hans, and Rik Pieters (2003), "The Structural Influence of Marketing Journals: A Citation Analysis of the Discipline and Its Subareas Over Time," *Journal of Marketing*, 67(2), 123-39. <https://doi.org/10.1509/jmkg.67.2.123.18610>.
- University of California at Berkeley, "Genomics and Data Science." Accessed August 18, 2022. Genomics and Data Science | CDSS at UC Berkeley.
- Beadle, George W., and Edward L. Tatum (1941), "Genetic Control of Biochemical Reactions in Neurospora," *Proceedings of the National Academy of Sciences*, 27(11), 499-506. Genetic Control of Biochemical Reactions in Neurospora* (pnas.org)
- Begum, Ferdouse, Debashis Ghosh, George C. Tseng, and Eleanor Feingold (2012), "Comprehensive Literature Review and Statistical Considerations for GWAS Meta-Analysis," *Nucleic Acids Research*, 40(9), 3777-84. <https://doi.org/10.1093/nar/gkr1255>.
- Benson Dennis A, Mark Cavanaugh, Karen Clark, Illene Karsch-Mizrachi, David Lipman, James Ostell, and Eric W. Sayers (2013), "GenBank", *Nucleic Acids Research*, 41(Database issue). <https://doi.org/10.1093/nar/gks1195>.
- Bierut, Laura J., Arpana Agrawal, Kathleen K. Bucholz, Kimberly F. Doheny, Cathy Laurie, Elizabeth Pugh, Sherri Fisher, et al. (2010), "A Genome-Wide Association Study of Alcohol Dependence," *Proceedings of the National Academy of Sciences*, 107(11), 5082-7. <https://doi.org/10.1073/pnas.0911109107>.

- Biglan, Anthony, Brian R. Flay, Dennis D. Embry, and Irwin N. Sandler (2012), "The Critical Role of Nurturing Environments for Promoting Human Well-being," *American Psychologist*, 67(4), 257-71. <https://doi.org/10.1037/a0026796>.
- Bipp, Tanja, Ricarda Steinmayr, and Birgit Spinath (2008), "Personality and Achievement Motivation: Relationship Among Big Five Domain and Facet Scales, Achievement Goals, and Intelligence," *Personality and Individual Differences*, 44(7), 1454-64. <https://doi.org/10.1016/j.paid.2008.01.001>.
- Birchler, James A. (2015), "Mendel, Mechanism, Models, Marketing, and More," *Cell*, 163(1), 9-11. <https://doi.org/10.1016/j.cell.2015.09.008>.
- Boland, Wendy Attaya, Ingrid M. Martin, and Marlys J. Mason (2020), "In Search of Well-being: Factors Influencing the Movement Toward and Away from Maladaptive consumption," *Journal of Consumer Affairs*, 54(4), 1178-94. <https://doi.org/10.1111/joca.12324>.
- Bouchard, Thomas J. and Matt McGue (2003), "Genetic and Environmental Influences on Human Psychological Differences," *Journal of Neurobiology*, 54(1), 4-45. <https://doi.org/10.1002/neu.10160>.
- Bouchard Jr, Thomas J. (2004), "Genetic Influence on Human Psychological Traits: A Survey," *Current Directions in Psychological Science*, 13(4), 148-51. <https://www.jstor.org/stable/20182937>.
- Bouchard Jr, Thomas J., David T. Lykken, Matthew McGue, Nancy L. Segal, and Auke Tellegen (1990), "Sources of Human Psychological Differences: The Minnesota Study of Twins Reared Apart," *Science*, 250(4978), 223-8. <https://doi.org/10.1126/science.2218526>.
- Boutwell, Brian B., Scott Menard, J. C. Barnes, Kevin M. Beaver, Todd A. Armstrong, and Danielle Boisvert (2014). "The Role of Gene–Gene Interaction in the Prediction of Criminal Behavior," *Comprehensive Psychiatry*, 55(3), 483-8. <https://doi.org/10.1016/j.comppsy.2013.11.005>.
- Boyce, Angie M., and Brian T. Garibaldi (2019), "Genomics and High-Consequence Infectious Diseases: A Scoping Review of Emerging Science and Potential Ethical Issues," *Health Security*, 17(1), 62-8. <https://doi.org/10.1089/hs.2018.0108>.
- Brand, Angela, Helmut Brand, and Tobias Schulte in den Bäumen (2008), "The Impact of Genetics and Genomics on Public Health," *European Journal of Human Genetics*, 16(1), 5-13. <https://doi.org/10.1038/sj.ejhg.5201942>.
- Briley, Daniel A., and Elliot M. Tucker-Drob (2013), "Explaining the Increasing Heritability of Cognitive Ability Across Development: A Meta-Analysis of Longitudinal Twin and Adoption studies," *Psychological Science*, 24(9), 1704-13. <https://doi.org/10.1177/0956797613478618>.

- Britannica (2003), "Gene Summary," *Encyclopedia Britannica*, Accessed March 20, 2022. <https://www.britannica.com/summary/gene>.
- Broadfoot, Marla Vacek (2018) "The Gene-Editing Tool CRISPR, Explained" *Discovery's Edge: Mayo Clinic's Research Magazine*, July 24, 2018, Accessed July 28, 2022. The Gene-Editing Tool CRISPR, Explained - Discovery's Edge (mayo.edu).
- Burke, Adrienne (2012), "DNA Sequencing is Now Improving Faster Than Moore's Law," *Forbes*. January 12, 2012, Accessed December 7, 2022. DNA Sequencing Is Now Improving Faster Than Moore's Law! (forbes.com).
- Butcher, Lee M., Joanna KJ Kennedy, and Robert Plomin (2006), "Generalist Genes and Cognitive Neuroscience," *Current Opinion in Neurobiology*, 16(2),145-51. <https://doi.org/10.1016/j.conb.2006.03.004>.
- Carey, Nessa (2012), *The Epigenetics Revolution: How Modern Biology is Rewriting Our Understanding of Genetics, Disease and Inheritance*, London: Icon Books.
- Centers for Disease Control and Prevention (2022), "Polygenic Risk Scores", *Centers for Disease Control and Prevention*, Accessed April 8, 2023. Polygenic Risk Scores | CDC.
- Cesarini, David, Christopher T. Dawes, Magnus Johannesson, Paul Lichtenstein, and Björn Wallace (2009), "Genetic Variation in Preferences for Giving and Risk Taking," *The Quarterly Journal of Economics*, 124(2), 809-42. <https://www.jstor.org/stable/40506244>.
- Chabris, Christopher F., James J. Lee, David Cesarini, Daniel J. Benjamin, David I. Laibson (2015), "The Fourth Law of Behavior Genetics," *Current Directions in Psychological Science*, 24 (4), 304-12. <http://doi.org/10.1177/0963721415580430>.
- Cheema, Amar, and Dilip Soman (2008), "The Effect of Partitions on Controlling Consumption," *Journal of Marketing Research*, 45(6), 665-75. <https://www.jstor.org/stable/20618855>.
- Cherry, Kendra (2022), "What is Behaviorism?" *Verywell Mind*, Accessed March 29, 2022. <https://www.verywellmind.com/behavioral-psychology-4157183>.
- Church, Kenneth, and Patrick Hanks (1990), "Word Association Norms, Mutual Information, and Lexicography," *Computational Linguistics*, 16(1), 22-9. Word association norms, mutual information, and lexicography (acm.org).
- Clithero, John A., Uma R. Karmarkar, and Ming Hsu (2021), "Toward an Integrative Conceptualization of Maladaptive Consumer Behavior," *Journal of the Association for Consumer Research*, 6(3),334-41. <https://doi.org/10.1086/714364>.
- Cloninger, C. Robert (1987), "Neurogenetic Adaptive Mechanisms in Alcoholism," *Science* 236(4800), 410-6. <https://www.jstor.org/stable/1698998>.

- Cloninger, CR1, P. Van Eerdewegh, A. Goate, H. J. Edenberg, J. Blangero, V. Hesselbrock, T. Reich et al. (1998), "Anxiety Proneness Linked to Epistatic Loci in Genome Scan of Human Personality Traits," *American Journal of Medical Genetics*, 81(4), 313-317. [https://doi.org/10.1002/\(SICI\)1096-8628\(19980710\)81:4<313::AID-AJMG7>3.0.CO;2-U](https://doi.org/10.1002/(SICI)1096-8628(19980710)81:4<313::AID-AJMG7>3.0.CO;2-U).
- Cohen, Jon. "CRISPR, the Revolutionary Genetic 'Scissors', Honored by Chemistry Nobel," *Science*, October 7, 2020, <https://www.science.org/content/article/crispr-revolutionary-genetic-scissors-honored-chemistry-nobel>.
- Cold Harbor Springs Laboratory. "Johann Gregor Mendel (1822-1884): Father of Genetics," *DNA From the Beginning*, Access March 29, 2022. Mendelas the Father of Genetics :: DNA from the Beginning (dnaftb.org).
- Collins, Francis S. (1999), "Medical and Societal Consequences of the Human Genome Project," *New England Journal of Medicine*, 341(1) 28-37. Medical and Societal Consequences of the Human Genome Project (nejm.org).
- Conklin, Edwin G. (1940) "Cell and Protoplasm Concepts: Historical Account," *The Cell and Protoplasm*, edited by FR Moulton, 6-19. Washington DC: The Science Press.
- Costas, Javier (2015), "A Genomic Approach to Alcoholism," *Adicciones*, 27(2), 87-9. <https://doi.org/10.20882/adicciones.693>.
- Cox, Dena, Anthony D. Cox, and George P. Moschis (1990), "When Consumer Behavior Goes Bad: An Investigation of Adolescent Shoplifting," *Journal of Consumer Research*, 17(2), 149-59. <https://www.jstor.org/stable/2626807>.
- Crick, Francis H. (1958) "On Protein Synthesis," *Symposia of the Society for Experimental Biology*, (12), 138-63.
- Cronqvist, Henrik, Florian Munkel, and Stephan Siegel (2014), "Genetics, Homeownership, and Home Location Choice," *The Journal of Real Estate Finance and Economics*, 48, 79-111. <http://doi.org/10.1007/s11146-012-9373-0>.
- Darden, Lindley, and Nancy Maull (1977), "Interfield Theories," *Philosophy of Science*, 44(1), 43-64. <https://www.jstor.org/stable/187099>.
- Daviet, Remi, Gideon Nave, and Jerry Wind (2022), "Genetic Data: Potential Uses and Misuses in Marketing," *Journal of Marketing*, 86(1), 7-26. <http://doi.org/10.1177/0022242920980767>.
- de Mooij, Marieke and Geert Hofstede (2011), "Cross-Cultural Consumer Behavior: A Review of Research Findings," *Journal of International Consumer Marketing*, 23: (3-4), 181-92. Full article: Cross-Cultural Consumer Behavior: A Review of Research Findings (tandfonline.com).

