The Myth of DNA Trade Secrecy

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Are DNA sequences subject to trade secrecy protection? At least three decades of scholarship has assumed so even while there is no explicit statutory authority directly on point and very few reported decisions in the area. And yet, an investigation into the elements of trade secrecy law—read in light of rapid advances in DNA and genomic sequencing—suggests the answer is probably, no. Those advances include the rise of cheap, accurate, easy, fast, and readily available DNA sequencing services, including the recent availability of whole human genome sequencing for less than a monthly cell phone bill. This cuts against some of the elements required for trade secret subject matter, namely, whether the sought-to-be protected information is "readily ascertainable" to the public and whether the information derives "independent economic value" from its secrecy. To date, neither caselaw nor scholarly case studies concerning genomic trade secrets have engaged with these advances. Understanding that much genomic data may not be protectable as a trade secret has several practical consequences, including the difficulty of litigating non-trade secret "stolen data" cases in federal fora; variability in enforcing non-disclosure agreements; and diminished remedies for breaches of confidence. More broadly, seeing that technological advances can upend the protectability of information once thought to be a trade secret yields several theoretical insights. It suggests that trade secrets, like some servitudes, can be terminated when faced with changed conditions. It also suggests that several defenses of trade secrecy—ready accessibility, independent derivation, and reverse engineering—are much closer to one another than typically conceived. And it demonstrates, à la the "comedy of the commons," that work to remove trade secret protection may benefit both the former trade secret holder and the public at large. The omnipresence of next-generation DNA sequencing should spur a serious reexamination of DNA sequences as trade secrets, a belief that courts, policymakers, and scholars should now recognize is largely a myth.

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TABLE OF CONTENTS

INTRODUCTION

Are DNA sequences subject to trade secrecy protection? At least three decades of scholarship has assumed so.[1] But, in fact, there is no explicit statutory authority directly on point and very few reported decisions in the area. More importantly, however, an investigation into the elements of trade secrecy law—read in light of rapid advances and expansion of DNA sequencing—suggests the answer is probably, *no*. Generally, trade secrets constitute that information which is subject to "reasonable measures" to guard its secrecy; is not "readily ascertainable" to others; and derives "independent economic value" from its secrecy.[2] But given the ease and ubiquity of DNA sequencing, it's not clear whether DNA sequences can be "secret" at all. Rather, much of it is likely "readily ascertainable" if the underlying source is known.[3] Nor should it be assumed that keeping such information secret confers "independent economic value" to its owner.[4] The value to much DNA sequence information lies in its public disclosure and use with *other* information—not secrecy of the data itself.[5] Lastly, even assuming that some DNA sequence was once protectable, recent technological and market developments may have extinguished the secrecy and competitive advantage of such information.[6] This suggests that while DNA

1. *E.g.*, Rebecca S. Eisenberg, *Re-Examining the Role of Patents in Appropriating the Value of DNA Sequences*, 49 EMORY L.J. 783, 795 (2000) (assuming it is possible to rely "on trade secrecy to motivate investment in DNA sequence databases"); Alexander K. Haas, *The Wellcome Trust's Disclosures of Gene Sequence Data into the Public Domain & the Potential for Proprietary Rights in the Human Genome*, 16 BERKELEY TECH. L.J. 145, 162 (2001) ("Trade secret protection [is] . . . perhaps applicable to the kind of information that genome companies have as long as it is secret . . . ."); Anna B. Laakmann, *The New Genomic Semicommons*, 5 U.C. IRVINE L. REV. 1001, 1021 (2015) ("Trade secrecy might, in some circumstances, be a better legal mechanism than patents to facilitate sharing of genomics research."); Robert Mitchell, John M. Conley, Arlene M. Davis, R. Jean Cadigan, Allison W. Dobson & Ryan Q. Gladden, *Genomics, Biobanks, and the Trade-Secret Model*, 332 SCIENCE 309, 309–10 (2011) (advocating the use of a trade secrecy model to simplify informed consent for DNA databases).

2. *E.g.*, 18 U.S.C. § 1839(3); UNIF. TRADE SECRETS ACT § 1(4) (UNIF. L. COMM'N 1985). *See also* MELVIN F. JAGER & BRAD LANE, 1 TRADE SECRETS LAW § 3:2 (2023) [hereinafter TRADE SECRETS LAW]; ROGER M. MILGRIM & ERIC E. BENSEN, 1 MILGRIM ON TRADE SECRETS § 1.01(2)(c)(iii) (2022) [hereinafter MILGRIM ON TRADE SECRETS].

3. *Cf.* RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. f (AM. L. INST. 1995) (likening information that is "readily ascertainable" to a "person who actually acquires the information through an examination of a publicly available product").

4. *See* Camilla A. Hrdy, *The Value in Secrecy*, 91 FORDHAM L. REV. 557, 593–606 (2022) (discussing courts' failures in making assumptions about secrets' independent economic value).

5. James Brian Byrd, Anna C. Greene, Deepashree Venkatesh Prasad, Xiaoqian Jiang & Casey S. Greene, *Responsible, Practical Genomic Data Sharing That Accelerates Research*, 21 NATURE REVS.: GENETICS 615, 624 (2020) (describing the increased value to genomic data through sharing); Barbara J. Evans, *Genomic Data Commons*, *in* GOVERNING MEDICAL KNOWLEDGE COMMONS 74, 77 (Katherine J. Strandburg, Brett M. Frischmann & Michael J. Madison eds., 2017) ("[Genomic] inferences – in other words, useful knowledge about the clinical meaning of particular genetic variants – can only be made by pooling genetic and other types of health data for large samples of the human population."); Robert L. Grossman, Allison P. Heath, Vincent Ferretti, Harold E. Varmus, Douglas R. Lowy, Warren A. Kibbe & Louis M. Staudt, *Toward a Shared Vision for Cancer Genomic Data*, 375 NEW ENG. J. MED. 1109, 1109 (2016) (discussing the value of genomic data sharing).

6. *See infra* Part I.C.

sequences could be *de facto* secrets, some—perhaps a good many—may not be *trade* secrets.

For trade secret law practitioners and scholars, or for those working in the general area of law and genomics, this is a provocative thesis. But the launching point for this provocation begins on fairly orthodox grounds: a straightforward history of DNA sequencing, then and now. Then is largely before 2001, the year when the first draft sequence of the human genome was completed.[7] Prior to then, DNA sequencing was a costly, uncertain, and difficult endeavor.[8] Sequencing even a single human gene, head to tail, provoked high-profile races among researchers.[9] Commercial diagnostic services—like Myriad Genetics, Inc. and an arm of the Miami Children's Hospital—sprang up to offer tests that specialized in the personalized sequencing of individual genes.[10] DNA sequencing was difficult; the information it generated was valuable; and the process was priced accordingly.

The 2001 draft completion of the Human Genome Project—an effort to sequence the entirety of the DNA of an organism, its "genome"—sparked a revolution in sequencing technology more generally. In 2005, a biotech startup called Solexa sequenced the entire genome of a bacteria-attacking virus.[11] This contributed little to an understanding of the virus—its genome sequence had been known for decades and was, in fact, the first genome of anything ever sequenced.[12] Rather, Solexa's announcement was revolutionary for its method—a high-fidelity, automated approach to DNA sequencing that cut down both sequencing time and cost by many orders of magnitude.[13] This

7. International Human Genome Sequencing Consortium, *Initial Sequencing and Analysis of the Human Genome*, 409 NATURE 860, 860 (2001) [hereinafter IHGSC, *Initial Analysis*]. A (mostly) complete draft wasn't completed until 2004. International Human Genome Sequencing Consortium, *Finishing the Euchromatic Sequence of the Human Genome*, 431 NATURE 931, 931 (2004) [hereinafter IHGSC, *Euchromatic Sequence*]. The actual complete, end-to-end sequence wasn't completed until 2022. Sergey Nurk et al., *The Complete Sequence of a Human Genome*, 376 SCIENCE 44, 44 (2022).

8. *See* T. Hunkapiller, R. J. Kaiser, B. F. Koop & L. Hood, *Large-Scale and Automated DNA Sequence Determination*, 254 SCIENCE 59, 66–67 (1991) (discussing challenges with traditional sequencing methods).

9. *See, e.g.*, KEVIN DAVIES & MICHAEL WHITE, BREAKTHROUGH: THE RACE TO FIND THE BREAST CANCER GENE, at vi (1996) (discussing the race to find and sequence *BRCA1*, a gene strongly implicated in early onset breast and ovarian cancer, between Mary-Claire King at the University of California, and Mark Skolnick, at the University of Utah).

10. JORGE L. CONTRERAS, THE GENOME DEFENSE: INSIDE THE EPIC LEGAL BATTLE TO DETERMINE WHO OWNS YOUR DNA 78–79, 86–96 (2021) (recounting the development of Miami Children's Hospital and Myriad Genetics' businesses).

11. Press Release, Solexa, Solexa Completes First Full Genome Sequence with Cluster-SBS Technology (Mar. 10, 2005), https://www.innovations-report.com/life-sciences/report-41607 [https://web.archive.org/web/20060822175604/http://www.solexa.com/news/2005/100305.htm] [hereinafter *Solexa Press Release*]; *see also* Caitlin Smith, *Getting Down to Details*, 435 NATURE 991, 994 (2005) (announcing Solexa's technology).

12. F. Sanger, A. R. Coulson, T. Friedmann, G. M. Air, B. G. Barrell, N. L. Brown, J. C. Fides, C. A. Hutchinson III, P. M. Slocombe & M. Smith, *The Nucleotide Sequence of Bacteriophage φX174*, 125 J. MOLECULAR BIOLOGY 225, 225 (1978); *see also Solexa Press Release*, *supra* note 11 ("The first complete sequence of a genome was ØX174 in 1978 by Fred Sanger and co-workers.").

13. Smith, *supra* note 11, at 994 (predicting a $1,000 genome); *Solexa Press Release*, *supra* note 11 (predicting significant cost savings).

technology—dubbed "sequencing-by-synthesis"—became one of several "next-generation sequencing" (NGS) technologies to make their debut in the mid-2000s.[14] The tiny company Solexa became Illumina, the genomic sequencing juggernaut of today, commanding ninety percent of the U.S. sequencing market.[15]

Today, *far* from being costly, uncertain, and difficult, obtaining DNA sequences—and genomic data of all stripes—is cheap, accurate, easy, and fast. How cheap? Well, sequence data for an entire human genome costs—retail—$249, and at a better level of fidelity than the original Human Genome Project.[16] And what took the Human Genome Project *decades* now takes *hours*.[17] Indeed, so much DNA sequencing has been done since the NGS revolution that simply *storing* the data has proven challenging, not unlike an out-of-control shopper with too little closet space.[18] Besides unlocking the mysteries of nature or using DNA sequences for clinical purposes, DNA sequencing is now used (often, inaccurately) for seemingly trivial purposes, including art, shopping discounts, and predicting one's preferences for certain wine varietals.[19] Today, there is virtually no hurdle between knowing the *source* of a DNA sequence and obtaining the sequence itself. Genomic data—standing alone—can no longer be

14. Michael L. Metzker, *Emerging Technologies in DNA Sequencing*, 15 GENOME RSCH. 1767, 1768 (2005); Catherine Shaffer, *Next-Generation Sequencing Outpaces Expectations*, 25 NATURE BIOTECHNOLOGY 149, 149 (2007).

15. Shaffer, *supra* note 14; Complaint at 1, Illumina Inc. & Pac. Biosciences of CA, Inc., FTC Docket No. 9387 (Dec. 17, 2019) ("In the United States, Illumina has complete dominance over the market for . . . [next-generation sequencing] products, with a share of over 90%.").

16. *What Does Your DNA Say About Your Health and Ancestry?: Choose Your Genome Sequencing Bundle*, NEBULA GENOMICS, https://nebula.org/whole-genome-sequencing-dna-test [https://perma.cc/TZ5R-5A7Z] (last visited Feb. 14, 2024). "Fidelity" is, perhaps, an inartful term. What I mean is *coverage*—how many times a given region of the genome is sequenced. While the finer differences between the two are beyond the scope of this paper, it's worth mentioning that the original Human Genome Project had a coverage of roughly 3 to 4X, while Nebula Genomics has a 30X product. *See* IHGSC, *Initial Analysis*, *supra* note 7, at 931.

17. John E. Gorzynski et al., *Ultrarapid Nanopore Genome Sequencing in a Critical Care Setting*, 386 NEW ENGL. J. MED. 700, 700 (2022) (reporting a time, from blood sample to diagnosis, of 7 hours and 18 minutes).

18. Mikel Hernaez, Dmitri Pavlichin, Tsachy Weissman & Idoia Ochoa, *Genomic Data Compression*, 2 ANN. REV. BIOMEDICAL DATA SCI. 19, 20 (2019) ("[T]he storage and acquisition of . . . [genomic] data are becoming a major bottleneck . . . .").

19. *DNA Sequencing + Personalized Genomic Art,* NEBULA GENOMICS, https://nebula.org/human-art-project/product [https://perma.cc/TK5Q-QEB2?type=image] (last visited Feb. 11, 2024); DHOSTUDIOS, *Award-Winning DNA DISCOUNTS Advertisement for "AeroMexico" Airlines*, YOUTUBE (May 25, 2018), https://www.youtube.com/watch?v=2sCeMTB5P6U [https://web.archive.org/web/20190201151502/https://www.youtube.com/watch?v=2sCeMTB5P6U] [hereinafter AeroMexico Ad]; Rebecca Robbins, *Fruity with a Hint of Double Helix: A Startup Claims to Tailor Wine to Your DNA*, STAT (Oct. 27, 2016), https://www.statnews.com/2016/10/27/wine-dna-genetics [https://perma.cc/7JB8-4JTU]; *Stranger Visions*, *Projects*, HEATHER DEWEY-HAGBORG, https://deweyhagborg.com/projects/stranger-visions [https://perma.cc/4VJ2-SHWA] (last visited Feb. 11, 2024).

said to be economically valuable. And, at $249—a 99.99999% discount off the original Human Genome Project—it has been repriced accordingly.[20]

Take these facts about DNA sequence data and apply them to the law of trade secrets; it's a tenuous fit at best. Trade secret protection extends only to information that derives "independent economic value" from its secrecy.[21] But raw DNA sequences—apart from being of little economic value—aren't likely to derive value *from* their secrecy. To the contrary, the most economically valuable DNA sequences are those that are disclosed and used in conjunction with other data, namely, public DNA databases linked to identified Internet users or those otherwise connected with electronic medical records.[22] Whatever value such databases have, it is not from the secrecy of their genomic components, but from inferences drawn from the combination of DNA sequences and other data—a value two steps removed from the DNA sequences themselves. Trade secret law also denies protection to information "readily accessible" to the public.[23] But ready accessibility is precisely what enables surreptitious DNA sequencing, the act of collecting genomic material without the knowledge or consent of the source and running it through a sequencer.[24] Neither cost, nor effort, nor expertise are major barriers to obtaining genomic sequences from anywhere.[25]

Beyond this simple statutory reading of trade secrecy law, there is also a sheer paucity of case law directly on point. Of the thousands of trade secrecy cases filed since the advent of NGS, a mere handful have yielded reported decisions that grapple with the relationship between genomic data and trade secrecy's statutory subject matter.[26] And many of these cases are largely idiosyncratic—driven by the particulars of the industry they operate, not the realities about simplicity and ease with which we have found ourselves in "The Age of the Genome."[27] Even fewer—possibly *none*—have taken the recent ubiquity and ease of DNA sequencing into account.

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20. Assuming its budgeted cost of $3 billion. *Human Genome Project Information Archive 1990–2003*, *Budget*, OAK RIDGE NAT'L LAB'Y (Apr. 23, 2019), https://doe-humangenomeproject.ornl.gov/human-genome-project-budget [https://perma.cc/7QUQ-2ATJ].

21. 18 U.S.C. § 1839(3); UNIF. TRADE SECRETS ACT § 1(4) (UNIF. L. COMM'N 1985).

22. Evans, *supra* note 5, at 77–79.

23. § 1839(3); UNIF. TRADE SECRETS ACT § 1(4).

24. *See* Yaniv Heled & Liza Vertinsky, *Genetic Paparazzi: Beyond Genetic Privacy*, 82 OHIO ST. L.J. 409, 411 (2021) (noting the connection between the ubiquity of genomic sequencing and "the press obtain[ing] the genetic material of public figures"); Elizabeth E. Joh, *DNA Theft: Recognizing the Crime of Nonconsensual Genetic Collection and Testing*, 91 B.U. L. REV. 665, 669 (2011) ("With DNA theft, the incentives exist, the technology is available, and the costs for engaging in it are decreasing all the time."); Mark A. Rothstein, *Genetic Stalking and Voyeurism: A New Challenge to Privacy*, 57 U. KAN. L. REV. 539, 541 (2009) ("For a fee, virtually any source of DNA that can be tested will be tested—with or without consent.").

25. Yaniv Erlich, *A Vision for Ubiquitous Sequencing*, 25 GENOME RSCH. 1411, 1414–15 (2015) (discussing the democratization of genome sequencing across a variety of applications).

26. *See infra* Part II.C.

27. Erlich, *supra* note 25.

And yet, scholars and practitioners continue to assume—as they have for more than a quarter-century—that genomic data and DNA sequences are subject to trade secret protection.[28] Law review articles, briefs, and practitioner analyses routinely invoke trade secret law as protecting various types of DNA data.[29] The source for this authority is often, if not exclusively, a description of a single database owned by a single company: Myriad Genetics' database of genetic variants of *BRCA1* and *BRCA2*—human genes tightly implicated in early-onset breast and ovarian cancer.[30] But while it is true that Myriad Genetics has such a database and guards it as if it were a trade secret,[31] that does not necessarily make it one. Its value likely lies in its size and connection with patient health reports, not the sequences themselves.[32] The sequences themselves are easy to reconstruct—and indeed have been by medical practitioners with a bone to pick against the company.[33] And the database—as a trade secret—has never been tested in court. The story about trade secrecy protecting Myriad Genetics' database seems to be the same as the story about trade secrecy protecting genomic sequences generally: it's a myth.

But like all myths, this story contains a grain of truth. Databases, after all, are routinely covered by trade secrecy protection—and what is a collection of DNA sequence data other than a database?[34] Many classes of information contained in databases are similarly easy to reconstruct, not defined by statute, and thinly litigated.[35] Does the myth extend to them, too? Perhaps! But understanding how DNA sequence data are poorly sheltered under the umbrella of trade secrecy suggests that the importance of genetic information isn't the sequence data itself but what *else* is in the database. The more valuable and

28. *See* sources cited *supra* note 1.

29. *Id.*; Brief of the Biotechnology Industry Organization as Amicus Curiae Supporting Appellants and in Favor of Reversal, Ariosa Diagnostics, Inc. v. Sequenom, Inc., 788 F.3d 1371 (5th Cir. 2015) (Nos. 2014-1139, 2014-1142, 2014-1144); Jessica Marks, *Gene Patents Won't Disappear Post-Myriad*, LAW360 (July 22, 2013, 12:50 PM EDT), https://www.law360.com/articles/455655/gene-patents-won-t-disappear-post-myriad [https://perma.cc/U76A-BGFZ].

30. *E.g.*, John M. Conley, Robert Cook-Deegan & Gabriel Lazaro-Munoz, *Myriad After Myriad: The Proprietary Data Dilemma*, 15 N.C. J.L. & TECH. 597, 599–600, 616 (2014); Chris Palmer, *The Myriad Decision: A Move Toward Trade Secrets?*, NIH CATALYST 9, 9 (2014); Charlotte A. Tschider, *Metaphor After* Myriad*: The Effect of Legal Rhetoric on Intellectual Property Protection for Biological Sequences*, 57 IDEA 519, 563–69 (2017).

31. Conley et al., *supra* note 30, at 616.

32. Robert Cook-Deegan, John M. Conley, James P. Evans & Daniel Vorhaus, *The Next Controversy in Genetic Testing: Clinical Data as Trade Secrets?*, 21 EUR. J. HUMAN GENETICS 585, 585 (2013) ("Interpreting the clinical significance of genomic information depends on broad access to DNA sequence variants and clinical information about those tested. . . . Myriad notes that nearly one million patients have had BRCA testing, and it has payment agreements with 2500 insurers or payers.").

33. Gina Kolata, *DNA Project Aims to Make Public a Company's Data on Cancer Genes*, N.Y. TIMES (Apr. 12, 2013), https://www.nytimes.com/2013/04/13/health/dna-project-aims-to-make-companys-data-public.html [https://perma.cc/KVW7-GBXC]; *see also* Christi J. Guerrini, Amy L. McGuire & Mary A. Majumder, *Myriad Take Two: Can Genomic Databases Remain Secret?*, 356 SCIENCE 586, 587 (2017).

34. *See* RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. d (AM. L. INST. 1995) (noting that databases are protectable as trade secrets).

35. *See id.*

secret the surrounding data, the more significant the connection to DNA becomes because the more difficult it is to ascertain the same information as a whole. And the more likely, then, it is for the database—again, as a whole—to derive independent economic value from its secrecy. DNA sequence data plugged into valuable, confidential, patient health information may, therefore, be a trade secret—not *because* of its inclusion of DNA information but, counterintuitively, *despite it*. Consequently, the myth—like all good myths—is true only as a didactic: It teaches that the *class* of information sought to be protected matters; that not everything counts; and that DNA sequence data *can* be a trade secret—but only the further and further away it gets from itself.

For many proud of their modernity, it's fun to poke holes in myths as inaccurate or antiquated. But countering the narrative of DNA trade secrecy isn't just fun; it has real consequences, both practical and theoretical. On the practical side, the absence of trade secret protection for DNA means an absence of trade secret misappropriation claims; one cannot misappropriate a de facto secret as opposed to a de jure one.[36] This means that disputes centering on the appropriation of genomic data can't be brought under the Defend Trade Secrets Act (DTSA), placing them largely outside federal court.[37] Assuming such claims also don't satisfy state-law Uniform Trade Secrets Act (UTSA) requirements either, this leaves plaintiffs with—at best—contract or breach of loyalty claims, causes of action that are highly variable from state to state.[38] And in those cases, remedies tend to be much more circumscribed: Damages, on the whole, are less; injunctions, if they're available, are narrower.[39] This ultimately may lead to an arms race to protect genomic data, either through legal mechanisms, like more robust non-disclosure agreements (NDAs) or physical ones, like encryption.[40] These solutions—if they can be called that—to the "problem" of DNA trade secrecy are not cost-free; they may ultimately stymie the very sort of open uses of DNA data we have since come to take for granted.[41]

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36. *See* Sharon K. Sandeen, *The Untold Story of Trade Secret Law*, 4 J. INTELL. PROP. L. & PRAC. 841, 842 (2009) ("The secret to understanding trade secret law is to realize that not all secrets are trade secrets . . . .").

37. Of course, breach of confidentiality claims could still find their way into federal court through diversity jurisdiction. 28 U.S.C. § 1332.

38. 47 RICHARD E. KAYE, CAUSES OF ACTION § 4 (2d ed. 2022) ("The enforceability of a confidentiality or nondisclosure agreement depends on the particular jurisdiction's approach to such agreements."); JOHN G. SPRANKLING & THOMAS G. SPRANKLING, UNDERSTANDING TRADE SECRET LAW § 8.03(C)(2) (2020) (noting a diversity of approaches to enforcing non-disclosure agreements protecting confidential information that does not qualify as a trade secret).

39. SPRANKLING & SPRANKLING, *supra* note 38, § 8.03(C)(3).

40. Mark A. Lemley, *The Surprising Virtues of Treating Trade Secrets as IP Rights*, 61 STAN. L. REV. 311, 332–37 (2008).

41. *See, e.g.*, Jorge L. Contreras, *Pathogen Genomes as Global Public Goods (And Why They Should Not Be Patented)*, 55 N.Y.U. J. INT'L L. & POL. 533, 541–543 (2023) (discussing the advantages of genomic data sharing for pathogen sequences); Jorge L. Contreras, *Bermuda's Legacy: Policy, Patents, and the Design of the Genome Commons*, 12 MINN. J.L. SCI. & TECH. 61, 97–111, 119–22 (2011) (discussing the trend, and variations, of open genomic data).

On the theoretical side, upending the myth of genomic trade secrecy suggests the existence of an unrecognized defense to trade secrecy misappropriation claims: termination. Under the law of servitudes, once-recognized covenants can be terminated if changing circumstances make it such that they can no longer be practically enforced.[42] So too, it may seem, for trade secrets governing information that has since become cheap and easy to obtain through a ubiquitous technology. Relatedly, the ease and ubiquity of DNA sequencing blurs the already fine lines separating three independent trade secrets defenses: lack of subject matter due to ready accessibility, independent development, and reverse engineering. Finally, the explosion of DNA data also sheds some insight into the tension between intellectual property and the "comedy of the commons," the state of affairs where an absence of clearly defined property boundaries enriches—rather than diminishes—individual property holders.[43] That is, becoming wise to DNA trade secrecy as a myth may actually explain the massive rise of DNA data commons often seen today.

Part I describes the genetic data revolution and its current incarnation as, essentially, a commodity service. Part II then explores the law surrounding DNA data as a trade secret, assessing whether it constitutes a trade secret under various statutes or case law. Answering that question, *no*, the Article then revisits the historical pedigree behind the myth of DNA trade secrecy and probes several arguments to the contrary. Rather than simply batting those away, the Article finds in them some hidden truths behind the nature of trade secrecy, generally. Part III then analyzes some practical effects of having some DNA data be unprotectable by trade secrecy. And Part IV provides some greater theoretical consequences of these findings to trade secret law and DNA, generally. The Article concludes with some prescriptive suggestions, which include—among other practical advice—doing nothing at all.

I. THE GENOMIC DATA REVOLUTION

A. DNA SEQUENCING AND THE AGE OF THE GENOME

On April 25, 1953, James D. Watson and Francis H.C. Crick announced their discovery of the molecular of structure of DNA, and, by now, everyone seems to understand the basics: DNA constitutes the genetic code of life, consists of individual genes, and is made up of four bases of nucleic acids, commonly lettered A (adenosine), C (cytosine), G (guanine), and T (thymine), that predictably pair together (A to T, C to G).[44] Beyond these basics, the sum total of DNA within a cell is its "genome."[45] According to one popular

42. RESTATEMENT (THIRD) OF PROP. (SERVITUDES) § 7.11 cmt. a (AM. L. INST. 2000).

43. *See* Carol Rose, *The Comedy of the Commons: Custom, Commerce, and Inherently Public Property*, 53 U. CHI. L. REV. 711, 723 (1986).