- de Villiers, Chantal Babb, Mark Kroese, and Sowmiya Moorthie (2020), "Understanding Polygenic Models, Their Development and the Potential Application of Polygenic Scores in Healthcare," *Journal of Medical Genetics*, 57(11), 725-32. <http://dx.doi.org/10.1136/jmedgenet-2019-106763>.
- Doudna, Jennifer A. and Emmanuelle Charpentier (2014), "The New Frontier of Genome Engineering with CRISPR-Cas9," *Science*, 346(6213), 1077-87. DOI: 10.1126/science.1258096.
- Doudna, Jennifer A. and Samuel Sternberg (2017), *A Crack in Creation: Gene Editing and the Unthinkable Power to Control Evolution*, New York: Houghton Mifflin Harcourt.
- Dudbridge, Frank (2013), "Power and Predictive Accuracy of Polygenic Risk Scores," *PLoS Genetics*, 9(3). Power and Predictive Accuracy of Polygenic Risk Scores.: EBSCOhost.
- Dunbar, Cynthia E., Katherine A. High, J. Keith Joung, Donald B. Kohn, Keiya Ozawa, and Michel Sadelain, (2018), "Gene Therapy Comes of Age," *Science*, 359(6372). DOI: 10.1126/science.aan4672
- Dunn, Erin C., Ruth C. Brown, Yael Dai, Jonathan Rosand, Nicole R. Nugent, Ananda B. Amstadter, and Jordan W. Smoller (2015), "Genetic Determinants of Depression: Recent Findings and Future Directions," *Harvard Review of Psychiatry*, 23(1), 1. doi: 10.1097/HRP.0000000000000054.
- Durme, Benjamin, and Ashwin Lall (2009), "Streaming Pointwise Mutual Information," *Advances in Neural Information Processing Systems* 22. Streaming Pointwise Mutual Information (neurips.cc).
- Eaves, Lindon J., and Hans J. Eysenck (1974), "Genetics and the Development of Social Attitudes," *Nature*, 249(5454), 288-9. <https://doi.org/10.1038/249288a0>.
- Edenberg, Howard J., and Tatiana Foroud (2006), "The Genetics of Alcoholism: Identifying Specific Genes Through Family Studies," *Addiction Biology*, 11(3-4), 386-96. <https://doi.org/10.1111/j.1369-1600.2006.00035.x>.
- Edenberg, Howard J., and Tatiana Foroud (2013), "Genetics and Alcoholism," *Nature Reviews Gastroenterology & Hepatology*, 10(8), 487-94. <https://doi.org/10.1038/nrgastro.2013.86>.
- Edenberg, Howard J., Joel Gelernter, and Arpana Agrawal (2019), "Genetics of Alcoholism," *Current Psychiatry Reports*, 21, 1-7. <https://doi.org/10.1007/s11920-019-1008-1>.
- ENCODE Project Consortium (2012), "An Integrated Encyclopedia of DNA Elements in the Human Genome," *Nature*, 489 (7414), 57. <https://doi.org/10.1038/nature11247>.

- Enoch, Mary-Anne (2013), "Genetic Influences on the Development of Alcoholism," *Current Psychiatry Reports* 15, 1-9. <https://doi.org/10.1007/s11920-013-0412-1>.
- Erevelles, Sunil, Kriti Bordia, Brian Whelan, Julia Canter, and Elise Guimont-Blackburn (2022), "Blockchain and the Transformation of Customer Co-creation," *Journal of Indian Business Research*, 14 (2), 88-107. <http://doi.org/10.1108/JIBR-03-2021-0085>.
- Erevelles, Sunil, Nobuyuki Fukawa, and Linda Swayne (2016), "Big Data Consumer Analytics and the Transformation of Marketing" *Journal of Business Research*, 69(2), 897-904. <https://doi.org/10.1016/j.jbusres.2015.07.001>.
- Erevelles, Sunil, Layne McGuire, and Anthony Erevelles (2022) "Genetic Data and the Transformation of Marketing" Paper presented at *Society for Marketing Advances: 2022 SMA Conference*, Charlotte, North Carolina, November 3, 2022.
- Erevelles, Sunil, Anthony Erevelles, Camelia Taheri, and Layne McGuire (2022) "The Genomics Blockchain," Paper presented at *Duke Center for Health Informatics*, Duke University School of Medicine, November 2, 2022.
- Euesden, Jack, Cathryn M. Lewis, and Paul F. O'Reilly (2015), "PRSice: Polygenic Risk Score Software," *Bioinformatics*, 31 (9), 1466-8. <https://doi.org/10.1093/bioinformatics/btu848>.
- Evans, David M and Nicholas G. Martin (2000), "The Validity of Twin Studies," *GeneScreen*, 1 (2), 77-79. <https://doi.org/10.1046/j.1466-9218.2000.00027.x>.
- Evitt, Niklaus H., Shamik Mascharak, and Russ B. Altman (2015), "Human Germline CRISPR-Cas Modification: Toward a Regulatory Framework," *The American Journal of Bioethics*, 15(12), 25-9. <https://doi.org/10.1080/15265161.2015.1104160>.
- Faber, Ronald J., Gary A. Christenson, Martina De Zwaan, and James Mitchell (1995), "Two Forms of Compulsive Consumption: Comorbidity of Compulsive Buying and Binge Eating," *Journal of Consumer Research*, 22(3), 296-304. <https://www.jstor.org/stable/2489615>.
- Faber, Ronald J., and Thomas C. O'Guinn (1992), "A Clinical Screener for Compulsive Buying," *Journal of Consumer Research*, 19(3), 459-69. <https://www.jstor.org/stable/2489402>.
- Farris, Sean P., Andrzej Z. Pietrzykowski, Michael F. Miles, Megan A. O'Brien, Pietro P. Sanna, Samir Zakhari, R. Dayne Mayfield, and R. Adron Harris (2015), "Applying the New Genomics to Alcohol Dependence," *Alcohol*, 49(8), 825-36. <https://doi.org/10.1016/j.alcohol.2015.03.001>.
- Feick, Lawrence F., and Linda L. Price (1987), "The Market Maven: A Diffuser of Marketplace Information," *Journal of Marketing*, 51(1), 83-97. <https://doi.org/10.2307/1251146>.

- Finegold, David N. (2021), "Overview of Genetics," In *Merck Manual Professional Version*, Accessed July 20, 2022. Overview of Genetics - Special Participants - Merck Manuals Professional Edition.
- Firestein, Stuart (2012), *Ignorance: How it Drives Science*, New York: Oxford University Press.
- Fisher, Ronald A. (1919), "XV. —The Correlation Between Relatives on the Supposition of Mendelian Inheritance," *Earth and Environmental Science Transactions of the Royal Society of Edinburgh*, 52(2), 399-433. 9.pdf (adelaide.edu.au).
- Frankwick, Gary L., Beth A. Walker, and James C. Ward (1994), "Belief structures in conflict: Mapping a strategic marketing decision," *Journal of Business Research*, 31(2-3), 183-95. [https://doi.org/10.1016/0148-2963\(94\)90082-5](https://doi.org/10.1016/0148-2963(94)90082-5).
- Francis, Richard C. (2012), *Epigenetics: How Environment Shapes our Genes*, New York: W.W. Norton.
- Friend, Angela, John C. DeFries, and Richard K. Olson (2008), "Parental Education Moderates Genetic Influences on Reading Disability," *Psychological Science*, 19(11), 1124-30. <https://www.jstor.org/stable/40064899>.
- Fukawa, Nobuyuki, and Sunil Erevelles (2014), "Perceived Reasonableness and Morals in Service Encounters." *Journal of Business Ethics*, 125(3), 381-400. <https://doi.org/10.1007/s10551-013-1918-5>.
- Galton, Francis (1875), "The History of Twins, As a Criterion of the Relative Powers of Nature and Nurture," *Fraser's Magazine*, 12, 566–76, Accessed March 26, 2022. <http://galton.org/essays/1870-1879/galton-1875-history-twins.pdf> .
- Garcia, Justin R., James MacKillop, Edward L. Aller, Ann M. Merriwether, David Sloan Wilson, and J. Koji Lum (2010), "Associations Between Dopamine D4 Receptor Gene Variation with Both Infidelity and Sexual Promiscuity, " *PLOS One* 5(11), e14162. doi:10.1371/journal.pone.0014162.
- Gayon, Jean (2016), "From Mendel to Epigenetics: History of Genetics," *Comptes Rendus Biologies*, 339(7-8), 225-30. <https://doi.org/10.1016/j.crv.2016.05.009>
- Gene Heritage, "What is Raw DNA Data?", Accessed August 18, 2022. What is Raw DNA Data? (geneheritage.com).
- Goenka, Shreyans, and Stijn MJ Van Osselaer (2023), "Why Is It Wrong to Sell Your Body? Understanding Liberals' Versus Conservatives' Moral Objections to Bodily Markets," *Journal of Marketing*, 87(1), 64-80. <https://doi.org/10.1177/00222429211046936>.