44. J. D. Watson & F. H. C. Crick, *Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid*, 171 NATURE 737, 737 (1953).

45. IHGSC, *Initial Analysis*, *supra* note 7, at 860.

metaphor, the genome serves as a cell's software code, "programming" the cell's functions and operations.[46] But at a more specific (and perhaps more accurate) level, the genome codes for proteins that are the workhorses of cellular activity.[47] Proteins give the cell structure, move things around the cell, perform chemical reactions, and signal all this to other cells.[48] The genomic code determines the proteins that constitute a cell, and so determining that code—that is, determining the order, or sequence, of As, Cs, Ts, and Gs in the genome—is important to understanding how a cell works.[49]

Genetic sequencing is—or, more to the point for this paper, *was*—very difficult to do for decades after Watson and Crick's announcement; no practically good method was invented until 1977.[50] Even then, it was a laborious and time-consuming process that required a good amount of grunt work; it was finicky and subject to significant trial and error; and it was not something, in the beginning, that could be technologically automated.[51] For researchers who wanted to uncover genes' sequences, this required them to make hard choices about which genes to sequence.[52] Even with these decisions made, simply finding genes of interest in the larger genome could be astonishingly difficult.[53] This led competing laboratories to race among themselves to be the first to find, and then sequence, genes of interest.[54]

One of highest profile races centered on the discovery and race to sequence *BRCA1* and *BRCA2*, genes strongly implicated in heritable early-onset breast and ovarian cancer.[55] That race was completed in 1994, with Mark Skolnick and his laboratory at the University of Utah hitting the ribbon just before Mary Claire King at the University of California, Berkeley.[56] This was historically important because Skolnick was also the CEO of Myriad Genetics, a company devoted to a single service: the sequencing of just two genes, *BRCA1* and *BRCA2*, in individual patients.[57] Myriad, in turn, kept a database of this sequence information, and paired the sequences alongside clinical information the

46. Tschider, *supra* note 30, at 559–60.

47. IHGSC, *Initial Analysis*, *supra* note 7, at 860.

48. DANIEL L. HARTL, ESSENTIAL GENETICS AND GENOMICS 9 (7th ed. 2018).

49. *Id.*

50. F. Sanger, S. Nicklen & A. R. Coulson, *DNA Sequencing with Chain-Terminating Inhibitors*, 74 PROC. NAT'L ACAD. SCIS. U.S.A. 5463, 5463 (1977).

51. Hunkapiller et al., *supra* note 8, at 62–67.

52. DAVIES & WHITE, *supra* note 9, at 112.

53. *Id.* (describing sequencing difficulties of the era).

54. *Id.* (describing the race to identify and sequence *BRCA1* and *BRCA2*).

55. *Id.*

56. Lori S. Friedman, Elizabeth A. Ostermeyer, Csilla I. Szabo, Patrick Dowd, Eric D. Lynch, Sarah E. Rowell & Mary-Claire King, *Confirmation of* BRCA1 *by Analysis of Germline Mutations Linked to Breast and Ovarian Cancer in Ten Families*, 8 NATURE GENETICS 399, 399 (1994); Yoshio Miki et al., *A Strong Candidate for the Breast and Ovarian Cancer Susceptibility Gene* BRCA1, 266 SCIENCE 66, 66 (1994).

57. Jacob S. Sherkow & Christopher Scott, *Myriad Stands Alone*, 32 NATURE BIOTECHNOLOGY 620, 620 (2014).

company received from patients seeking treatment.[58] Narrow though this business model may sound, it made a mint for Myriad; the company was valued at $4.306 billion at its peak.[59] And it was in good company, with other outfits, like the Miami Children's Hospital, offering similar services for different individual genes.[60]

At the same time, Myriad Genetics' scientific and business model underscored a significant problem of scope. In a universe of what was then thought to be as many as 100,000 human genes,[61] sequencing one of them was myopic, like using a telescope only good for spying on a single planet while otherwise ignoring the surrounding galaxy. Something more expansive was needed to truly understand the "genome" as an integrated whole. In 1986, researchers convened in Santa Fe, New Mexico to discuss the usefulness of sequencing a canonical version of an entire human genome, a Human Genome Project.[62] "Useful" is an understatement; the Project was then likened to "cracking the code of the mystery of life," in addition to numerous other breathless metaphors.[63] And so, a consortium of research institutes, under the auspices of the Department of Energy and the National Institutes of Health, embarked, in 1990, on a journey to sequence the human genome in its entirety—all *six billion* base pairs' worth. By way of comparison, the *BRCA1* gene, which took roughly three years to sequence, was a mere 110,000 base pairs long—a miniscule 0.0018% of the genomic total.[64] There was a lot of work to do.

By 2000, researchers Francis Collins and Craig Venter announced—with President Bill Clinton upfront and U.K. Prime Minister Tony Blair, by satellite—that the human genome had been sequenced.[65] In reality, a *draft* sequence was completed, with large sections missing or of suspect accuracy.[66] This was the result of not oversight or sloth, but rather, complex reasons related to physical chemistry of the genome. Some parts of the genome were "stickier"

58. Conley et al., *supra* note 30, at 614, 616; Palmer, *supra* note 30, at 9.

59. This occurred on Apr. 13, 2009 according to the market cap tracker on https://www.ycharts.com. A screenshot is on file with the author.

60. CONTRERAS, *supra* note 10, at 86–96.

61. G. D. Schuler et al., *A Gene Map of the Human Genome*, 274 SCIENCE 540, 540 (1996).

62. James D. Watson, *The Human Genome Project: Past, Present, and Future*, 248 SCIENCE 44, 45 (1990); James Dewey Watson & Robert Mullan Cook-Deegan, *Origins of the Human Genome Project*, 5 FASEB J. 8, 9 (1991).

63. David Whitehouse, *Cracking the Code for the Mystery of Life*, 127 NEW STATESMAN 20, 20 (1998); *see also, e.g.*, *The Human Genome Project: Past, Present, and Future*, *supra* note 62, at 44 ("When finally interpreted, the genetic messages encoded within our DNA molecules will provide the ultimate answers to the chemical underpinnings of human existence."); LAWRENCE BERKELEY LAB'Y, MAPPING THE HUMAN GENOME 2 (1989) ("It is no overstatement to say that to decode these 100,000 genes in some fundamental way would be the most dramatic step we could take toward unraveling the manifold mysteries of life.").

64. *See* Friedman et al., *supra* note 56, at 399; Miki et al., *supra* note 56, at 66.

65. *Reading the Book of Life; White House Remarks on Decoding of Genome*, N.Y. TIMES (June 27, 2000), https://www.nytimes.com/2000/06/27/science/reading-the-book-of-life-white-house-remarks-on-decoding-of-genome.html#:~:text=We%2C%20all%20of%20us%2C%20share,creator%20or%20invade%20individual%20privacy [https://perma.cc/KVW7-GBXC].

66. *See* IHGSC, *Euchromatic Sequence*, *supra* note 7, at 931.

than others, and hard to read, like say, fragile pages of a book stuck together or to something else.[67] Nonetheless, even the draft sequence was monumental—and even more so, given that *all of it* was made publicly available, free of charge, a decision made—forcefully—by researchers involved in the beginning of the project at a conference in Bermuda.[68] These "Bermuda Principles" of rapid, open deposit of sequence information continue to live on today in what is now the "Age of the Genome."[69]

B. NEXT GENERATION SEQUENCING AND SEQUENCERS

Whether the Human Genome Project lived up to its hype is difficult to say.[70] The real fruits of the Project were not the genomic sequences it generated, but rather, the related advanced sequencing technologies developed during the course of the work. In 2005, a small biotech company, Solexa, announced it had sequenced the genome of an entire virus, φX174.[71] That, perhaps was remarkable news standing alone. But it was revolutionary for how it did it—not the laborious, largely manual, finicky process used in the Human Genome Project, "Sanger sequencing," but an automated, high-tech, high-fidelity process, "sequencing by synthesis."[72] While the mechanical details of sequencing by synthesis are beyond the scope of this Article, it's hard to overstate the technology's impact on genomics. The method, almost instantly called, "next generation sequencing" or NGS technology, transformed genomic sequencing from a monumental endeavor—one that required the oversight of national agencies and the White House, as well as international coordination—to something that bordered on routine.[73] Since SBS technology debuted, an average of *twenty-seven* new, complete genomes have been sequenced *every week*.[74] And there is currently a project to sequence one representative of *every* multicellular organism on the planet—hundreds of thousands if not millions of species—in the same time it took to do the first human one.[75] One famous

67. *See id.* (describing technical difficulties in finishing the complete sequence).

68. *Pathogen Genomes as Global Public Goods (And Why They Should Not Be Patented)*, *supra* note 41, at 541–42, 577–78; Kathryn Maxson Jones, Rachel A. Ankeny & Robert Cook-Deegan, *The Bermuda Triangle: The Pragmatics, Policies, and Principles for Data Sharing in the History of the Human Genome Project*, 51 J. HIST. BIOLOGY 693, 728–51 (2018).

69. *See Pathogen Genomes as Global Public Goods (And Why They Should Not Be Patented)*, *supra* note 41, at 541–42, 577–78; Erlich, *supra* note 25, at 1413–14.

70. *See* Frank Emmert-Streib, Matthias Dehmer & Olli Yli-Harja, *Lessons from the Human Genome Project: Modesty, Honesty, and Realism*, 8 FRONTIERS GENETICS 184, 184 (2017) (providing a mixed assessment of the project).

71. *Solexa Press Release*, *supra* note 11; *see also* Smith, *supra* note 11, at 994.

72. Robert F. Service, *The Race for the $1000 Genome*, 311 SCIENCE 1544, 1545 (2006).

73. *See id.* at 1544.

74. And I'm just including eukaryotes; the number dramatically escalates if we're talking about sequencing bacteria or archaea. *Genome Information by Organism*, *Genome*, NAT'L LIBR. MEDICINE, https://www.ncbi.nlm.nih.gov/genome/browse#!/eukaryotes/ (last visited Aug. 24, 2022).

75. Harris A. Lewin et al., *Earth BioGenome Project: Sequencing Life for the Future of Life*, 115 PROC. NAT'L ACAD. SCIS. U.S.A. 4325, 4325, 4327 (2018); Harris A. Lewin et al., *The Earth BioGenome Project 2020: Starting the Clock*, 119 PROC. NAT'L ACAD. SCIS. U.S.A. 1, 2 (2022).

measure of this advance is the cost, per base (that is, per A, C, T, or G) for sequencing. Since NGS technology debuted, it has fallen from $1 million per million bases sequenced to $0.01 per million bases—yes, *1¢*—a real price decrease wholly without rival for any technology before or since.[76] And it is expected to go even lower.[77]

Solexa has since become Illumina: the genetic sequencing juggernaut that has come to dominate sequencing across much of the globe.[78] Unlike Myriad Genetics, which did all of its own sequencing in-house in order to corner the *BRCA1* and *BRCA2* market, Illumina has put its technology in virtually every academic and industrial laboratory everywhere. This has led to a proliferation of DNA services laboratories, facilities that will sequence, well, anything, for a fee.[79] This includes human genomes, of course, but it also includes the single genes, multigene panels, and the genomes of almost any species—known or unknown—for almost any purpose.[80]

Illumina's success has spawned competitors, some of which use different technology from Illumina's and others that outstrip Illumina in total sequencing capacity even if not global reach. The Beijing Genomics Institute, branded as BGI, now has the capacity to sequence roughly fifty percent of the world's genomic data outside of China—and virtually all, within it.[81] Others, like Nanopore, can complete sequences in very long runs, rapidly speeding up the time it takes to product a draft genomic sequence of a new species.[82] Like any mature technology, this competition has spawned a rats' nest of patent suits, with Illumina and its rivals trying to elbow one another out of each other's market share.[83]

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76. *DNA Sequencing Costs: Data*, NAT'L HUM. GENOME RSCH. INST. (May 16, 2023), https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data [https://perma.cc/8FZ7-A7HL].

77. Elizabeth Pennisi, *Upstart DNA Sequencers Could Be a "Game Changer,"* 376 SCIENCE 1257, 1258 (2022) (predicting $0.005 per base, a 10-fold reduction from current prices).

78. Complaint at 1, Illumina Inc. & Pac. Biosciences of CA, Inc., FTC Docket No. 9387 (Dec. 17, 2019); Prior Notification of a Concentration (Case M.10188 — Illumina/GRAIL), 2021 O.J. (C 248) 1,1.

79. *E.g.*, *DNA Services*, ROY J. CARVER BIOTECHNOLOGY CTR., https://biotech.illinois.edu/htdna (last visited Feb. 13, 2024).

80. *Id.* (listing different services).

81. MARK KAZMIERCZAK, RYAN RITTERSON, DANIELLE GARDNER, ROCCO CASAGRANDE, THILO HANEMANN & DANIEL H. ROSEN, GRYPHON SCI., RHODIUM GRP., CHINA'S BIOTECHNOLOGY DEVELOPMENT: THE ROLE OF US AND OTHER FOREIGN ENGAGEMENT 25–26 (2019), https://www.uscc.gov/sites/default/files/Research/US-China%20Biotech%20Report.pdf [https://perma.cc/UW5V-V3VD].