- Gomes Alcoforado, Daniela, and Francisco Vicente Sales Melo (2021), "Depression in Consumer Research: an Integrative Review and Research Agenda." *ACR North American Advances*. <http://www.acrwebsite.org/volumes/3000414/volumes/v49/NA-49>.
- Gonçalves, Giulliana, Augusta Rangel, and Raquel de Melo Alves Paiva (2017), "Gene Therapy: Advances, Challenges and Perspectives," *Einstein (Sao Paulo)*, 15(2017): 369-75. doi: 10.1590/S1679-45082017RB4024.
- Green, Eric D., James D. Watson, and Francis S. Collins (2015), "Human Genome Project: Twenty-five Years of Big Biology," *Nature* 526, (7571), 29-31. <https://doi.org/10.1038/526029a>.
- Greenspan, Ralph J (2008), "The Origins of Behavioral Genetics," *Current Biology* 18(5), 192-8. <https://doi.org/10.1016/j.cub.2008.01.015>.
- Gregory-Smith, Diana, and Danae Manika (2017), "Consumers' Identities and Compartmentalisation Tendencies in Alcohol Consumption," *Journal of Marketing Management*, 33(11-12), 942-72. <https://doi.org/10.1080/0267257X.2017.1310126>.
- Grilo, Carlos M., and Michael F. Pogue-Geile (1991), "The Nature of Environmental Influences on Weight and Obesity: A Behavior Genetic Analysis," *Psychological Bulletin*, 110(3), 520. <http://dx.doi.org/10.1037/0033-2909.110.3.520>.
- Grishin, Dennis, Kamal Obbad, and George M. Church (2019), "Data Privacy in the Age of Personal Genomics," *Nature Biotechnology*, 37(10), 1115-7. <https://doi.org/10.1038/s41587-019-0271-3>.
- Harden, Paige K & Philipp D. Koellinger (2020), "Using Genetics for Social Science," *Nature: Human Behavior* 4, (6), 567-76. <https://doi.org/10.1038/s41562-020-0862-5>.
- Haworth, Claire MA, and Robert Plomin (2010), "Quantitative Genetics in the Era of Molecular Genetics: Learning Abilities and Disabilities As an Example," *Journal of the American Academy of Child & Adolescent Psychiatry*, 49(8),783-93. <https://doi.org/10.1016/j.jaac.2010.01.026>.
- Haworth, Claire MA, Oliver SP Davis, and Robert Plomin (2012), "Twins Early Development Study (TEDS): A Genetically Sensitive Investigation of Cognitive and Behavioral Development from Childhood to Young Adulthood," *Twin Research and Human Genetics*, 16(1), 117-25. <https://doi.org/10.1017/thg.2012.91>.
- Haworth, Catherine MA, Margaret J. Wright, Michelle Luciano, Nicholas G. Martin, Eco JC de Geus, Catharina EM van Beijsterveldt, Meike Bartels, et al. (2010), "The Heritability of General Cognitive Ability Increases Linearly from Childhood to Young Adulthood," *Molecular Psychiatry*, 15(11), 1112-20. <https://doi.org/10.1038/mp.2009.55>.

- Hirsch, Francois, Ron Iphofen, and Zvonimir Koporc (2019), "Ethics Assessment in Research Proposals Adopting CRISPR Technology," *Biochemia Medica*, 29(2), 206-13. <https://doi.org/10.11613/BM.2019.020202>.
- Hirschman, Elizabeth C. (1992), "The Consciousness of Addiction: Toward a General Theory of Compulsive Consumption," *Journal of Consumer Research*, 19(2), 155-79. <https://www.jstor.org/stable/2489326>.
- Hirschman, Elizabeth C., and Barbara B. Stern (2001), "Do Consumers' Genes Influence Their Behavior? Findings on Novelty Seeking and Compulsive Consumption," In *Advances in Consumer Research Volume 28*, edited by Mary C. Gilly and Joan Meyers-Levy, 403-10. Valdosta, GA: Association for Consumer Research. Do Consumers' Genes Influence Their Behavior? Findings on Novelty Seeking and Compulsive Consumption | ACR (acrwebsite.org).
- Hoekstra, Rosa A., Meike Bartels, and Dorret I. Boomsma (2007), "Longitudinal Genetic Study of Verbal and Nonverbal IQ from Early Childhood to Young Adulthood," *Learning and Individual Differences*, 17(2), 97-114. <https://doi.org/10.1016/j.lindif.2007.05.005>.
- Hofacker, Charles F., Edward Carl Malthouse, and Fareena Sultan (2016), "Big Data and Consumer Behavior: Imminent Opportunities," *Journal of Consumer Marketing*, 33(2), 89-97. <https://doi.org/10.1108/JCM-04-2015-1399>.
- Hoffman, Donna, C. Page Moreau, Stefan Stremersch, and Michel Wedel (2022), "The Rise of New Technologies in Marketing: A framework and Outlook," *Journal of Marketing*, 86(1), 1-6. <https://doi.org/10.1177/00222429211061636>.
- Horowitz, N. H. (1948), "The One Gene-One Enzyme Hypothesis," *Genetics*, 33 (6), 612. <https://pubmed.ncbi.nlm.nih.gov/18207813/>.
- Hunt, Shelby D. (2011), "On The Intersection of Marketing History and Marketing Theory." *Marketing Theory*, 11(4), 483-9. <https://doi.org/10.1177/1470593111418802>.
- Hunt, Shelby D. (2011), "Theory Status, Inductive Realism, and Approximate Truth: No Miracles, No Charades" *International Studies in the Philosophy of Science*, 25(2), 159-78. <https://doi.org/10.1080/02698595.2011.574858>.
- Hunt, Shelby D (2013), "The Inductive Realist Model of Theory Generation: Explaining the Development of a Theory of Marketing Ethics," *Academy of Marketing Science Review*, 3(2), 61-73. <https://doi.org/10.1007/s13162-013-0040-2>.
- Hunt, Shelby D. (2020), "Indigenous Theory Development in Marketing: The Foundational Premises Approach," *Academy of Marketing Science Review*, 10, 8-17. <https://doi.org/10.1007/s13162-020-00165-w>.

- Inouye, Michael, Gad Abraham, Christopher P. Nelson, Angela M. Wood, Michael J. Sweeting, Frank Dudbridge, Florence Y. Lai et al. (2018), "Genomic Risk Prediction of Coronary Artery Disease in 480,000 Adults: Implications for Primary Prevention," *Journal of the American College of Cardiology*, 72(16), 1883-93.
<https://doi.org/10.1016/j.jacc.2018.07.079>.
- Ioannidis, John PA. (2005), "Why Most Published Research Findings are False, " *PLoS Medicine*, 2(8), 0696-0701.
<https://doi.org/10.1371/journal.pmed.0020124>.
- Isaacson, Walter (2021), *The Codebreaker: Jennifer Doudna, Gene Editing, and the Future of the Human Race*, New York: Simon & Schuster.
- Jacob, Raphaëlle, Vicky Drapeau, Angelo Tremblay, Véronique Provencher, Claude Bouchard, and Louis Pérusse (2018), "The Role of Eating Behavior Traits in Mediating Genetic Susceptibility to Obesity," *The American Journal of Clinical Nutrition*, 108(3), 445-52.
<https://doi.org/10.1093/ajcn/nqy130>.
- Jacoby, Jacob (1978), "Consumer Research: How Valid and Useful Are All Our Consumer Behavior Research Findings? A State of the Art Review," *Journal of Marketing*, 42(2), 87-96. <https://doi.org/10.2307/1249890>.
- The Jackson Laboratory. "Minute to Understanding: What is a Chromosome?" Accessed August 18, 2022. What is a chromosome and what does it do? Find out in this Minute to Understanding from the Jackson Laboratory! (jax.org)
- Jang, Kerry L., W. John Livesley, and Philip A. Vernon (1996), "Heritability of the Big Five Personality Dimensions and Their Facets: A Twin Study," *Journal of Personality*, 64(3), 577-92. <https://doi.org/10.1111/j.1467-6494.1996.tb00522.x>
- J. Craig Venter Institute, "Overview, JCVI Fact Sheet" *JCVI: J. Craig Venter Institute*, Accessed June 14, 2022, <https://www.jcvi.org/sites/default/files/assets/news/JCVI-Fact-Sheet.pdf>.
- Johnson, Wendy, Eric Turkheimer, Irving I. Gottesman, and Thomas J. Bouchard Jr. (2009), "Beyond Heritability: Twin Studies in Behavioral Research," *Current Directions in Psychological Science*, 18(4), 217-20. <https://www.jstor.org/stable/20696034>.
- Kahn, Scott D. (2011), "On the Future of Genomic Data," *Science*, 331(6018), 728-9. DOI: 10.1126/science.1197891.
- Kaiser, Jocelyn (2016), "The Gene Editor CRISPR Won't Fully Fix Sick People Anytime Soon. Here's Why", *Science*, May 3, 2016. Accessed July 28, 2022.
 Doi:10.1126/science.aaf5689.
- Kaur, Sukhvinder, Arif Ali, Uzair Ahmad, Yaser Siahbalei, A. K. Pandey, and Balkirat Singh (2019), "Role of Single Nucleotide Polymorphisms (SNPs) in Common Migraine," *The*