82. Miten Jain, Hugh E. Olsen, Benedict Paten & Mark Akeson, *The Oxford Nanopore MinION: Delivery of Nanopore Sequencing to the Genomics Community*, 17 GENOME BIOLOGY 239, 239, 241, 246 (2016).

83. *E.g.*, Complaint for Pat. Infringement & Declaratory Judgment for Pat. Infringement at 1, 10X Genomics, Inc. v. Parse Biosciences, Inc., No. 1:22-cv-01117-UNA (D. Del. Aug. 24, 2022); Complaint for Pat. Infringement & Demand for Jury Trial at 1, Illumina, Inc. v. Oxford Nanopore Techs. Ltd., No. 3:16-cv-00477-LAB-MDD (S.D. Cal. Feb. 23, 2016); Complaint for Pat. Infringement of U.S. Pat. No. 8,129,930 & Jury Trial Demanded at 1, Illumina, Inc. v. Complete Genomics, Inc., No. 3:12-cv-01465-AJB-BGS (S.D. Cal. June 15, 2012).

Today, sequencing is largely a commodity business—in a literal sense.[84] If you want to sequence some genetic material, you can shop around your sample to several DNA services laboratories—all of which largely do the same thing—and haggle over nothing but price per volume and ancillary services. As but one example, you could get a quote for a human whole genome sequence from the Genomics Core Facility at the Icahn School of Medicine at Mount Sinai in New York City.[85] If you didn't like the price, you could simply take your sample on the subway downtown—eight stops on the Q train—to the New York Genome Center on Canal Street, and get another quote.[86] But you don't need to be in New York City—or any city—to take advantage of the ubiquity of DNA services. Because genomic DNA is generally stable, and shipping is easy, you could just as easily mail off your sample to any of the dozens of DNA services laboratories around the United States.[87] Your results are delivered the same way they would be if your sample was local: online, typically in the BAM file format.[88] And in all of these instances, given the advance in sequencing technology, it's likely to be a better level of fidelity than the original human genome project.[89]

C. USERS AND USES OF GENOMIC SEQUENCES

Like any piece of government instantiated technology—the Internet, GPS, cell phones—DNA sequencing has now gone fully direct-to-consumer, becoming a piece of Americana in the process. Direct-to-consumer genomic sequencing companies now abound, with companies offering whole genome

84. Precisely articulating the definition of "commodity" has long plagued economists. Daniel V. Gordon, Rögnvaldur Hannesson & William A. Kerr, *What is a Commodity? An Empirical Definition Using Time Series Econometrics*, 10 J. INT'L FOOD & AGRIBUSINESS MKTG 1, 3–6 (1999). Nonetheless, the *sine qua non* of a commodity is it being "[a] comparatively homogeneous product that can typically be bought in bulk." MATTHEW BISHOP, THE ECONOMIST, ECONOMICS: AN A-Z GUIDE (2016). The upshot of that requirement is that the only difference in price across producers is the quantity demanded and, in some cases, ancillary services related to purchasing, e.g., faster delivery times.

85. *Genomics Core Facility*, ICAHN SCH. MED. MOUNT SINAI, https://icahn.mssm.edu/research/genomics/core-facility [https://perma.cc/6WBK-L9SV] (last visited Feb. 14, 2024).

86. *See* N.Y. GENOME CTR., GENOMICS SERVICES 3, 6–7, http://www.nygenome.org/wp-content/uploads/NYGC-nopricing.pdf [https://web.archive.org/web/20150701020307/http://www.nygenome.org:80/wp-content/uploads/NYGC-nopricing.pdf] (last visited Feb. 14, 2024); *see also* Subway Directions from 96 St. to Canal St., GOOGLE MAPS, https://goo.gl/maps/y344exDcpYLmmsep8 [https://perma.cc/C76A-JD9H] (follow "Directions" hyperlink; then search starting point field for "96 Street, New York, NY" and search destination field for "Canal Street, New York, NY").

87. *See, e.g.*, *Returning DNA Sample to the Lab*, 23ANDME, https://customercare.23andme.com/hc/en-us/articles/202904570-Returning-DNA-Sample-to-the-Lab [https://perma.cc/D8AG-F4CA] (last visited Feb. 14, 2024).

88. *See, e.g.*, *How to Start Exploring Your Raw Genomic Data*, NEBULA GENOMICS, https://nebula.org/blog/how-to-start-exploring-your-raw-genomic-data [https://perma.cc/3U9C-XVF3] (last visited Feb. 14, 2024).

89. *Cf.* IHGSC, *Initial Analysis*, *supra* note 7, at 931.

sequences for $299—on sale![90] There are television ads for DNA sequencing services that reference sports, traffic on health fads, and promise human "connection."[91] People give DNA sequencing kits as Christmas stocking stuffers.[92] One of the most prominent proponents of genomic sequencing for the purposes of tracing genealogy is the Mormon Church.[93] Over a hundred million people worldwide have used a direct-to-consumer DNA sequencing service.[94] DNA sequencing is everywhere.

Indeed, DNA sequencing has become so prevalent, sequence information has been used for purely trivial things. It can, in perhaps its most popular consumer use, determine ethnic ancestry, validating—or finally interring—family lore about where one's ancestors came from.[95] One company has used—or, to be a bit more accurate, *claims* to have used—DNA to predict one's preferred wine varietals.[96] And, in one ad campaign, equal parts racist and inaccurate, claims to have determined discounts on an airline's airfare based on one's percentage of "Mexican ancestry."[97] To be clear, these examples are obvious *misuses* of genomic data; that is, that companies' interpretations of DNA sequences data do not do what they purport them to do. But the point here is that the *data* itself is genuine. The "calls"—that is, the As, Cs, Ts, and Gs that are the output of sequencing runs—are largely correct even if the company doing the sequencing incorrectly tells you that your genomic data suggests you prefer Chablis to chardonnay.[98]

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90. *Choose Your Genome Sequencing Bundle*, *DNA Test*, NEBULA GENOMICS, https://nebula.org/whole-genome-sequencing-dna-test/ [https://perma.cc/TZ5R-5A7Z] (last visited Feb. 14, 2024).

91. *E.g.*, Ancestry, *Imagine What's Possible | Ancestry*, YOUTUBE (Mar. 4, 2019), https://www.youtube.com/watch?v=kxGT0LJVPSw [https://web.archive.org/web/20200301195037/https://www.youtube.com/watch?v=kxGT0LJVPSw]; *"ROOT FOR YOUR ROOTS" with Fox Sports & 23andMe*, FOX SPORTS (June 19, 2018), https://www.foxsports.com/watch/1259084867769 [https://perma.cc/NU93-QLJK]; 23andMe, *DNA and Fitness: Josh Hockett's 23andMe Story*, YOUTUBE (Dec. 26, 2016), https://www.youtube.com/watch?v=7V7KE_pgjMQ.

92. Marcus Wohlsen, *Getting Your DNA Scanned Now Costs Less Than an iPhone 5*, WIRED (Dec. 11, 2012, 5:19 PM), https://www.wired.com/2012/12/23andme-99-dollar-dna-scan [https://web.archive.org/web/20140409234451/https://www.wired.com/2012/12/23andme-99-dollar-dna-scan/].

93. *See* JULIA CREET, THE GENEALOGICAL SUBLIME 38–39 (2020) (recounting the connection between the direct-to-consumer genomics industry and the Church of Jesus Christ of Latter-Day Saints).

94. NAT'L ACADS. SCIS., ENG'G, & MED., EXPLORING THE CURRENT LANDSCAPE OF CONSUMER GENOMICS: PROCEEDINGS OF A WORKSHOP 38 (2020).

95. *Id.* at 25–26.

96. Robbins, *supra* note 19.

97. AeroMexico Ad, *supra* note 19; *see generally* CHRISTINA A. SUE, LAND OF THE COSMIC RACE: RACE MIXTURE, RACISM, AND BLACKNESS IN MEXICO (2013) (analyzing how a genetically singular concept of a "Mexican race" marginalizes Indigenous, Mestizo, and Black Mexicans, among other groups).

98. Why capitalize "Chablis" but not "chardonnay"? Simple: Chablis is a geographic region in France, and therefore deserves capitalization as a proper noun; chardonnay is simply a type of grape and, therefore, does not. This comports with William Safire's famous series of rules regarding wine capitalization, which—for the sticklers among us—has been tepidly (or perhaps at a cellar temperature) endorsed by the *Chicago Manual of Style*. William Safire, *Wines Without Caps*, N.Y. TIMES, Aug. 25, 1985, sec. 6, at 12; *Capitalization*, CHI. MANUAL STYLE ONLINE, https://www.chicagomanualofstyle.org/qanda/data/faq/topics/Capitalization/faq0049.html [https://perma.cc/5R4R-XHH4] (last visited Apr. 5, 2024).

These trivial uses even go beyond sequencing one's *own* DNA. At a one cent per million bases, genomic sequencing has become so easy, people can obtain DNA sequences surreptitiously—that is, without the source of the DNA even knowing about it.[99] This has been used for the greater good—to solve criminal cold cases, for example—but also for the more pedestrian, such as determining paternity.[100] Surreptitious DNA sequencing has been used more creatively, such as an art project that reconstitutes people's faces using "discarded" DNA,[101] and as a celebrity relic—what one suite of commentators have dubbed the "genetic paparazzi."[102] And in a less benign, albeit ridiculous example, surreptitious DNA sequencing has been used by jealous country club members to blackmail their rivals.[103] Going from sample to sequence is no longer a decades-long government project. It's as easy as mailing a plastic tube to a sequencing laboratory—and a small tube at that.

Today, so much genetic data now exists, that it's become almost impossible to store; genomic data is some of the biggest of big data. [104] Centering for a moment on DTC genomic data alone, there is now so much of it freely available online that virtually everyone of Western European ancestry in the United States—whether they've uploaded their sequence or not—can be paired to a close relative.[105] Even genomic data used for primarily research purposes is so expansive that it requires special bandwidth protocols for cloud computing,[106] and special compression algorithms to transmit.[107] With such a burden simply storing the stuff, genomic data is just as routinely created as it is lost, trashed, or abandoned. Other than those directly affected when their genomic information is lost, no one seems to care. Unlike even the recent past, genomic data is no longer a precious resource. Like a simple sauce spilled, it can just as easily be made again.

II. ARE GENOMIC DATA TRADE SECRETS?

A. THE ELEMENTS OF TRADE SECRECY

In the United States, trade secrecy is a creature of both state and federal law. To date, either forty-eight or forty-nine states—depending on how one

99. *See* sources cited *supra* note 24.

100. Natalie Ram, *Fortuity and Forensic Familial Identification*, 63 STAN. L. REV. 751, 793–94 (2011).

101. Eva Amsen, *These 3D Portraits Are Created from Strangers' DNA*, FORBES (Sept. 4, 2019, 11:34 AM EDT), https://www.forbes.com/sites/evaamsen/2019/09/04/these-3-d-portraits-are-created-from-strangers-dna/?sh=13dd367029f6 [https://perma.cc/AL7P-W26U].

102. Heled & Vertinsky, *supra* note 24, at 411.

103. Complaint at 2–3, Peerenboom v. Perlmutter, 362 So. 3d 217 (Fla. Cir. Ct. Apr. 7, 2017) (No. 2013-CA-015257).

104. Hernaez et al., *supra* note 18, at 20–21.

105. Yaniv Erlich, Tal Shor, Itsik Pe'er & Shai Carmi, *Identity Inference of Genomic Data Using Long-Range Familial Searches*, 362 SCIENCE 690, 690 (2018).

106. Ben Langmead & Abhinav Nellore, *Cloud Computing for Genomic Data Analysis and Collaboration*, 19 NATURE REVS. GENETICS 208, 211 (2018).

107. Hernaez et al., *supra* note 18, at 22, 28–30, 32.

counts—have adopted the Uniform Trade Secrets Act (UTSA).[108] And since 2016, the Defend Trade Secrets Act (DTSA) has created a federal cause of action for trade secrets violations.[109] Despite this overlapping jurisdiction, the definitional elements of a trade secret are largely the same between state and federal. A "trade secret" is "information" that "derives independent economic value" from being secret; is not "readily ascertainable by proper means"; and "is the subject of efforts that are reasonable under the circumstances to maintain its secrecy."[110] Outside the United States, the law is largely the same in the EU, especially after the 2016 Trade Secrets Directive, which had the effect of harmonizing basic trade secret law across much of Europe.[111]

The "independent economic value" requirement for trade secret subject matter means only that the holder of the contested information derives some form of competitive advantage—actual or potential—from keeping it secret.[112] Put another way, that the information is worth more as a secret than known.[113] This can include technical information about more efficient manufacturing processes, proprietary software code, or confidential market research on one's competitors—all give the holder of such information a leg up on the competition.[114] But it includes banal bits of information, too, like lists of customers, that improve business positioning in the marketplace.[115] Nonetheless, the root query for assessing whether information has "independent economic value" is what the information is worth.[116] Economically worthless information cannot be a trade secret.[117] Nor can information the competitive advantage of

108. While both New York and North Carolina have refused to formally adopt the UTSA, North Carolina's Trade Secrets Protection Act largely mirrors the uniform act, leaving New York as the only true outlier. *Compare* N.C. GEN. STAT. § 66-152(3) (1981) (defining "trade secret"), *with* UNIF. TRADE SECRETS ACT § 1(4) (UNIF. L. COMM'N 1985) (same).