- Egyptian Journal of Neurology, Psychiatry and Neurosurgery*, 55(1),1-7.
<https://doi.org/10.1186/s41983-019-0093-8>.
- Kean, Sam (2012), *The Violinist's Thumb: And Other Lost Tales of Love, War, and Genius, As Written By Our Genetic Code*, New York: Little, Brown and Company.
- Keeney, Ralph L. (2008), "Personal Decisions are the Leading Cause of Death," *Operations Research*, 56(6), 1335-47. <https://www.jstor.org/stable/25580892>.
- Kendler, Kenneth S. and Jessica H. Baker (2007), "Genetic Influences on Measures of the Environment: A Systematic Review," *Psychological Medicine*, 37 (5), 615-26.
<https://doi.org/10.1017/S0033291706009524>.
- Key, Thomas Martin, Terry Clark, O. C. Ferrell, David W. Stewart, and Leyland Pitt (2020), "Marketing's Theoretical and Conceptual Value Proposition: Opportunities to Address Marketing's Influence," *AMS Review*, 10, 151-67. <https://doi.org/10.1007/s13162-020-00176-7>.
- Khera, Amit V., Mark Chaffin, Krishna G. Aragam, Mary E. Haas, Carolina Roselli, Seung Hoan Choi, Pradeep Natarajan, et al. (2018), "Genome-wide Polygenic Scores for Common Diseases Identify Individuals With Risk Equivalent to Monogenic Mutations," *Nature genetics*, 50(9), 1219-24. <https://doi.org/10.1038/s41588-018-0183-z>.
- Khera, Amit V., Connor A. Emdin, Isabel Drake, Pradeep Natarajan, Alexander G. Bick, Nancy R. Cook, Daniel I. Chasman et al. (2016), "Genetic Risk, Adherence to a Healthy Lifestyle, and Coronary Disease," *New England Journal of Medicine*, 375(24), 2349-58.
<https://doi.org/10.1056/NEJMoa1605086>.
- Krych, Raymond (1989), "Abnormal Consumer Behavior: A Model of Addictive Behaviors," *ACR North American Advances*. Abnormal Consumer Behavior: a Model of Addictive Behaviors | ACR (acrwebsite.org)
- Lambert, Samuel A., Laurent Gil, Simon Jupp, Scott C. Ritchie, Yu Xu, Annalisa Buniello, Aoife McMahon, et al. (2021), "The Polygenic Score Catalog as An Open Database for Reproducibility and Systematic Evaluation," *Nature Genetics*, 53(4), 420-5.
<https://doi.org/10.1038/s41588-021-00783-5>.
- Landis, J. Richard, and Gary G. Koch (1977), "The Measurement of Observer Agreement for Categorical Data," *Biometrics*, 33(1), 159-174. <https://doi.org/10.2307/2529310>.
- Lau, Cia-Hin, and Yousin Suh (2017), "In Vivo Genome Editing in Animals Using AAV-CRISPR System: Applications to Translational Research of Human Disease," *F1000Research*, 6 (2017), 1-21. doi: 10.12688/f1000research.11243.1.
- Ledford, Heidi (2019), "CRISPR Babies: When Will the World Be Ready?" *Nature*, 570 (7761), 293-6. <https://doi.org/10.1038/d41586-019-01906-z>.

- Lee, James J., Robbee Wedow, Aysu Okbay, Edward Kong, Omeed Maghzian, Meghan Zacher, Tuan Anh Nguyen-Viet, et al. (2018), "Gene Discovery and Polygenic Prediction from a Genome-Wide Association Study of Educational Attainment in 1.1 Million Individuals," *Nature Genetics*, 50(8), 1112-21. <https://doi.org/10.1038/s41588-018-0147-3>.
- Lesieur, Henry, Sheila Blume, and Richard M. Zoppa (1986), "Alcoholism, Drug Abuse, and Gambling," *Alcoholism: Clinical and Experimental Research*, 10(1), 33-8. <https://doi.org/10.1111/j.1530-0277.1986.tb05610.x>.
- Lewis, Cathryn M., and Evangelos Vassos (2020), "Polygenic Risk Scores: from Research Tools to Clinical Instruments," *Genome Medicine*, 12(1), 1-11. <https://doi.org/10.1186/s13073-020-00742-5>.
- Li, Ming D. (2006), "The Genetics of Nicotine Dependence," *Current Psychiatry Reports*, 8(2), 158-164. <https://doi.org/10.1007/s11920-006-0016-0>.
- Lin, Bochao D., Gonneke Willemsen, Abdel Abdellaoui, Meike Bartels, Erik A. Ehli, Gareth E. Davies, Dorret I. Boomsma, and Jouke J. Hottenga (2016), "The Genetic Overlap Between Hair and Eye Color," *Twin Research and Human Genetics*, 19(6), 595-9. <https://doi.org/10.1017/thg.2016.85>.
- Linnér, Richard Karlsson, Travis T. Mallard, Peter B. Barr, Sandra Sanchez-Roige, James W. Madole, Morgan N. Driver, Holly E. Poore et al. (2012), "Multivariate Analysis of 1.5 Million People Identifies Genetic Associations With Traits Related to Self-Regulation and Addiction," *Nature Neuroscience*, 24(10), 1367-76. <https://doi.org/10.1038/s41593-021-00908-3>.
- Litman, Simon (1950), "The Beginnings of Teaching Marketing in American Universities," *Journal of Marketing*, 15(2), 220-3. <https://doi.org/10.2307/1247670>.
- Mack, T. M., Hamilton, A. S., Press, M. F., Diep, A., & Rappaport, E. B. (2002), "Heritable Breast Cancer in Twins," *British Journal of Cancer*, 87(3), 294-300. <https://doi.org/10.1038/sj.bjc.6600429>.
- Malaty, Hoda M, David Graham, Inger Isaksson, Lars Engstrand, and Nancy Pedersen (2000), "Are Genetic Influences on Peptic Ulcer Dependent or Independent of Genetic Influences for Helicobacter Pylori Infection?" *Archives of Internal Medicine*, 160(1), 105-9. doi: 10.1001/archinte.160.1.105.
- Malone John C. (2014), "Did John B. Watson Really 'Found' Behaviorism?" *The Behavior Analyst*, 37(1), 1–12. <https://doi.org/10.1007/s40614-014-0004-3>
- Manolio, Teri A., Francis S. Collins, Nancy J. Cox, David B. Goldstein, Lucia A. Hindorff, David J. Hunter, Mark I. McCarthy et al. (2009), "Finding the Missing Heritability of Complex Diseases," *Nature* 461(7265), 747-53. 10.1038/nature08494.

- Maas, Heike, and Frank M. Spinath (2012), "Personality and Coping with Professional Demands: A Behavioral Genetics Analysis," *Journal of Occupational Health Psychology*, 17(3), 376-85. <http://doi.org/10.1037/a0027641>.
- Mahner, Martin, and Michael Kary (1997), "What Exactly are Genomes, Genotypes and Phenotypes? And What About Phenomes?" *Journal of Theoretical Biology*, 186(1), 55-63. <https://doi.org/10.1006/jtbi.1996.0335>.
- Malin, Bradley A. (2005), "An Evaluation of the Current State of Genomic Data Privacy Protection Technology and a Roadmap for the Future," *Journal of the American Medical Informatics Association*, 12(1), 28-34. <https://doi.org/10.1197/jamia.M1603>.
- Malthus, Thomas R. (1798), *An Essay on the Principle of Population*, London: A Public Domain Book. <http://www.esp.org/books/malthus/population/malthus.pdf>.
- Manousaki, Despoina, Vincenzo Forgetta, Julyan Keller-Baruch, Kaiqiong Zhao, Celia MT Greenwood, Vincent Mooser, JH Duncan Bassett, et al., "A Polygenic Risk Score as a Risk Factor for Medication-Associated Fractures," *Journal of Bone and Mineral Research*, 35(10), 1935-41. <https://doi.org/10.1002/jbmr.4104>.
- Manyiwa, Simon, and Ross Brennan (2012), "Fear Appeals in Anti-Smoking Advertising: How Important is Self-Efficacy?" *Journal of Marketing Management*, 28(11-12), 1419-37. <https://doi.org/10.1080/0267257X.2012.715092>.
- Martin, Ingrid M., Michael A. Kamins, Dante M. Pirouz, Scott W. Davis, Kelly L. Haws, Ann M. Mirabito, Sayantani Mukherjee, et al. (2013), "On the Road to Addiction: The Facilitative and Preventive Roles of Marketing Cues," *Journal of Business Research*, 66(8), 1219-26. <https://doi.org/10.1016/j.jbusres.2012.08.015>.
- Maté, Gabor (2010), *In the Realm of Hungry Ghosts: Close Encounters with Addiction*, Berkeley: North Atlantic Books.
- Mathaiyan, Jayanthi, Adithan Chandrasekaran, and Sanish Davis (2013), "Ethics of Genomic Research," *Perspectives in Clinical Research*, 4(1), 100-4. Ethics of genomic research - PMC (nih.gov).
- Maynard, Harold H. (1941), "Marketing Courses Prior to 1910," *Journal of Marketing*, 5(4), 382-4. <https://doi.org/10.2307/1245554>.
- McCain, Katherine, and Kathleen Turner (1989), "Citation Context Analysis and Aging Patterns of Journal Articles in Molecular Genetics," *Scientometrics*, 17(1-2), 127-163. <https://doi.org/10.1007/BF02017729>.

- McEvoy, Brian P., and Peter M. Visscher (2009), "Genetics of Human Height," *Economics & Human Biology*, 7(3), 294-306. <https://doi.org/10.1016/j.ehb.2009.09.005>.
- McGue, Matt, and Kaare Christensen (2013), "Growing Old But Not Growing Apart: Twin Similarity in the Latter Half of the Lifespan," *Behavior Genetics*, 43(1), 1-12. <https://doi.org/10.1007/s10519-012-9559-5>.
- Meehl, Paul E. (1978), "Theoretical Risks and Tabular Asterisks: Sir Karl, Sir Ronald, and the Slow Progress of Soft Psychology." *Journal of Consulting and Clinical Psychology*, 46, 806-34. Theoretical Risks and Tabular Asterisks:.
- Mendel, Gregor, (Available online (1996), "Experiments in Plant Hybridization (1865)," *Verhandlungen des Naturforschenden Vereins Brünn*, 1-39. gm-65-a.pdf (esp.org).
- Merriam-Webster. (n.d.), "Behavioral," In *Merriam-Webster.com*, Accessed March 26, 2022, <https://www.merriam-webster.com/dictionary/behavioral>.
- Merriam-Webster. (n.d). "Gene," In *Merriam-Webster.com*, Accessed March 26, 2022, <https://www.merriam-webster.com/dictionary/gene>.
- Merriam-Webster. (n.d), "Trait," In *Merriam-Webster.com*, Accessed March 26, 2022, <http://www.merriam-webster.com/dictionary/trait>.
- Merriman, Curtis. "The intellectual resemblance of twins", *Psychological Monographs* 33, no. 5 (1924): i. <https://doi.org/10.1037/h0093212>.
- Middleton, Anna, Richard Milne, Mohamed A. Almarri, Shamim Anwer, Jerome Atutornu, Elena E. Baranova, Paul Bevan et al. (2020), "Global Public Perceptions of Genomic Data Sharing: What Shapes the Willingness to Donate DNA and Health Data?" *The American Journal of Human Genetics*, 107(4), 743-52. <https://doi.org/10.1016/j.ajhg.2020.08.023>.
- Miller, Madeline (2012), *The Song of Achilles*, New York: HarperCollins Publishers Inc.
- Möller, Sören, Lorelei A. Mucci, Jennifer R. Harris, Thomas Scheike, Klaus Holst, Ulrich Halekoh, Hans-Olov Adami et al. (2016), "The Heritability of Breast Cancer Among Women in the Nordic Twin Study of Cancer", *Cancer Epidemiology, Biomarkers & Prevention*, 25(1), 145-50. <https://doi.org/10.1158/1055-9965.EPI-15-0913>.
- Moore, David S. (2015), *The Developing Genome: An Introduction to Behavioral Epigenetics*, New York: Oxford University Press.
- Moore, Gordon E. (1965), "Cramming More Components Onto Integrated Circuits," *Electronics*, 38(8), 114-7. moores paper (weka-fachmedien.de).

- Moorman, Christine, Harald J. van Heerde, C. Page Moreau, and Robert W. Palmatier (2022), "From Vision to Reality: Lessons in Creating a Marketplace of Ideas." *Journal of Marketing*, 86(6), 4-12. <https://doi.org/10.1177/00222429221129661>.
- Montessori, Maria (1959), *The Absorbent Mind*, New York: Start Publishing, 2012. Kindle
- Morgan, Thomas Hunt (1917), "The Theory of the Gene," *The American Naturalist*, 51(609), 513-44. <https://www.jstor.org/stable/2456204>.
- Moschis, George P. (2007), "Stress and Consumer Behavior," *Journal of the Academy of Marketing Science*, 35, 430-444. <https://doi.org/10.1007/s11747-007-0035-3>.
- Mukherjee, Siddhartha (2016), *The Gene: An Intimate History*, New York: Simon & Schuster Inc.
- Nagel, Ronald L. (2005). "Epistasis and the Genetics of Human Diseases," *Comptes Rendus Biologies*, 328(7), 606-15. <https://doi.org/10.1016/j.crv.2005.05.003>.
- Nanda, Ambika Prasad, and Ranjan Banerjee (2021), "Consumer's Subjective Financial Well-being: A Systematic Review and Research Agenda," *International Journal of Consumer Studies*, 45(4), 750-76. <https://doi.org/10.1111/ijcs.12668>.
- National Cancer Institute, *NCI Dictionary of Genetic Terms*, Accessed March 26, 2022. www.cancer.gov/publications/dictionaries/genetics-dictionary/expand/G.
- National Human Genome Research Institute, "Chromosome Fact Sheet" *National Institutes of Health, National Human Genome Research Institute*, Accessed June 14, 2022. Chromosomes Fact Sheet (genome.gov).
- National Human Genome Research Institute, "Double Helix" *National Institutes of Health, National Human Genome Research Institute*, Accessed April 20, 2023. Double Helix (genome.gov).
- National Human Genome Research Institute, "Epistasis" *National Institutes of Health, National Human Genome Research Institute*, Accessed April 15, 2023. Epistasis (genome.gov).
- National Human Genome Research Institute, "Eugenics: Its Origin and Development (1883-Present)" *National Institutes of Health, National Human Genome Research Institute*, Accessed June 14, 2022. <https://www.genome.gov/about-genomics/educational-resources/timelines/eugenics>.
- National Human Genome Research Institute, "Gene," *National Institutes of Health, National Human Genome Research Institute*, Accessed March 26, 2022. Gene (genome.gov).

National Human Genome Research Institute, “Genetic Map,” *National Institutes of Health, National Human Genome Research Institute*, Accessed July 21, 2023. Genetic Map (genome.gov).

National Human Genome Research Institute, “Genetic Marker,” *National Institutes of Health, National Human Genome Research Institute*, Accessed April 20, 2023. Genetic Marker (genome.gov).

National Human Genome Research Institute, “Genetics Timeline,” *National Institutes of Health, National Human Genome Research Institute*, Accessed June 13, 2022. <https://www.genome.gov/about-genomics/teaching-tools/Genetic-Timeline>.

National Human Genome Research Institute, “Genome-Wide Association Studies (GWAS),” *National Institutes of Health, National Human Genome Research Institute*, Accessed July 21, 2022. Genome-Wide Association Studies (GWAS).

National Human Genome Research Institute, “Genomics,” *National Institutes of Health, National Human Genome Research Institute*, Accessed July 21, 2022. Genomics (genome.gov).

National Human Genome Research Institute, “Human Genome Project Timeline of Events,” *National Institutes of Health, National Human Genome Research Institute*, Accessed June 13, 2022. <https://www.genome.gov/human-genome-project/Timeline-of-Events>.

National Human Genome Research Institute, “Genomic Data Science,” *National Institutes of Health, National Human Genome Research Institute*, Accessed August 19, 2022. Genomic Data Science Fact Sheet (genome.gov).

National Human Genome Research Institute, “Locus,” *National Institutes of Health, National Human Genome Research Institute*, Accessed April 15, 2023. Locus (genome.gov).

National Human Genome Research Institute, “Messenger RNA(mRNA),” *National Institutes of Health, National Human Genome Research Institute*, Accessed August 28, 2022. Messenger RNA (mRNA) (genome.gov).

National Human Genome Research Institute, “Polygenic Risk Scores,” *National Institutes of Health, National Human Genome Research Institute*, Accessed October 6, 2022. Polygenic Risk Scores (genome.gov).

National Institute on Drug Abuse, “Genetics and Epigenetics of Addiction Drug Facts,” *National Institutes of Health, National Institute on Drug Abuse*, Accessed February 2, 2023. <https://nida.nih.gov/publications/drugfacts/genetics-epigenetics-addiction>.

National Institute of General Medical Sciences, “Genetics” *National Institutes of Health, National Institute of General Medical Sciences*, Accessed July 21, 2022. Genetics (nih.gov).

- National Library of Medicine, "How is Genetic Testing Done?" *National Institutes of Health, National Library of Medicine*, Accessed July 13, 2022. How is genetic testing done?: MedlinePlus Genetics.
- National Library of Medicine, "What are Proteins and What Do They Do?" *National Institutes of Health, National Library of Medicine*, Accessed July 21, 2022. What are proteins and what do they do?: MedlinePlus Genetics.
- National Library of Medicine, "What are Single Nucleotide Polymorphisms (SNPs)?" *National Institutes of Health, National Library of Medicine*, Accessed April 20, 2023. What are single nucleotide polymorphisms (SNPs)?: MedlinePlus Genetics.
- National Library of Medicine, "What Can Raw Data From a Direct-to-Consumer Genetic Test Tell Me?" *National Institutes of Health, National Library of Medicine*, Accessed August 18, 2022. What can raw data from a direct-to-consumer genetic test tell me?: MedlinePlus Genetics.
- National Library of Medicine, "What is DNA?" *National Institutes of Health, National Library of Medicine*, Accessed August 18, 2022. What is DNA?: MedlinePlus Genetics.
- National Library of Medicine Genome Research Institute, "Human Genome Project Timeline of Events." Timeline," *National Institutes of Health, National Human Genome Research Institute*, Accessed June 13, 2022. <https://www.genome.gov/human-genome-project/Timeline-of-Events>.
- National Library of Medicine, "What Are Genome Editing and CRISPR-CAS9?" *National Institutes of Health, National Library of Medicine*, Accessed August 26, 2022. What are genome editing and CRISPR-Cas9?: MedlinePlus Genetics
- Niemiec, Emilia, and Heidi Carmen Howard (2016), "Ethical Issues in Consumer Genome Sequencing: Use of Consumers' Samples and Data," *Applied & Translational Genomics* 8, 23-30. <https://doi.org/10.1016/j.atg.2016.01.005>.
- Nguyen, Tuan V., and John A. Eisman (2020), "Post-GWAS Polygenic Risk Score: Utility and Challenges," *Journal of Bone and Mineral Research Plus*, 4(11), 1-5. <https://doi.org/10.1002/jbm4.10411>.
- November, Joseph (2018), "More than Moore's Mores: Computers, Genomics, and the Embrace of Innovation," *Journal of the History of Biology*, 51(4), 807-40. <https://www.jstor.org/stable/44980449>.
- O'Guinn, Thomas C., and Ronald J. Faber (1989), "Compulsive Buying: A Phenomenological Exploration," *Journal of Consumer Research*, 16(2), 147-57. <https://www.jstor.org/stable/2489314>.