109. 18 U.S.C. § 1839(3).

110. *Id.*; UNIF. TRADE SECRETS ACT § 1(4).

111. Directive (EU) 2016/943 of the European Parliament and of the Council of 8 June 2016 on the Protection of Undisclosed Know-How and Business Information (Trade Secrets) Against Their Unlawful Acquisition, Use and Disclosure, 2016 O.J. (L 157) 8 (EU Trade Secrets Directive).

112. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. e (AM. L. INST. 1995).

113. This is shorthand—and a contestable proposition. Information could, in theory, be *independently* economically valuable, through licensing, even if worth *more* known than secret. One may still need to license it, and by consequence, the secrecy imparts value on the information. Were this the correct interpretation of the independent economic value requirement, though, it would apply to literally *all secret information*, including information courts and the Restatement have rejected as meeting the standard. After all, *anything* I know, and you don't, I could license to you for money. Regardless: this statement is shorthand for the general proposition that some value must derive from the *information*'s secrecy, not the *secrecy*, alone; the better interpretation given, the few cases that have rejected a more expansive view of the principle.

114. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. d.

115. *Id.*

116. *Id*. § 39 cmt. e ("A trade secret must be of sufficient value in the operation of a business or other enterprise to provide an actual or potential economic advantage over others who do not possess the information."); Hrdy, *supra* note 4, at 593–95 (describing the problem of "amount failure").

117. Hrdy, *supra* note 4, at 593–95.

which is purely abstract or indefinite.[118] If the keeper of the guarded information can't point to how the information's secrecy benefits them, or, for that matter, which particular aspects of the information are independently valuable, the information may not be a trade secret at all. In making these assessments, courts have looked at the usefulness of the information to the owner's business and the amount of effort or money it took to develop the information in question, among other factors.[119]

Trade secrets must also be subject to "reasonable" protections to maintain their secrecy.[120] Secret information poorly kept as a secret is not, whatever else it may be, a *trade* secret.[121] This does not (necessarily) mean that the information must continually be guarded under lock and key;[122] only that the information is protected from broader disclosure beyond those in whom it is entrusted.[123] There are no hard and fast rules about the mechanics of what constitutes a "reasonable" protection, any more than there are hard and fast rules about other areas of law grounded in "reasonableness." Like those areas—say, negligence's infamous "reasonable person"—the bar can be adjusted to account for underlying circumstances. In trade secrets law, this adjustment could take into account the value of the information, the nature of the information, and the cost of maintaining that information's secrecy.[124] Industry practice may be informative as well. If, for example, NDAs are common in the field, the absence of one may mean that the contested information was not subject to "reasonable" protections to guard its secrecy.[125]

The last of these statutory elements is a lack of "ready ascertainment"—that the sought-to-be-protected information cannot be "readily" discerned by competitors or the consuming public.[126] This can arise if the information was previously publicly disclosed—say, in a patent—or in the public domain.[127] Or even, as is more likely these days, dumped somewhere in the vast sea of the Internet. But information can also be "readily ascertainable" for trade secret law's purposes, in situations where a rival pieces together the supposedly secret information from publicly available materials or deduces the secret as a self-evident variation or modification from what is otherwise known. Nonetheless, "readily ascertainable" means *readily* ascertainable. If merely eyeballing a competitor's product yields the protected information, it's likely readily available enough to void trade secret protection. So is getting at that same

118. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39, Reporter's Note, cmt. d ("A lack of definiteness may also preclude proof of secrecy.").

119. *Id.*

120. *Id.* § 39 cmt. g.

121. *Id.* § 39 cmt. f.

122. *Id.* § 39 cmt. g.

123. *Id.*; Ari Ezra Waldman, *Trust: A Model for Disclosure in Patent Law*, 92 IND. L.J. 557, 589–90 (2017).

124. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. g.

125. *Id.*

126. *Id.* § 39 cmt. f.

127. *Id.*

information by routine physical inspection or duplication. But detailed statistical analyses of a swath of a rival's inventory is probably not.

So: if the information is, in fact, a trade secret, how can one police it? The answer is, *narrowly*. The rights of trade secret holders are much more limited than other forms of intellectual property. Trade secrets do not grant their holders the right to exclude others from their practice (like patents) or even the exclusive right to use them (like copyright). Rather trade secrecy is only a right to prevent "misappropriation," some form of possession or use that violates some duty to the information's holder.[128] By and large, this frequently comes up in the context of jealous (or negligent) former employees or in cases concerning corporate espionage.[129] But it can also occur where the information has been leaked following the breach of an NDA or through garden variety fraud. By contrast, trade secrets obtained by accident are just that—*accidents*, the line between *mis*appropriation and *appropriation*, and the boundary between being able to enforce a trade secret and having it succumb to the larger marketplace.[130]

Importantly, there are defenses to claims of misappropriation. These principally include independent discovery and reverse engineering. Independent discovery operates precisely as it sounds: as a defense that the contested information was not misappropriated but independently discovered by the defendant.[131] Again, unlike patents or copyrights, trade secret owners do not have the right to exclude others from the secret's practice or to exclusively use the information for themselves. So, a defendant's independent discovery of the same information leaves the secret holder out of luck.

Reverse engineering begins with the publicly available material of the trade secret holder and working backwards—often with some significant effort—to unlocking the underlying secret.[132] Despite the unseemliness of the practice (at least according to some), reverse engineering has long been a defense to claims of misappropriation and is considered "an essential part of innovation. . . . [that] often leads to significant advances in technology."[133] It is, in other words, "an important factor in maintaining balance in intellectual property law" among the often-competing goals of disclosure, economic protection, and technological advance.[134] In either case, getting the information yourself—whether from scratch or from a competitor's goods—is a perfectly valid defense to assertions of misappropriation.

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128. *See id.* § 40.

129. *See* Timothy Murphy, *How Can a Departing Employee Misappropriate Their Own Creative Outputs?*, 66 VILL. L. REV. 529, 540–41 (2021) (noting that this common feature of trade secrecy cases was not resolved by the UTSA).

130. *See* Hrdy, *supra* note 4, at 585 (noting that much trade secret litigation concerns information otherwise lawfully obtained).

131. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. f.

132. *See id.* § 43 cmt. b.

133. Bonito Boats, Inc. v. Thunder Craft Boats, Inc., 489 U.S. 141, 160 (1989).

134. Pamela Samuelson & Suzanne Scotchmer, *The Law and Economics of Reverse Engineering*, 111 YALE L.J. 1575, 1583 (2002).

B. DNA AS A STATUTORY TRADE SECRET?

Do these elements cover DNA sequences? Perhaps not. The requirements of trade secrecy—in light of how commoditized DNA data is now—don't seem to read on much of the genomic information that currently exists or is in the process of being continually created on the cheap. Granted, a given dataset of DNA sequences can certainly be subject to reasonable efforts to maintain its secrecy. And many are. But it's not clear that DNA sequences are no longer "readily ascertainable" or if they "derive independent economic value" from their secrecy.

To start at the beginning: While the contours of ready ascertainment are a source of significant dispute, courts have primarily focused on the effort or expense in recreating the information. Information that is "easy" and "economically feasible" to discover from its original source, for example, is "readily ascertainable" and therefore not a trade secret. This can involve, for example, combing the prior literature for the components of the alleged secret, building one's own database from public information, or hiring those with experience in the field to recreate the information otherwise locked away—all seemingly greater efforts than sending off samples to a commercial DNA services provider for fractions of a cent per base.[135]

Of course, one needs to obtain a sample to sequence first. But, for some DNA sequences, this may be an easily surmounted hurdle. For basic human genomic information—especially where the underlying humans in the secret database are known—much of that information may already be on the Internet. To date, more than one hundred million people have made use of a direct-to-consumer genomic sequencing service, with tens of millions of those underlying sequences being put online.[136] Much of the time, those sequences are identifiable, either because the user has voluntarily identified themselves or because re-identifying a user can be accomplished using other information, like zip code and birth year.[137] And even if a given user has not uploaded their own genomic information, such information can now be *inferred*—that is, accurately predicted—if the user's relatives have uploaded such information, given the heritable nature of DNA. This is more far-reaching than it may sound to the uninitiated: a 2018 estimate calculated that genomic information could be inferred for more than sixty percent of *all Americans* with European ancestry.[138]

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135. *See* MILGRIM ON TRADE SECRETS, *supra* note 2, § 1.01[2][a] n. 47 (providing examples of ready ascertainability).

136. Antonio Regalado, *More than 26 Million People Have Taken an At-Home Ancestry Test*, MIT TECH. REV. (Feb. 11, 2019), https://www.technologyreview.com/2019/02/11/103446/more-than-26-million-people-have-taken-an-at-home-ancestry-test/ [https://perma.cc/MY9P-2KRA].

137. Shuang Wang, Xiaoqian Jiang, Siddharth Singh, Rebecca Marmor, Luca Bonomi, Dov Fox, Michelle Dow & Lucila Ohno-Machado, *Genome Privacy: Challenges, Technical Approaches to Mitigate Risk, and Ethical Considerations in the United States*, 1387 ANNALS N.Y. ACAD. SCIS. 73, 77, 79 (2017).

138. Erlich et al., *supra* note 105, at 690.

By today, that number has been estimated to be as high as 99.98%.[139] Dystopia or not, a vast swath of human genomic information is accessible using simple computational tools.

This is to say nothing of surreptitious sequencing—obtaining DNA from an individual's leavings, like loose strands of hair or shed skin, or from tissue left behind on discarded items like coffee cups or chewing gum.[140] Obtaining DNA sequence information here would require more than simply scraping the internet; it would require someone to prep the samples and send them to a sequencing lab. But that's simple—no more than putting a Q-tip in a plastic tube and sending it off in the mail. And importantly—that's all it would take. The idea of surreptitious sequencing may seem fanciful—who would go through the trouble?—but it's been done (and reported as having been done) in a variety of cases for seemingly frivolous purposes, including making art, creating celebrity memorabilia, and in one famous instance, exacting revenge on a country club rival.[141] At its current cost of fractions of a cent per base, it would fall far below the cost obtaining other information courts have deemed readily accessible.[142]

Separately, it's not clear that DNA sequence information derives independent economic value from its secrecy because it's not clear that keeping DNA sequences secret drives value in and of itself. What value is there to purely secret DNA sequence data? Even assuming there is some value, DNA is generally perceived as being valuable only in concert with other information, such as clinical information about a given patient.[143] To a typical genomicist, awash in raw genomic data, this should make perfect sense. A string of DNA sequence information—without knowing its provenance—is just noise. It's only the information's combination with other, real-world information—what some call "annotation"—that gives DNA sequences any value at all. Indeed, raw genomic data—even in commercially lucrative fields like immunology and drug development—are routinely dumped online, en masse, for public use, in the hope that it can be aggregated with other data to bring it value.[144] This is the basis, for example, of several public-private research consortia, such as the Structural Genomics Consortium, the Cancer Genomics Consortium, and the Adaptive Immune Receptor Repertoire Community, all of which recognize that genomic sequences, standing alone, are "pre-competitive" data, *improved* by

139. Luc Rocher, Julien M. Hendrickx & Yves-Alexandre de Montjoye, *Estimating the Success of Re-Identifications in Incomplete Datasets Using Generative Models*, 10 NATURE COMMC'NS 1, 5 (2019).

140. *See* sources cited *supra* note 24.

141. *See* sources cited *supra* note 19; Amended Counterclaim at 6–11, Peerenboom v. Perlmutter, 362 So. 3d 217 (Fla. Cir. Ct. Apr. 7, 2017) (No. 2013-CA-015257); *see also* Jessica L. Roberts, *Progressive Genetic Ownership*, 93 NOTRE DAME L. REV. 1105, 1109 (2018) (discussing the *Peerenboom v. Perlmutter* case).

142. *Cf.* MILGRIM ON TRADE SECRETS, *supra* note 2, § 1.01[2][a] n. 47 (collecting activities that constitute "ready accesibility").

143. *See* sources cited *supra* note 5.

144. Jorge L. Contreras & Liza S. Vertinsky, *Pre-Competition*, 95 N.C. L. REV. 67, 81–82 (2016).

their disclosure not their restriction.[145] If there's value to genomic information, it's not to genomic information standing alone.

A recent review of the independent economic value requirement—Camilla A. Hrdy's, *The Value of Secrecy*—both recognizes that courts have, in the past, rubber stamped the "independent economic value" requirement and, recently, are beginning to push back against it.[146] The framework courts have correctly begun to employ, in Hrdy's analysis, is whether the information—as a secret—is worth more than the information were it publicly disclosed.[147] Or better yet, taking into account the realities of litigation, whether it is *provable* that the underlying data is worth more, and more than a trivial amount more, if it's secret.[148] As noted by Hrdy, much of the courts' lack of a serious analysis of the independent economic value requirement suffers from a "causation failure"—a failure to recognize that the element mandates that what makes the information valuable is *because* it is kept secret.

DNA, by contrast, is often kept secret for reasons having nothing to do with competitive advantage, including overzealous fears of health privacy regulations. And, on the margins, some courts have conflated the independent economic value of the information to the "sweat work" used to create it—the effort, time, and money expended to bring it into being. This has, of course, been substantially depreciated since the rise of NGS technologies. With Hrdy's perspective, claims to DNA as being universally, or even widely, "independently economically valuable" are questionable.