- Olson, James M., Philip A. Vernon, Julie Aitken Harris, and Kerry L. Jang (2001), "The Heritability of Attitudes: A Study of Twins," *Journal of Personality and Social Psychology*, 80(6), 845. <https://doi.org/10.1037/0022-3514.80.6.845>.
- Onnis, Luca (2017), "Caregiver Communication to the Child as Moderator and Mediator of Genes for Language", *Behavioural Brain Research*, 325:197-202. <https://doi.org/10.1016/j.bbr.2017.02.003>.
- Orgogozo, Virginie, Baptiste Morizot, and Arnaud Martin (2015), "The Differential View of Genotype–Phenotype Relationships," *Frontiers in Genetics*, 6(179),1-14. <https://doi.org/10.3389/fgene.2015.00179>.
- Orphanides, George, and Danny Reinberg (2002), "A Unified Theory of Gene Expression," *Cell*, 108(4), 439-451. [https://doi.org/10.1016/S0092-8674\(02\)00655-4](https://doi.org/10.1016/S0092-8674(02)00655-4).
- Ozimec, Ana-Marija, Martin Natter, and Thomas Reutterer (2010), "Geographical Information Systems—Based Marketing Decisions: Effects of Alternative Visualizations on Decision Quality," *Journal of Marketing*, 74(6), 94-110. <https://www.jstor.org/stable/25764285>.
- Ozercan, Halil Ibrahim, Atalay Mert Ileri, Erman Ayday, and Can Alkan (2018), "Realizing the Potential of Blockchain Technologies in Genomics," *Genome Research*, 28(9), 1255-63. <https://doi.org/10.1101/gr.207464.116>.
- Paulhus, Delroy L., Paul D. Trapnell, and David Chen (1999), "Birth Order Effects on Personality and Achievement Within Families," *Psychological Science*, 10 (6), 482-8. <https://doi.org/10.1111/1467-9280.00193>.
- Pawlowski, Suzanne D., Evgeny A. Kaganer, and John J. Cater III (2007), "Focusing the Research Agenda on Burnout in IT: Social Representations of Burnout in the Profession," *European Journal of Information Systems*, 16(5), 612-27. <https://doi.org/10.1057/palgrave.ejis.3000699>.
- Pearson, Helen (2006). "What is a Gene?" *Nature* 441(7092), 398-402. <https://doi.org/10.1038/441398a>.
- Peighambari, Kaveh, Setayesh Sattari, Arash Kordestani, and Pejvak Oghazi (2016), "Consumer Behavior Research: A Synthesis of the Recent Literature," *Sage Open*, 6(2), 1-9. <https://doi.org/10.1177/2158244016645638>.
- Penders, Bart, and A. Cecile JW Janssens (2022), "Do We Measure or Compute Polygenic Risk Scores? Why Language Matters," *Human Genetics*, 141(5), 1093-7. <https://doi.org/10.1007/s00439-021-02262-7>.
- Petty, Richard E., and John T. Cacioppo (1996), "Addressing Disturbing and Disturbed Consumer Behavior: Is it Necessary to Change the Way We Conduct Behavioral Science?" *Journal of Marketing Research*, 33(1),1-8. <https://doi.org/10.2307/3152008>.

- Pich, Christopher, Dianne Dean, and Khanyapuss Punjaisri (2016), "Political Brand Identity: An Examination of the Complexities of Conservative Brand and Internal Market Engagement During the 2010 UK General Election Campaign," *Journal of Marketing Communications*, 22(1), 100-17. <https://doi.org/10.1080/13527266.2013.864321>.
- Phillips, Patrick C. (1998), "The Language of Gene Interaction," *Genetics*, 149(3), 1167-71. <https://doi.org/10.1093/genetics/149.3.1167>.
- Polderman, Tinca JC, Beben Benyamin, Christiaan A. De Leeuw, Patrick F. Sullivan, Arjen Van Bochoven, Peter M. Visscher, and Danielle Posthuma (2015), "Meta-analysis of the Heritability of Human Traits Based on Fifty Years of Twin Studies," *Nature Genetics*, 47(7), 702-9. <https://doi.org/10.1038/ng.3285>.
- Pope, Alexander (1734), "An Essay on Man: Epistles II," In *The Collected Major Works*, Colombia, South Carolina; Annotated Editions.
- Plomin, Robert (2019), *Blueprint: How DNA Makes Us Who We Are*, Cambridge: The MIT Press.
- Plomin, Robert (1986), "Multivariate Analysis and Developmental Behavioral Genetics: Developmental Change as Well as Continuity," *Behavior Genetics*, 16(1), 25-43. <https://doi.org/10.1007/BF01065477>.
- Plomin, Robert (1990), "The Role of Inheritance in Behavior," *Science*, 248 (4952), 183-88. DOI: 10.1126/science.2183351.
- Plomin, Robert (2023), "Celebrating a Century of Research in Behavioral Genetics," *Behavior Genetics*, 53, 75-84. <https://doi.org/10.1007/s10519-023-10132-3>.
- Plomin, Robert, and Cindy S. Bergeman (1991), "The Nature of Nurture: Genetic Influence on 'Environmental' Measures," *Behavioral and Brain Sciences*, 14(3), 373-86. <https://doi.org/10.1017/S0140525X00070278>.
- Plomin, Robert, and Ian Craig (1997), "Human Behavioural Genetics of Cognitive Abilities and Disabilities," *Bioessays*, 19(12), 1117-24. <https://doi.org/10.1002/bies.950191211>.
- Plomin, Robert, and Oliver SP Davis (2009), "The Future of Genetics in Psychology and Psychiatry: Microarrays, Genome-wide Association, and Non-Coding RNA," *Journal of Child Psychology and Psychiatry*, 50(1-2), 63-71. <https://doi.org/10.1111/j.1469-7610.2008.01978.x>.
- Plomin, Robert, Claire MA Haworth, Emma L. Meaburn, Thomas S. Price, Wellcome Trust Case Control Consortium 2, and Oliver SP Davis (2013), "Common DNA Markers Can Account for More Than Half of the Genetic Influence on Cognitive Abilities," *Psychological Science*, 24(4), 562-8. doi: 10.1177/0956797612457952.

- Plomin, Robert, Michael J. Owen, and Peter McGuffin (1994), "The Genetic Basis of Complex Human Behavior," *Science*, 264 (5166), 1733-39
<https://doi.org/10.1126/science.8209254>.
- Plomin, Robert, and John C. DeFries (1980), "Genetics and Intelligence: Recent Data," *Intelligence*, 4(1), 15-24. [https://doi.org/10.1016/0160-2896\(80\)90003-3](https://doi.org/10.1016/0160-2896(80)90003-3).
- Plomin, Robert, John C. DeFries, Valerie S. Knopik, and Jenae Neiderhiser (2016), "Top 10 Replicated Findings from Behavioral Genetics," *Perspectives on Psychological Science: A Journal of the Association for Psychological Science*, 11(1), 3-23.
<https://doi.org/10.1177/1745691615617439>.
- Plomin, Robert, and Richard Rende (1991), "Human Behavioral Genetics," *Annual Review of Psychology*, 42(1), 161-90. <https://doi.org/10.1146/annurev.ps.42.020191.001113>.
- Plomin, Robert, and Michael Rutter (1998), "Child Development, Molecular Genetics, and What To Do With Genes Once They are Found," *Child Development*, 69(4), 1223-42.
<https://doi.org/10.1111/j.1467-8624.1998.tb06169.x>.
- Plomin, Robert and Sheila O. Walker (2003), "Genetics and educational psychology," *British Journal of Educational Psychology*, 73(1), 3-14.
<https://doi.org/10.1348/000709903762869888>.
- Plomin, Robert and Michael A. Simpson (2013), "The Future of Genomics for Developmentalists," *Development and Psychopathology*, 25(4pt2), 1263-78.
<https://doi.org/10.1017/S0954579413000606>.
- Plomin, Robert, and Sophie Von Stumm (2018). "The New Genetics of Intelligence," *Nature Reviews Genetics*, 19(3), 148-59. DOI: 10.1038/nrg.2017.104.
- Plomin, Robert, and Sophie Von Stumm (2022). "Polygenic Scores: Prediction Versus Explanation," *Molecular Psychiatry*, 27(1), 49-52. <https://doi.org/10.1038/s41380-021-01348-y>.
- Portin, Petter, and Adam Wilkins (2017). "The Evolving Definition of the Term 'Gene'," *Genetics*, 205(4), 1353-64. <https://doi.org/10.1534/genetics.116.196956>.
- Qu, Hongzhu, and Xiangdong Fang (2013), "A Brief Review on the Human Encyclopedia of DNA Elements (ENCODE) Project," *Genomics, Proteomics & Bioinformatics*, 11(3), 135-141. <https://doi.org/10.1016/j.gpb.2013.05.001>.
- Rao, Li-Lin, Yuan Zhou, Dang Zheng, Liu-Qing Yang, and Shu Li (2018), "Genetic Contribution to Variation in Risk Taking: A Functional MRI Twin Study of the Balloon Analogue Risk Task," *Psychological Science*, 29(10), 1679-91.
<https://doi.org/10.1177/0956797618779961>.

- Ramanan, Vijay K., Li Shen, Jason H. Moore, and Andrew J. Saykin (2012), "Pathway Analysis of Genomic Data: Concepts, Methods, and Prospects for Future Development, " *Trends in Genetics*, 28(7), 323-32. <https://doi.org/10.1016/j.tig.2012.03.004>.
- Karlsson Linnér R, Mallard TT, Barr PB, Sanchez-Roige S, Madole JW, Driver MN, et al. (2021), "Multivariate Genomic Analysis of 1.5 Million People Identifies Genes Related to Addiction, Antisocial Behavior, and Health," *Nature Neuroscience*, 24, 1367–76. <https://doi.org/10.1038/s41593-021-00908-3>.
- Recchia, Gabriel, and Michael N. Jones (2009), "More Data Trumps Smarter Algorithms: Comparing Pointwise Mutual Information with Latent Semantic Analysis," *Behavior Research Methods*, 41, 647-56. <https://doi.org/10.3758/BRM.41.3.647>.
- Reimann, Martin and Shailendra Pratap Jain (2021), "Maladaptive Consumption: Definition, Theoretical Framework, and Research Propositions." *Journal of the Association for Consumer Research*, 6(3), 307-14. <https://doi.org/10.1086/714822>.
- Rende, Richard D., Robert Plomin, and Steven G. Vandenberg (1990), "Who Discovered the Twin Method?" *Behavior Genetics*, 20(2), 277-85. <https://doi.org/10.1007/BF01067795>.
- Rhea, Sally-Ann, Josh B. Bricker, Sally J. Wadsworth, and Robin P. Corley (2013), "The Colorado Adoption Project," *Twin Research and Human Genetics*, 16(1), 358-65. <https://doi.org/10.1017/thg.2012.109>.
- Ridley, Matt (1993), *The Red Queen: Sex and the Evolution of Human Nature*, New York: Harper Collins.
- Ridley, Matt (2003), *The Agile Gene: How Nature Turns on Nurture*, New York: Harper Collins.
- Rimfeld, Kaili, Margherita Malanchini, Eva Krapohl, Laurie J. Hannigan, Philip S. Dale, and Robert Plomin (2018), "The Stability of Educational Achievement Across School Years is Largely Explained by Genetic Factors, " *NPJ: Science of Learning*, 3(1), 1-10. <https://doi.org/10.1038/s41539-018-0030-0>.
- Rimfeld, Kaili, Nicholas G. Shakeshaft, Margherita Malanchini, Maja Rodic, Saskia Selzam, Kerry Schofield, Philip S. Dale, Yulia Kovas, and Robert Plomin (2017), "Phenotypic and Genetic Evidence for a Unifactorial Structure of Spatial Abilities," *Proceedings of the National Academy of Sciences*, 114(10), 2777-82. <https://www.jstor.org/stable/26480105>.
- Rindfleisch, Aric, James E. Burroughs, and Frank Denton (1997), "Family Structure, Materialism, and Compulsive Consumption," *Journal of Consumer Research*, 23(4), 312-25. <https://www.jstor.org/stable/2489568>.