Even so, it's not clear the value that DNA information adds to such databases causes them to possess the *independent* economic value required of trade secrets law. In many cases, the value of proprietary genomics databases—like those belonging to NantOmics, Wuxi NextCode, and Human Longevity, Inc.—seem to have nothing to do with the *secrecy* of those databases but the ability to license them to other research partners.[149] Again, it's not the *secrecy* that's doing the work here, but the ancillary value of attaching the sequence information with other information out there. Like robust, searchable databases of public information, the value in these cases has little to do with the underlying information's proprietary nature. Even then, some of the licensees to these

145. Molly Morgan Jones, Sophie Castle-Clarke, Daniel Brooker, Edward Nason, Farah Huzair & Joanna Chataway, *The Structural Genomics Consortium: A Knowledge Platform for Drug Discovery*, RAND HEALTH Q. 1, 1 (2014); Jacob S. Sherkow, *Cancer's IP*, 96 N.C. L. REV. 297, 304 (2018); Jacob S. Sherkow & Timo Minssen, *AIRR Data Under the EU Trade Secrets Directive: Aligning Scientific Practices with Commercial Realities*, *in* THE HARMONIZATION AND PROTECTION OF TRADE SECRETS IN THE EU 237 (Jens Schovsbo, Timo Minssen & Thomas Riis, Edward Elgar Publ'g 2020).

146. Hrdy, *supra* note 4, at 587–88.

147. *Id.* at 587–93.

148. *See id.* at 599 ("Recent DTSA cases have been dismissed due to plaintiffs' failures to allege value due specifically to secrecy.").

149. StartUp Health, *The Rise of the Private Genome Databases*, MEDIUM (May 11, 2017), https://healthtransformer.co/the-rise-of-the-private-genome-databases-42a14d5988f5 [https://perma.cc/4FXL-RRTN].

databases have plans to *publicize* aspects of the underlying databases across a variety of research products.[150] The value, here, likely lies in the activity of formatting, collecting, and annotating data, and putting it all together in a research-friendly format. This is not unlike caselaw databases available on WestLaw and Lexis Nexis, the underlying sources of which—publicly available judicial decisions—are indisputably *not* trade secrets. And when DNA data is so cheap and easy to come by, licensing business models like these suggest this calculus will only become *truer* over time. Besides, under the same requirement, value derived from the secret information "must at least be connected to [a] business or to some form of wealth-seeking activity"[151]—something not true of all private genomic databases.[152] Naked claims that secrecy will allow their holders to maintain a "competitive advantage" are not universally countenanced by the courts.[153]

Even if a genomic dataset otherwise passes the threshold of trade secret subject matter, it may be quite susceptible—depending upon the allegations of misappropriation—to independent derivation and reverse engineering defenses. Perhaps ironically, much of the information from large, proprietary DNA datasets can be—for practical purposes—independently derived from public ones; whatever uniqueness a given genomic dataset holds is likely to come out in the wash as compared against hundreds of thousands or millions of freely available samples. This is the spirit, even if not the word, of large-scale national genomics efforts, such as NIH's All of Us Initiative—roughly 250,000 whole human genome sequences—and the UK Biobank—roughly 150,000 whole human genome sequences.[154] Relatedly, information from some proprietary genomic datasets can easily be reversed engineered from freely national data. As but one example, researchers at Purdue University were able to reverse engineer some genomic data from the publication of summary statistics about the data, a common practice in reporting research results from proprietary datasets.[155] Of course, independent derivation and reverse engineering are defenses to claims of misappropriation—not a denial of the trade secret subject

150. *See id.* (discussing licensees).

151. Hrdy, *supra* note 4, at 563.

152. For example, CanCORS, a proprietary genomic dataset, is owned by an unincorporated consortium of research scientists, and licenses its data—when it does—for free. *See* Sherkow, *supra* note 145, at 356.

153. Hrdy, *supra* note 4, at 590.

154. All of Us *Research Program Makes Nearly 250,000 Whole Genome Sequences Available to Advance Precision Medicine*, NAT'L INSTS. HEALTH (Apr. 20, 2023), https://allofus.nih.gov/news-events/announcements/all-us-research-program-makes-nearly-250000-whole-genome-sequences-available-advance-precision-medicine#:~:text=Advance%20Precision%20Medicine-,All%20of%20Us%20Research%20Program%20Makes%20Nearly%20250%2C000%20Whole,Available%20to%20Advance%20Precision%20Medicine&text=All%20of%20Us%20genomic%20dataset,way%20to%20advance%20precision%20medicine [https://perma.cc/7QPP-FR3F]; Bjarni V. Halldorsson et al., *The Sequences of 150,119 Genomes in the UK Biobank*, 607 NATURE 732, 732 (2022).

155. Zhiyu Yang, Peristera Paschou & Petros Drineas, *Reconstructing SNP Allele and Genotype Frequencies from GWAS Summary Statistics*, 12 SCI. REPORTS 1, 1–2 (2022).

matter of the underlying information. Nonetheless, the genomic data revolution has made such defenses an ongoing and active area of genomic research itself.

C. CASES ON DNA SEQUENCE DATA AS TRADE SECRETS

If DNA sequences are, in fact, trade secrets—and if they're truly valuable, as claimed—then there's likely to be *some* litigation surrounding them. But a review of cases on trade secret claims, both state and federal, yields all of *thirty* unique cases with published decisions that even *mention* DNA sequences or genomic data alongside a related trade secrecy claim.[156] Importantly, several of these cases explicitly *reject* genomic sequences as trade secret subject matter. Take, for example, *SinoMab Bioscience Ltd. v. Immunomedics, Inc.*, a case surrounding a collection of genetic sequences covering certain antibodies.[157] The facts in *SinoMab* were simple: the plaintiff, Immunomedics, alleged a former employee, Leung, took some of these sequences with him to join defendant as an employee, and this constituted trade secret misappropriation.[158] The Chancery Court of Delaware rejected this claim outright, on the grounds that the sequences in question did not constitute protectable subject matter under New Jersey's implementation of the UTSA:

156. Before we move on, let's unpack the methodology. First: I define a "unique case" as a dispute between the same or related parties arising from the same factual nexus, analogous to the standard used to determine supplemental jurisdiction. *Cf.* 28 U.S.C. § 1367. This avoids the artificiality of treating separately filed complaints arising from the same conduct—say, one affirmative complaint and one declaratory judgment arising from the same—as multiple lawsuits. It also avoids incorrectly listing, as separate cases, multiple *opinions* in the same case; an order regarding a motion to dismiss and another order regarding a motion for summary judgment in the same case still make *one* case. For example: *XY, LLC v. Trans Ova Genetics, LC*, a case about sperm-sorting technology useful in animal breeding, yielded six court opinions even though the lawsuit arose from the same underlying facts. That's one lawsuit—not six.

Second: my search is confined to those decisions made available on Westlaw, using the following search criteria in Westlaw's "ALLCASES" database: (genomic genetic DNA) /100 (trade /1 (secret secrecy)). As of October 9, 2023, this yielded 261 decisions arising from 206 unique cases. Relatedly, I do not confine myself to only those decisions that have been officially reported. A decision is a decision, as far as I'm concerned, irrespective of whether the Federal Supplement thinks so.

Third: I then went through the available opinions and underlying complaints, if available on Westlaw, to determine whether the plaintiff alleged the misappropriation of a trade secret pertaining to anything related to DNA or genomic sequences as opposed to, say, a piece of document imaging software called "Doc DNA." *See, e.g.*, Advanced Tech. Servs., Inc. v. KM Docs, LLC, No. 1:11-CV-3121-TWT, 2011 WL 5870545, at *3–4 (N.D. Ga. Nov. 21, 2011). For my purposes, I discounted cases that alleged misappropriation of crop *seeds*, rather than crop DNA or genomic information. *See, e.g.*, Biochron, Inc. v. Blue Roots, LLC, 529 P.3d 464, 478 (Wash. Ct. App. 2023) (alleging misappropriation of genetically unique marijuana cultivars—but not misappropriation of the genetic information itself). I also discounted cases that alleged misappropriation of DNA sequencing *technology*—rather than the sequences themselves. *See, e.g.*, Gene Codes Corp. v. Thomson, No. 09-cv-14687, 2011 WL 611957, at *2 (E.D. Mich. Feb. 11, 2011). All told, this step yielded thirty unique disputes.

After that, I went through whatever opinions were available through Westlaw to see whether the defendant raised the objection that the purported genomic trade secret was not—as is the point of this Article—trade secret subject matter—a grant total of *nine* cases. A spreadsheet documenting this analysis is available at https://doi.org/10.7910/DVN/I1UU02.

157. No. 2471-VCS, 2009 WL 1707891, at *1 (Del. Ch. June 16, 2009).

158. *Id.* at *1.

> With respect to the DNA sequence that Immunomedics claims that Leung took, I find that this sequence is not the type of protectable information that New Jersey protects as a trade secret. It was a slight variation on publicly known information which Leung created in a few hours using publicly known methods. And, there is no record evidence that this sequence was particularly valuable to either Leung or Immunomedics or that the Sequence gave Leung some unfair advantage vis-a-vis his former employer. Thus, Leung's use of the DNA sequence in question is not actionable as the misappropriation of a trade secret.[159]

Or, take *Brigham Young University v. Pfizer, Inc.*, a case about whether Pfizer's use of genomic sequences and cells from a certain mouse model constituted trade secrets misappropriation.[160] There, the District Court specifically separated the plaintiff's trade secrets claims covering the allegedly pilfered genomic sequences from the cells themselves, finding that because the underlying genomic information was "readily available," it could not constitute a trade secret.[161] It contrasted this with Pfizer's use of cells provided to it by the plaintiff, which the court described as "difficult."[162] A variety of cases in a diversity of contexts have similarly cast aspersions on whether genomic data is protectable as a trade secret.[163]

Meanwhile, other cases—those which allowed some form of trade secret claim to genomic data to proceed to trial—are not what one would expect from the broader proposition that DNA sequence data are trade secrets. They're almost exclusively about animal breeding and largely idiosyncratic—if not entirely unique—to the facts of the underlying industry in which the purported trade secret was alleged to have been misappropriated. Take, for example, *North American Deer Registry, Inc. v. DNA Solutions, Inc.*, a case centered on a genetic registry of domesticated deer for breeding purposes.[164] Genomic sequencing of a breeding population of deer allowed the plaintiff, North American Deer Registry, Inc., to build a lineage database, allowing purchasers of buck semen to both value their purchase and verify its provenance.[165] The defendant, DNA Solutions, Inc., allegedly took portions of this database in confidence.[166] The U.S. District Court for the Eastern District of Texas granted a motion for a preliminary injunction, and rejected DNA Solutions' argument that the database was not a trade secret.[167] But in doing so, the court rejected DNA Solutions' subsidiary argument that only "the biological material and genetic data create

159. *Id.*

160. No. 2:06-CV-890, 2012 WL 1029289, at *1 (D. Utah Mar. 26, 2012).

161. *Id.* at *4.

162. *Id.*

163. *E.g.*, Yoder Bros. v. Cal.–Fla. Plant Corp., 537 F.2d 1347, 1365 (5th Cir. 1976); N.C. Farm P'ship v. Pig Improvement Co., 593 S.E.2d 126, 128 (N.C. Ct. App. 2004).

164. No. 4:17-CV-00062, 2017 WL 2402579, at *1 (E.D. Tex. June 2, 2017).

165. *Id.*

166. *Id.* at *2.

167. *Id.* at *10–11.

the 'database.'"[168] Rather, the court found that only the *entirety* of the database was a trade secret.[169] Moreover, the plaintiff's own expert "testified that the economic value of the Registry flows from the *deer lineages*," not the genomic information.[170] This the court agreed with, noting "the economic value of each trade secret is derived from the compilation of many data points that are not readily ascertainable by the public."[171] Equally important, though, is what the court did not ultimately acknowledge. The bulk of the database was created in 2007—back when NGS was still, itself, a fawn. Even if the genomic information was costly to produce and keep secret in 2007; that's simply not true today, where breeding lineage sequencing costs—again, retail—three hundred dollars, a price discounted to *zero* if you're willing to pay stud fees.[172] But to take a step back for a moment: the vagaries and business models involved in ungulate breeding are likely specific to their facts rather than generalizable propositions that genomic data are trade secrets.

In another recently decided case—this one about shrimp rather than deer breeding—a jury found that the defendant, American Mariculture, Inc., misappropriated TB Food USA's trade secrets in brood shrimp (for use in aquaculture) and "biologic information and markers of animals including genetic information."[173] This finding was affirmed by the district court over the defendant's strenuous objections that the plaintiff did not know the shrimp brood genomic sequences and that "no court in the United States has ever found that the genetics of bred animals constitute a trade secret under the DTSA or the FUTSA."[174] But the district court did not explicitly adopt the position that genomic sequences were necessarily protectable information. To the contrary, the district court lay the decision at the jury's feet, noting, simply, "There was sufficient evidence admitted at trial from which a reasonable jury could find that there was 'information' in this case which qualified as a trade secret," further noting, that "much of the evidence was disputed" and the case's procedural posture compelled it read the record in the light most favorable to TB Food.[175] Despite some hyperbolic reporting on the case about a court finding trade secrets covering a "living creature,"[176] this isn't exactly a full-throated defense of genomic information as being trade secret subject matter.