- Redondo, Maria J., Andrea K. Steck, and Alberto Pugliese (2017), "Genetics of type 1 diabetes." *Pediatric diabetes*, 19(3), 346-53. <https://doi.org/10.1111/pedi.12597>.
- Rietveld, Cornelius A., Sarah E. Medland, Jaime Derringer, Jian Yang, Tõnu Esko, Nicolas W. Martin, Harm-Jan Westra et al. (2013), "GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment," *Science*, 340(6139), 1467-71. DOI: 10.1126/science.1235488.
- Rose, Richard J. (1995) "Genes and Human Behavior," *Annual Review of Psychology*, 46, 625-54. <https://doi.org/10.1146/annurev.ps.46.020195.003205>.
- Robinson, Gene E (2004), "Beyond Nature and Nurture," *Science*, 304 (5669), 397-99. <https://doi.org/10.1126/science.1095766>.
- Roselius, Ted (1971), "Consumer Rankings of Risk Reduction Methods," *Journal of Marketing*, 35(1), 56-61. <https://doi.org/10.2307/1250565>.
- Rowell, Sarah, Beth Newman, Jeff Boyd, and Mary-Claire King (1994). "Inherited Predisposition to Breast and Ovarian Cancer," *American Journal of Human Genetics*, 55(5), 861. Inherited predisposition to breast and ovarian cancer. - PMC (nih.gov).
- Ruvio, Ayalla, Eli Somer, and Aric Rindfleisch (2014), "When Bad Gets Worse: The Amplifying Effect of Materialism on Traumatic Stress and Maladaptive Consumption," *Journal of the Academy of Marketing Science*, 42, 90-101. <https://doi.org/10.1007/s11747-013-0345-6>.
- Samanthi, Udayangani (2011), "Difference Between Allele and Locus", *Difference Between Allele and Locus, Difference Between.Com*, Accessed August 1, 2023. [Allele and Locus | Compare the Difference Between Similar Terms.](#)
- Same, Robert V., David I. Feldman, Nishant Shah, Seth S. Martin, Mahmoud Al Rifai, Michael J. Blaha, Garth Graham, and Haitham M. Ahmed (2016), "Relationship Between Sedentary Behavior and Cardiovascular Risk," *Current Cardiology Reports*, 18 (6), 1-7. <https://doi.org/10.1007/s11886-015-0678-5>.
- Sandler, Irwin, Erin Schoenfelder, Sharlene Wolchik, and David MacKinnon (2011), "Long-term impact of prevention programs to promote effective parenting: Lasting effects but uncertain processes." *Annual Review of Psychology* 62, 299. 10.1146/annurev.psych.121208.131619.
- Sariyar Murat, Stephanie Suhr, and Irene Schlünder (2017), "How Sensitive Is Genetic Data?" *Biopreservation and Biobanking*, 15(6):494-501. <https://doi.org/10.1089/bio.2017.0033>.
- Savage Jeanne, Philip Jansen, Sven Stringer, Kyoko Watanabe, Julien Brio's, Christiaan de Leeuw, Mats Nagel, Swapnil Awasthi, et al. (2018), "Genome-wide Association Meta-

- Analysis in 269,867 Individuals Identifies New Genetic and Functional Links to Intelligence,” *Nature Genetics*, 50, 912–9. <https://doi.org/10.1038/s41588-018-0152-6>.
- Schmidt, Bertil, and Andreas Hildebrandt (2017), "Next-Generation Sequencing: Big Data Meets High Performance Computing," *Drug Discovery Today*, 22(4), 712-17. <https://doi.org/10.1016/j.drudis.2017.01.014>.
- Schutte, Nienke M., Charlotte Huppertz, Stieneke Doornweerd, Meike Bartels, Eco JC de Geus, and Hidde P. van Der Ploeg (2020), "Heritability of Objectively Assessed and Self-Reported Sedentary Behavior," *Scandinavian Journal of Medicine & Science in Sports*, 30(7), 1237-47. <https://doi.org/10.1111/sms.13658>.
- Schmidt, Louis A., Nathan A. Fox, and Dean H. Hamer (2007), "Evidence for a Gene–Gene Interaction in Predicting Children's Behavior Problems: Association of Serotonin Transporter Short and Dopamine Receptor D4 Long Genotypes with Internalizing and Externalizing Behaviors in Typically Developing 7-Year-Olds," *Development and Psychopathology*, 19(4), 1105-16. <https://doi.org/10.1017/S0954579407000569>.
- Segal, Nancy L. (1993), "Twin, Sibling, and Adoption Methods: Tests of Evolutionary Hypotheses," *American Psychologist*, 48(9), 943-56. <http://dx.doi.org/10.1037/0003-066X.48.9.943>.
- Schilling, David Russell (2013), "Knowledge Doubling Every 12 Months, Soon to be Every 12 Hours," *Industry Tap* 19, Accessed February 20, 2023. Knowledge Doubling Every 12 Months, Soon to be Every 12 Hours - Industry Tap.
- Shabani, Mahsa (2019), "Blockchain-based Platforms for Genomic Data Sharing: A Decentralized Approach in Response to the Governance Problems?" *Journal of the American Medical Informatics Association*, 26(1), 76-80. <https://doi.org/10.1093/jamia/ocy149>.
- Shabani, Mahsa, and Pascal Borry (2018), "Rules for Processing Genetic Data for Research Purposes in View of the New EU General Data Protection Regulation." *European Journal of Human Genetics*, 26(2), 149-56. [10.1038/s41431-017-0045-7](https://doi.org/10.1038/s41431-017-0045-7).
- Shakeshaft, Nicholas G., and Robert Plomin (2015), "Genetic Specificity of Face Recognition," *Proceedings of the National Academy of Sciences*, 112(41), 12887-92. <https://doi.org/10.1073/pnas.1421881112>.
- Shampo, Marc A., and Robert Kyle (2011), "J. Craig Venter--The Human Genome Project," *Mayo Clinic Proceedings*, 86(4), e26-27. [10.4065/mcp.2011.0160](https://doi.org/10.4065/mcp.2011.0160).
- Sherman, Steven J., and Russell H. Fazio (1983), "Parallels Between Attitudes and Traits as Predictors of Behavior," *Journal of Personality*, 51(3), 308-45. <https://doi.org/10.1111/j.1467-6494.1983.tb00336.x>.

- Sheth, Jagdish (2021), "New Areas of Research in Marketing Strategy, Consumer Behavior, and Marketing Analytics: The Future is Bright," *Journal of Marketing Theory and Practice*, 29(1), 3-12. <https://doi.org/10.1080/10696679.2020.1860679>.
- Simonson, Itamar (2008), "Regarding Inherent Preferences," *Journal of Consumer Psychology*, 18(3), 191-6. <https://doi.org/10.1016/j.jcps.2008.04.007>.
- Simonson, Itamar (2008), "Will I like a “Medium” Pillow? Another Look at Constructed and Inherent Preferences," *Journal of Consumer Psychology*, 18(3), 155-169. <https://doi.org/10.1016/j.jcps.2008.04.002>.
- Simonson, Itamar and Aner Sela (2011), “On the Heritability of Consumer Decision Making: An Exploratory Approach for Studying Genetic Effects on Judgement and Choice,” *Journal of Consumer Research*, 37(6), 951-66. <https://doi.org/10.1086/657022>.
- Speed, Richard, Patrick Butler, and Neil Collins (2015), "Human Branding in Political Marketing: Applying Contemporary Branding Thought to Political Parties and Their Leader," *Journal of Political Marketing*, 14(1-2), 129-51. <https://doi.org/10.1080/15377857.2014.990833>.
- Steiger, David M., and Natalie M. Steiger (2008) "Instance-based Cognitive Mapping: A Process for Discovering a Knowledge Worker's Tacit Mental Model," *Knowledge Management Research & Practice*, 6(4), 312-21. <https://doi.org/10.1057/kmrp.2008.19>.
- Stein, Lincoln D. (2010), "The Case for Cloud Computing in Genome Informatics," *Genome Biology*, 11(5), 1-7. <https://doi.org/10.1186/gb-2010-11-5-207>.
- Stephens, Zachary D., Skylar Y. Lee, Faraz Faghri, Roy H. Campbell, Chengxiang Zhai, Miles J. Efron, Ravishankar Iyer, Michael C. Schatz, Saurabh Sinha, and Gene E. Robinson (2015), "Big Data: Astronomical or Genomical?" *PLOS Biology*, 13(7), e1002195. <https://doi.org/10.1071/journal.pbio.1002195>.
- Sugrue, Leo P., and Rahul S. Desikan (2019), "What Are Polygenic Scores and Why Are They Important?" *Journal of the American Medical Association*, 321(18), 1820-1. <https://doi.org/10.1001/jama.2019.3893>.
- Tarter, Ralph E. (1988), "Are There Inherited Behavioral Traits That Predispose to Substance Abuse?" *Journal of Consulting and Clinical Psychology*, 56(2), 189-96. <http://dx.doi.org/10.1037/0022-006X.56.2.189>.
- Taylor, Amy E., George Davey Smith, and Marcus R. Munafò (2018), "Associations of Coffee Genetic Risk Scores with Consumption of Coffee, Tea and Other Beverages in the UK Biobank," *Addiction*, 113 (1), 148-57. <https://doi.org/10.1111/add.13975>.