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168. *Id.* at *7.

169. *Id.* at *7–8.

170. *Id.* at *8.

171. *Id.* at *7.

172. *Genetics*, VICTORY ROSE THOROUGHBREDS, https://web.archive.org/web/20220819150425/https://www.victoryrose.com/genetics (last visited Apr. 5, 2024)

173. TB Food USA, LLC v. Am. Mariculture, Inc., No. 2:17-cv-9-FtM-29NPM, 2022 WL 3028061, at *3 (M.D. Fla. Aug. 1, 2022).

174. *Id.*

175. *Id.*

176. Kyle Jahner, *Shrimp Genetics Case Dips Into Uncharted Trade Secret Realm (2)*, BLOOMBERG L. (Aug. 19, 2022, 9:08 AM PDT), https://www.bloomberglaw.com/bloomberglawnews/ip-law/XFUS7MI4000000 [https://perma.cc/MLM8-64JP].

There are also several earlier cases finding trade secret subject matter in novel genetic variants of agricultural products—the "germplasm" cases, so called, because the item purported to be protected by a trade secret was the product's germplasm, meaning, the genetic material in a living cell often used for seed development.[177] In all of those cases, though, the courts faced with the issue of whether the germplasm was protectable by a trade secret went to pains to distinguish the *germplasm*—that is, a living cell that happened to contain DNA—from the DNA sequences themselves.[178] In *Del Monte Fresh Product Co. v. Dole Food Co.*, Del Monte alleged that one of its former employees took its prized pineapple variety to its competitor—and new employer—Dole Food Co.[179] Dole moved to dismiss, in part, on the grounds that the pineapple's genetic information could not be protected by trade secrecy under either California or Florida law.[180] While the court did not adopt Dole's argument, it did conclude that—at least for purposes of surviving a motion to dismiss—a physical instance of the pineapple itself could potentially be a trade secret even though it was not purely information but would, unlike genetic data, "will eventually develop into an edible plant when planted and watered."[181] Furthermore, the court took Del Monte to task for not alleging, with particularity, whether the pineapple's genetic sequence was the information sought to be protected—a missing allegation all the more surprising if genomic information was clearly protectable by trade secrets law.[182] In fairness to Del Monte, it was probably hesitant to hang its trade secrecy hat on its pineapple's DNA because in another germplasm case, *Yoder Bros., Inc. v. Cal.–Fla. Plant Corp.*, the U.S. Court of Appeals for the Fifth Circuit has this to say about the relationship between secret germplasm, genomics, and ready accessibility:

> We reject Yoder's suggested analogy to trade secret law, claiming that the plant's genetic code is the secret. In one sense, the genetic code always remains a secret, even to the breeder. In the more common sense, however, as soon as the plant is released, so are its secrets. We prefer the latter view as the one more in accordance with experience.[183]

177. *E.g.*, Pioneer Hi–Bred Int'l v. Holden Found. Seeds, Inc., 35 F.3d 1226, 1228, 1240 (8th Cir. 1994); Yoder Bros. v. Cal.–Fla. Plant Corp., 537 F.2d 1347, 1351–52, 1382 (5th Cir. 1976); Del Monte Fresh Produce Co. v. Dole Food Co., 136 F.Supp. 2d 1271, 1291–93 (S.D. Fla. 2001); . Note: I *excluded* these from my count of DNA trade secrecy cases but am discussing them there for the sake of completeness.

178. *Del Monte Fresh Produce Co.*, 136 F.Supp. 2d at 1293; *Pioneer Hi–Bred Int'l*, 35 F.3d at 1233; *Yoder Bros.,* 537 F.2d at 1365 n.16.

179. *Del Monte Fresh Produce Co.*, 136 F. Supp. 2d at 1276.

180. *Id.* at 1283.

181. *Id.* at 1292.

182. *Id.* at 1292–93 ("While it is clear that Del Monte seeks to protect MD-2 [the pineapple variety], Dole correctly states that 'it is unclear exactly what aspect of MD–2 Del Monte claims is entitled to trade secret protection.' Def.'s 12(b)(6) Mtn. to Dismiss at p. 7. Does Del Monte seek to protect MD–2's genetic code, growth technique, or some other quality? Because this case involves complex factual matters, Dole's motion to dismiss count II is granted without prejudice so that Del Monte can plead more specifically what aspect of MD–2 it seeks to protect as a trade secret.").

183. *Yoder Bros.,* 537 F.2d at 1365 n.16.

And that was back in 1976, even before the advent of first-generation DNA sequencing![184]

All put together, there's a shocking paucity of cases finding, as fact, the protectability of trade secrecy in DNA sequences. This is astonishing given the body of literature tethering genomic data to trade secrecy—and the wringing of its authors' collective hands over the prospect. And it is all the more fantastical given the banality of trade secrets cases for *other* forms of "pure" data, including things like lists of customers and computer algorithms. If genomic data is valuable as a trade secret, litigation, at least, has not proven it.

D. SCHOLARLY ASSUMPTIONS ON DNA AS TRADE SECRETS

Despite all of this, a raft of legal scholarship has been underwritten on the premise that genomic data are, by and large, protectable as trade secrets. In 2000, Rebecca S. Eisenberg assumed that such protection would be possible as an alternative to patents;[185] Alexander K. Haas made a similar observation a year later.[186] Anna B. Laakmann proposed that "[t]rade secrecy might, in some circumstances, be a better legal mechanism than patents to facilitate sharing of genomics research."[187] In one highly influential article, John M. Conley, Robert Cook-Deegan, and Gabriel Lázaro-Muñoz detailed the clinical concerns about the use of trade secrecy in proprietary genomic databases.[188] A trio of health policy experts from Baylor College of Medicine—Christi J. Guerrini, Amy L. McGuire, and Mary A. Majumder—similarly did so in the pages of *Science* in 2017, under the subtitle, "Trade-secrecy laws clash with a right to one's health data."[189] Alexis K. Juergens and Leslie P. Francis began with the premise that genomic databases are protectable as trade secrets to explore ways to upend them.[190] Recently, David S. Levine noted that genomic trade secrets were responsible, in part, for innovation policy deficiencies in COVID-19 research.[191] And I made similar assumptions about genomic sequences in cancer research.[192]

A closer examination of this body of scholarship, however, uncovers three, curious facets about their grounding assumptions. One: The vast bulk of this work relies on a single or few narrow examples: namely, Myriad Genetics' claim that its database of sequences of patients' *BRCA1* and *BRCA2* genes—genes implicated in early onset breast and ovarian cancers—are a trade secret.[193]

184. *See supra* notes 50–54 and accompanying text.

185. Eisenberg, *supra* note 1, at 795.

186. Haas, *supra* note 1, at 162.

187. Laakmann, *supra* note 1, at 1021.

188. Conley et al., *supra* note 30, at 613–16.

189. Guerrini et al., *supra* note 33, at 586.

190. Alexis K. Juergens & Leslie P. Francis, *Protecting Essential Information About Genetic Variants as Trade Secrets: A Problem for Public Policy?*, 5 J.L. & BIOSCIENCES 682, 682–83 (2018).

191. David S. Levine, *Trade Secrets and the Battle Against Covid*, 15 J. INTELL. PROP. L. & PRAC. 849, 849 (2020).

192. Sherkow, *Cancer's IP*, *supra* note 145, at 341–46.

193. *See, e.g.*, Conley et al., *supra* note 30, at 613–16.

Indeed, in hundreds of articles about genomics and trade secrets, Myriad's database is *the only* concrete example. This isn't terribly problematic for articles about Myriad's database *specifically*—but it casts doubt on extending Myriad to stand for the larger proposition that DNA databases, today, are trade secrets. The creation of Myriad's database dates back to the pre-NGS days when sequencing even single genes was indeed an expensive and uncertain process. Today, this is simply no longer the case. In addition, the value in Myriad's database was never the sequence data themselves—information Myriad openly *shared* with patients and clinicians—but their pairing with patients' clinical outcomes. This ultimately says little about whether the underlying genomic data are themselves trade secret subject matter. And lastly, scholars' heavy reliance on Myriad as an example of genomic trade secrets—combined with the paucity of other examples—suggests that either the practice is simply not widespread, or—given everything else—whatever Myriad has may not be trade secrets. Bluntly: If Myriad's database isn't sufficient evidence that genomic data can be protected by trade secrets, much scholarship on DNA trade secrecy may rest on nothing.

Two: As evidence of the general argument that genomic data are trade secrets, scholars have often largely recited the same basic elements of trade secret eligibility detailed here—namely, that the information is subject to reasonable efforts to maintain its secrecy, derives independent economic value from its secrecy, and is not readily ascertainable. But this is often done with little, if any, probing analysis into what those elements *mean*. And again, what analysis there is—even recently—largely fails to grapple with the exponential rise of NGS. For example, in assessing the protectability of Myriad's database as a trade secret, Conley, Cook-Deegan, and Lázaro-Muñoz call the matter "straightforward," cite the elements Uniform Trade Secrets Act, and then conclude—with little interrogation—that Myriad's "thus-far proprietary [variant of unknown significance] data would clearly satisfy this definition."[194] There is no discussion about whether the database's secrecy indeed drives its independent value, whether the genetic information within the database is nonetheless readily ascertainable, or whether the calculus of any of that had changed, by the article's publication date in 2014. By that time, the cost of genomic sequencing had fallen to a dime per million bases—eight orders of magnitude fewer since the *BRCA1* and *BRCA2* genes were first sequenced. Countless other genomics scholars' interpretations of trade secrecy statutes fall along similar lines.[195]

Three: Almost no scholarship cites actual U.S. caselaw that concludes that genomic data are protectable by trade secrets.[196] That is, of course, because—as

194. *Id.* at 616.

195. *See, e.g.*, sources cited *supra* notes 164–171.

196. This was, in fact, the impetus for this Article. In trying to "reassess" cases concluding that genomic data were trade secrets in light of genomic sequencing advances, I was struck by the total absence of any cases cited in the literature—a true oddity for a claim so widely held. That reassessment became, simply, an assessment; that's this Article.

discussed above—little readily exists. But that's the point: Of the *hundreds* of law review articles discussing trade secrets in the context of genomics, none—at least as far as I have read—have found a body of cases conclusively demonstrating that courts tend to view genomic data as trade secrets. It seems implausible to attribute this absence of recited cases to other factors—search difficulties, unimportance, scholarly ineptitude—so much as yet further proof that the underlying claim simply is founded on myth. All in all, scholarly claims to genomic data as being unquestionably trade secrets are, themselves, at least questionable.

To be fair, there are some excellent counterexamples.[197] In 1994, Dan L. Burk—as if peering into a crystal ball—had this to say about biotechnology, generally, and trade secrecy's ready accessibility bar:

> Several factors in the Restatement test for trade secrecy tend to favor such protection for biological materials. . . . At the same time, the rapid advance of biological research and the academic character of the biotechnology industry may work to frustrate the requirement of secrecy. For example, in the litigation between Eli Lilly and Genentech [Case No. IP 87-219-C (S.D. Ind. 1990)] Lilly alleges that Genentech's purported trade secrets were available publicly and from third parties, and so fall outside the purview of trade secrecy. Overcoming such a defense—proving that claimed trade secrets were *not* publicly available—may be extremely difficult in biotechnology. . . . For example, in the case of a recombinant plasmid such as that supplied by Genentech under its agreement with Eli Lilly, the DNA gene sequence that codes for the desired pharmaceutical product is likely to be proprietary. However, the other individual genetic elements that will be incorporated into the plasmid may be well known in the literature. Their combination is also likely to be apparent from the literature, because the placement of the genetic elements is constrained by the way the plasmid operates . . . . Assembly of such genetic elements may be too obvious from the literature to constitute a "secret."[198]

In a 2011 response letter in *Science*, critiquing another paper's repetition of the myth, Edward S. Dove, Yann Joly, and Bartha M. Knoppers hit the nail on the head of independent value: "Trade-secret information, by definition, must confer an economic benefit on the holder, deriving specifically from the fact that the information is not generally known. Genetic information is financially worthless absent outsourced scientific interpretation and technological application (and even then, there is no guarantee of its financial worth)."[199] And Donna M. Gitter, in her review of the International HapMap Project—a set of genomic databases used "to determine the common patterns of DNA sequence

197. I owe a debt to Jorge L. Contreras for pointing many of these out.

198. Dan L. Burk, *Misappropriation of Trade Secrets in Biotechnology Licensing*, 4 ALB. L.J. SCI. & TECH. 121, 148–50 (1994).

199. Edward S. Dove, Yann Joly & Bartha M. Knoppers, *Trade-Secret Model: Legal Limitations*, 333 SCIENCE 1575, 1575 (2011).

variation in the human genome"[200]—wrote a detailed analysis of whether the databases qualified for trade secrecy protection under the UTSA.[201] But these are exceptions, not the rule; quiet heresies that ultimately did little to challenge the orthodoxy of genomic data as trade secrets.