- Taylor, James W. (1974), "The Role of Risk in Consumer Behavior: A Comprehensive and Operational Theory of Risk Taking in Consumer Behavior," *Journal of Marketing*, 38(2), 54-60. <https://doi.org/10.2307/1250198>.
- Thaler, Richard H., and Cass R. Sunstein (2009), *Nudge: Improving Decisions About Health, Wealth, and Happiness*, New York: Penguin.
- The Nobel Prize in Physiology or Medicine 1962, *NobelPrize.org.*, Accessed Wednesday. 27 Jul 2022. <https://www.nobelprize.org/prizes/medicine/1962/summary>.
- Torkamani, Ali, Nathan E. Wineinger, and Eric J. Topol (2018), "The Personal and Clinical Utility of Polygenic Risk Scores," *Nature Reviews Genetics*, 19(9), 581-90. <https://doi.org/10.1038/s41576-018-0018-x>.
- Trzaskowski, Maciej, Nicholas G. Shakeshaft, and Robert Plomin (2013), "Intelligence Indexes Generalist Genes for Cognitive Abilities," *Intelligence* 41(5), 560-5. <https://doi.org/10.1016/j.intell.2013.07.011>.
- Turel, Ofir, and Antoine Bechara (2021), "A Triple-System Neural Model of Maladaptive Consumption," *Journal of the Association for Consumer Research*, 6(3), 324-33. <https://doi.org/10.1086/714366>.
- Turkheimer, Eric (2000), "Three Laws of Behavior Genetics and What They Mean," *Current Directions in Psychological Science*, 9 (5), 160-64. <https://doi.org/10.1111/1467-8721.00084>.
- Turkheimer, Eric, Brian M. D'Onofrio, Hermine H. Maes, and Lindon J. Eaves (2005), "Analysis and Interpretation of Twin Studies Including Measures of the Shared Environment," *Child Development*, 76(6), 1217-33. <https://www.jstor.org/stable/20696034>.
- Turney, Peter D. (2002), "Thumbs Up or Thumbs Down? Semantic Orientation Applied to Unsupervised Classification of Reviews," *arXiv preprint cs/0212032*. Microsoft Word - turney-acl02-final.doc (arxiv.org)
- Turner, Rick, and Marc Gellman (2013), "Allele," *Encyclopedia of Behavioral Medicine*, 1689-91. https://doi.org/10.1007/978-1-4419-1005-9_676.
- Uffelmann, Emil, Qin Qin Huang, Nchangwi Syntia Munung, Jantina De Vries, Yukinori Okada, Alicia R. Martin, Hilary C. Martin, Tuuli Lappalainen, and Danielle Posthuma (2021), "Genome-Wide Association Studies," *Nature Reviews Methods Primers*, 1(59), 1-21. <https://doi.org/10.1038/s43586-021-00056-9>.
- University of Edinburgh Roslin Institute. "The Life of Dolly," The Life of Dolly | Dolly the Sheep (ed.ac.uk), Accessed July 11, 2022. The Life of Dolly | Dolly the Sheep (ed.ac.uk).
- Vandenbergh, David J., Richard J. O'Connor, Michael D. Grant, Akilah L. Jefferson, George P. Vogler, Andrew A. Strasser, and Lynn T. Kozlowski (2007), "Genetic Study: Dopamine

- Receptor Genes (DRD2, DRD3 and DRD4) and Gene–Gene Interactions Associated with Smoking-Related Behaviors," *Addiction Biology*, 12(1),106-16.
<https://doi.org/10.1111/j.1369-1600.2007.00054.x>.
- Van Noorden, Richard, Brendan Maher, and Regina Nuzzo (2014), "The Top 100 Papers," *Nature News*, 514(7524), 550-3. [nature291014-top100.pdf](https://doi.org/10.1038/nature291014-top100.pdf) (onr-russia.ru).
- Varadarajan, Rajan (2020), "Relevance, Rigor and Impact of Scholarly Research in Marketing, State of the Discipline and Outlook," *AMS Review*, 10 (2020), 199-205.
<https://doi.org/10.1007/s13162-020-00180-x>.
- Vargo, Stephen L. and Robert F. Lusch (2004), "Evolving to a New Dominant Logic for Marketing," *Journal of Marketing*, 68, 1-17. <https://doi.org/10.1509/jmkg.68.1.1.24036>.
- Vasiliou, Vasilis, Thomas L. Ziegler, Pequita Bludeau, Dennis R. Petersen, Frank J. Gonzalez, and Richard A. Deitrich (2006), "CYP2E1 and Catalase Influence Ethanol Sensitivity in the Central Nervous System," *Pharmacogenetics and Genomics*, 16(1), 51-8.
<https://doi.org/10.1097/01.fpc.0000182777.95555.56>.
- Venter, J. Craig, Mark D. Adams, Eugene W. Myers, Peter W. Li, Richard J. Mural, Granger G. Sutton, Hamilton O. Smith et al. (2001), "The Sequence of the Human Genome," *Science*, 291(5507), 1304-51. <https://doi.org/10.1126/science.1058040>.
- von Stumm, Sophie, and Robert Plomin (2021), "Using DNA to Predict Intelligence," *Intelligence*, 86 (101530). <https://doi.org/10.1016/j.intell.2021.101530>.
- Wedel, Michel, and P. K. Kannan (2016), "Marketing Analytics for Data-Rich Environments" *Journal of Marketing*, 80(6), 97-121. <https://doi.org/10.1509/jm.15.0413>.
- Weissenbach, Jean (2016), "The Rise of Genomics," *Comptes Rendus Biologies*, 339(7-8), 231-9.
<https://doi.org/10.1016/j.crv.2016.05.002>.
- Weld, Louis DH (1941), "Early Experience in Teaching Courses in Marketing, " *Journal of Marketing*, 5(4), 380-1. <https://doi.org/10.2307/1245553>.
- Wilkes, Robert E. (1978), "Fraudulent Behavior by Consumers: The Other Side of Fraud in the Marketplace: Consumer-Initiated Fraud against Business," *Journal of Marketing*, 42(4), 67-75. <https://doi.org/10.2307/1250088>.
- Williams, Sarah C.P. (2014), "Genes Don't Just Influence Your IQ: They Determine How Well You Do In School," *Science*, October 6, 2014. Genes don't just influence your IQ—they determine how well you do in school | Science | AAAS.
- Wojczynski, Mary K., and Hemant K. Tiwari (2008), "Definition of Phenotype," *Advances in Genetics*, 60, 75-105. [https://doi.org/10.1016/S0065-2660\(07\)00404-X](https://doi.org/10.1016/S0065-2660(07)00404-X).

- Xcode Life. "What is a DNA Raw Data File and How Does it Look Like." Accessed August 18, 2022. What is a DNA raw data file and how does it look like? (xcode.life).
- Zeithaml, Valerie A., Jaworski, Bernard J., Kohli, Ajay K., Tuli, Kapil R., Ulaga, Wolfgang, & Gerald Zaltman (2019). "A Theories-in-use Approach to Building Marketing Theory," *Journal of Marketing*, 84(1), 32–51. <https://doi.org/10.1177/0022242919888477>.
- Zemack-Rugar, Yael, Canan Cokus, and David Brinberg (2012), "The 'Response-to-Failure' Scale: Predicting Behavior Following Initial Self-Control Failure," *Journal of Marketing Research*, 49(6), 996-1014. <https://www.jstor.org/stable/41714483>.

Appendix: Survey Information

Survey for Data Collection

This appendix includes the instructions for participation in the survey and the three survey questions.

UNC Charlotte, Department of Marketing, Belk College of Business**Name of Investigator(s):** Layne McGuire**Title of Project:** The Genomics Revolution and the Transformation of Marketing**Request to Participate in Research**

We would like to invite you to take part in a research project. The purpose of this research is to ascertain understanding, perceptions, and concerns around the use of genomic data.

You must be at least 18 years old to be in this research project.

The study will take about 25-30 minutes. If you decide to participate in this study, we will ask you to complete three survey questions about genomic data, how it can potentially be used in marketing, and concerns about using your genomic data.

There are no foreseeable risks or discomforts to you for taking part in this study.

There are no direct benefits to you for participating in the study. However, your answers may help us to learn more about how people understand genomic data and its uses, as well as their concerns about using it.

Your part in this study will be handled in a confidential manner. Only the researchers will know that you participated in this study. Any reports or publications based on this research will use only group data and will not identify you or any individual as being of this project. After this study is complete, study data may be shared with other researchers for use in other studies without asking for your consent again. The data we share will NOT include information that could identify you.

The decision to participate in this research project is up to you. You do not have to participate and can refuse to answer any question. Even if you begin the study, you may withdraw at any time.

You will receive extra credit for participating in this research.

If you have any questions about this study, please contact Layne McGuire (mmcgui31@uncc.edu), the Principal Investigator.

If you have any questions about your rights in this research, you may contact the Office of Research Protections and Integrity at uncc-irb@uncc.edu.

Questions:

1. Please describe, in detail, at least three key aspects or attributes of genomic data.

2. **Please explain how genomic data can potentially be used to understand consumer behavior better and be used in marketing strategy. Describe, in detail, at least three key potential ways that genomic data can be used to understand consumer behavior.**