E. THE TRUTH IN THE MYTH

But not so fast. Declaiming genomic data as not subject to trade secret protection is a bold provocation. It cuts against decades of scholarly and industry understanding of the field, and rests on several debatable propositions in trade secrecy law alongside little more than simple observations about the state of the world. Can it really be so? After all, there are other forms of secret information that are more easily ascertainable than DNA sequences that nonetheless are still protectable by trade secret law. There are yet others that are protectable even though they confer *less* economic value to their owners than genomic data might. And there are whole fields that similarly possess few—or fewer—trade secrecy cases than genomics, and similarly lack any explicit statutory recognition of their status. Perhaps the common wisdom is indeed wise—or, at a minimum, correct.[202]

These are good counterarguments to this Article's claim. But they don't disprove its central thesis: that much DNA sequence data, in the age of NGS, is unlikely to be trade secret subject matter. Still: Where's the engagement with NGS technologies? Where are the litigated cases? Where are the practices demonstrating the positive? And yet, such counterarguments are insightful because they illuminate this thesis's boundaries—and, in doing so, provide a more robust understanding of trade secrecy law, especially when faced with an encroachingly powerful technology. That is, they uncover a small bit of truth about genomic data and trade secrets—the underlying truth to the great myth.

Say, for example, you—a detractor of this Article's premise—disagree that genomic data is now, post the NGS era, "readily ascertainable" under trade secret doctrine. Our disagreement therefore likely falls along two axes: one, what ready ascertainment means under the law; and two, whether NGS falls within it. But this highlights the connection between "ready ascertainment" and technological intervention. Regardless of the particulars of what "readily ascertainable" means in practice, the *Restatement (Third) of Unfair Competition*

200. The International HapMap Consortium, *The International HapMap Project*, 426 NATURE 789, 789 (2003).

201. Donna M. Gitter, *Resolving the Open Source Paradox in Biotechnology: A Proposal for a Revised Open Source Policy for Publicly Funded Genomic Databases*, 43 HOUS. L. REV. 1475, 1509–16 (2007). Gitter ultimately concludes that the HapMap databases are protectable as trade secrets—an analysis I disagree with, especially given Gitter's gossamer thin assessment of the independent economic value prong—but it's at least an analysis!

202. *Cf.* Daniel A. Farber, *The Case Against Brilliance*, 70 MINN. L. REV. 917, 917 (1986) (arguing that "brilliance"— "insights that overturn conventional thinking and common sense"—"should count heavily against an economic or legal theory"). To be clear: I am not, in any way, suggesting this Article is "brilliant." That would be obnoxious. I am suggesting, though, that it's *right*.

has characterized it as turning on whether the secret can be revealed in a manner not "difficult, costly, or time-consuming."[203] This has long had an almost Luddite feel, equating such "readiness" with a virtual absence of technological intervention.[204] Technological discoveries of a trade secret, by contrast, have largely been shunted to the defense of reverse engineering.[205] But that's the rub: Our disagreement suggests that one plausible way to view the readily ascertainable prong is whether, in general, it becomes easier to meet as surrounding technologies become simpler, cheaper, and quicker to use—undoubtedly the case for genomic sequencing since the Human Genome Project. Perhaps you nonetheless think we're not there *yet* or that "resequencing" genomic data is still too much of a technological intervention to make genomic sequences "readily accessible." But the broader point stands that that is the direction we're headed—and, consequently, reexamining the myth is in order.

Similarly, perhaps you—the detractor, again—are a legal realist: courts have long given the "economic advantage" prong a free pass, cynically concluding that almost all secret information is valuable to someone. But giving such a requirement a free pass does not make it legally *correct*. As articulated by Hrdy, "[i]ndependent economic value cannot be presumed from the mere fact that the plaintiff kept information secret."[206] Doing so simply runs away from an assessment of what value *is* (to determine if something is valuable at all), let alone whether such value *derives* from the information's secrecy. And again, *naked* genomic data—that is, genomic data untethered to other valuable information—is likely to be of low-value.[207] Furthermore, such value is likely to be *improved* by its disclosure—not its secrecy—especially given the ability of large-scale genomic datasets to "extract value" from such information.[208] You may say, "Who cares? Courts don't look at this stuff that closely." But, again, that's the rub: The disagreement is interesting because it differentiates a realist view of the "independent economic value" prong from a positivist one. And a realist one that may very well need to change if, and when, such cases begin to be fully litigated—especially if cases like *SinoMab Bioscience Ltd. v. Immunomedics* or *Brigham Young University v. Pfizer, Inc.* are harbingers of the future.[209]

There are a number of additional objections—but none of them compelling. One lies in the observation that other areas of trade secrecy law are similarly thinly litigated and not subject to more particular statutes. "No one contests *those* as being protectable by trade secrets!," you might say. Perhaps so. But this does little to disprove that genomic data are *not* trade secrets. To the contrary, it

203. RESTATEMENT (THIRD) OF UNFAIR COMPETITION § 39 cmt. f (AM. L. INST. 1995).
204. *See, e.g.*, Richdale Dev. Co. v. McNeil Co., 508 N.W.2d 853, 857 (Neb. 1993).
205. *See infra* Part IV.B.
206. Hrdy, *supra* note 4, at 561.
207. Dove et al., *supra* note 199, at 1575.
208. *See supra* note 136 and accompanying text.
209. *See supra* notes 157–162 and accompanying text.

suggests—perhaps—that quite a significant amount of information widely assumed to be protectable by trade secrecy may not be. Other objections are appeals to either authority or history (or both): Some of the best scientists and lawyers at the forefront of the Human Genome Project assumed genomic data sets were protectable by trade secrets—and decades of practice have operated under that assumption. We should be careful before calling them wrong—or, at minimum, proving such claims incorrect should operate under an extraordinary burden of proof. But such objections prove nothing themselves: Neither history, nor intelligence, nor technical expertise are elements of trade secrecy. Such arguments certainly don't engage with any of the substantive analysis of whether DNA databases are "readily accessible" or possess "independent economic value." And besides, the same set of lawyers and scientists have been wrong about intellectual property coverage of genomic sequences before—*at least twice!* The first concerned the patentability of snippets of genomic data, "expressed sequence tags" (ESTs), which began in earnest around 1991.[210] Such efforts—widely thought to be suboptimal but legally sufficient—were mercilessly killed off in 2005 by the U.S. Court of Appeals for the Federal Circuit in *In re Fisher*.[211] There, the court found that ESTs failed to satisfy arguably the most basic of patentability requirements: utility.[212] Similarly, Myriad Genetics itself was on the losing end of a dispute concerning the patent eligibility of isolated genomic DNA, despite thousands of analogous patents and decades of practice in the area.[213] So much for the best of minds.

But back to the more salient counterarguments against this Article's thesis. What do they tell us about more broadly about genomic data as trade secrets? They likely suggest that, like many myths, therein lies a kernel of truth. It's not that *no* genomic data are protectable as trade secrets. Genomic databases that are truly not readily accessible or genuinely do contain information that derives independent value from its secrecy should—by this Article's same analysis—be protectable as a trade secret. Instead, the truth likely consists in the recognition that that genomic data are better considered on a spectrum of protectability. At one end, are naked genomic data—genomic data without any attachment to other valuable information. Such data, assuming the population of samples is known, is likely not a trade secret, being both "readily ascertainable" by virtue of improvements to sequencing equipment and lack of value in the *secrecy* of such information. At the other end of the spectrum are genomic data linked to valuable, difficult to derive information, and further analyzed for the meaning of such connections. The portion of Myriad Genetics' database on genetic "variants of unknown significance" is nothing more than a collection of raw

210. Robert Cook-Deegan & Christopher Heaney, *Patents in Genomics and Human Genetics*, 11 ANN. REV. GENOMICS & HUM. GENETICS 383, 400 (2010).

211. 421 F.3d 1365 (Fed. Cir. 2005).

212. *Id.* at 1369–78.

213. Ass'n for Molecular Pathology v. Myriad Genetics, Inc., 569 U.S. 576, 580 (2013).

genomic data—the sequence readout for *BRCA1* and *BRCA2* for a number of patients.[214] But its connection to those variants' effects on the development of certain cancers is more than that: It is a measurement of patient propensity for cancer linked to the (less valuable) raw genomic information. It's this aspect of Myriad's database—if any—that's not readily ascertainable information. Commentators' reliance on Myriad as a case study of genomic trade secrecy, therefore, makes *some* sense: it's a good edge case for when easily reconstructed genomic variant data tips the scale into something more.

At the same time, this doesn't make the rest of the myth true. In the middle of the two extremes—where most DNA sequence data lay—is an almost limitless number of databases that tether genomic information to basic information about their samples but little more. Whether such genomic information is a trade secret *should* turn on things like factual assessments of the state-of-the-art to determine their ready ascertainment and the value arising from such information's secrecy, rather than decades of orthodoxy.

III. PRACTICAL CONSEQUENCES TO THE MYTH OF DNA TRADE SECRECY

Determining whether DNA sequence data are protectable as trade secrets is more than a mere academic debate. It yields several, significant practical consequences. After all, there's no liability for misappropriating a trade secret if the underlying information is *not* a trade secret. So, when would there be liability, if ever? Getting a sense of that requires some thinking about what a failed genomic data misappropriation case would look like. And for that, some of the genomic data trade secrecy cases—the "close, but no potato"[215] ones presented earlier—provide realistic, workable examples.

Take the facts from *SinoMab Bioscience Ltd. v. Immunomedics, Inc.* as but one hypo.[216] In *SinoMab*, a former employee was alleged to have absconded with some genomic sequences to start his own company.[217] His former employer—without a trade secret claim—was forced to rely on a potpourri of causes of action, surrounding sundry things like patent assignments, a non-competition agreement, and a breach of an implied covenant of good faith and fair dealing.[218] As another example, how about the facts from *North American Deer Registry, Inc. v. DNA Solutions, Inc.*?[219] There, the defendant, DNA Solutions, a contractor to the plaintiff, North American Deer Registry, was

214. Cook-Deegan et al., *supra* note 32, at 585.

215. *Cf.* Close But No Potato (@ButNoPotato), TWITTER, https://twitter.com/ButNoPotato [https://web.archive.org/web/20180207074559/https://twitter.com/ButNoPotato]. The phrase—reminiscent of the more well-known, "Close, but no cigar"—is meant to convey someone on the verge of, but yet to arrive at, an intellectual breakthrough. And so, too, here: Cases like *TB Food USA, LLC v. Am. Mariculture, Inc.*, No. 2:17-cv-9-FtM-29NPM, 2022 WL 3028061, at *8 (M.D. Fla. Aug. 1, 2022), come *so close* to the understanding that genomic data may not be protectable by trade secrecy. But alas: no potato.

216. No. 2471-VCS, 2009 WL 1707891, at *1 (Del. Ch. June 16, 2009).

217. *Id.*

218. *Id.* at *20–21.

219. No. 4:17-CV-00062, 2017 WL 2402579, at *1 (E.D. Tex. June 2, 2017).

responsible for maintaining—and keeping confidential—North American Deer Registry's database of genomic deer lineages.[220] The trade secrets claim there turned on whether DNA Solutions failed to "return" the genomic data back to North American Deer Registry—and therefore, misappropriated it—by delivering a copy to North American Deer Registry while also keeping the same in its own, larger database.[221] But without a trade secrets claim, North American Deer Registry would have largely been left with a single claim for violation of constructive trust, akin to breach of a bailment.[222]

If these fact patterns are representative of a future without genomic trade secrecy, we can glean a few things. First, this means disputes surrounding genomic data will likely shift from federal to state court. Without a trade secret, there's no misappropriation claim under the DTSA, and without the DTSA, the bulk of cases will likely have no other federal cause of action. Absent diversity jurisdiction—always a possibility, sure—the remaining claims from *TB Food* and *North American Deer Registry* weren't federal ones. Second, and relatedly, a move from federal to state courts will result in varied dispositions on how far *non-trade secret* confidentiality provisions can be enforced. Third, whatever remedies are left after all of that are likely to be of low value—or, at least, lower value than claims sounding in trade secret misappropriation. Fourth, injunctive remedies will likely be unavailable to aggrieved genomic data holders. And fifth, at one level of remove, these diminished returns on litigating genomic trade secret cases may, at the margins, lead some to an arms race, of sorts, in protecting genomic data—a reality which, if true, is likely to have negative consequences for the field.

A. LITIGATION SHIFT FROM FEDERAL TO STATE COURT

There is, essentially, a single cause of action to police trade secrecy rights: misappropriation. One misappropriates a trade secret if—and only if—they acquired, disclosed, or used another's trade secret by "improper means."[223] Which means are, in fact, "improper" is pretty expansive, from violating the express terms of an NDA to the more loosey-goosey "standards of commercial morality in the business world."[224] But the threshold requirement to make such bad behavior actionable—at least under trade secrecy law—is whether the underlying information is definitionally a trade secret. If it's not, there is no misappropriation claim; it's a perfect defense.

If raw genomic data is not subject to trade secrecy protection, then for all practical purposes, the unauthorized disclosure of that portion of data or DNA

220. *Id.* at *1–2.

221. *Id.* at *8.

222. *Id.* at *2. North American Deer Registry also pleaded federal Lanham Act violations, but those turned on nuances of DNA Solutions' marketing to customers that are unlikely to be instructive for future cases. *Id.* at *5–7.

223. *See* 18 U.S.C. § 1836(b)(1)(2); UNIF. TRADE SECRETS ACT § 1–2 (UNIF. L. COMM'N 1985).

224. E. I. duPont deNemours & Co. v. Christopher, 431 F.2d 1012, 1015 (5th Cir. 1970).

sequences cannot give rise to a misappropriation claim. That would remove the federal DTSA arrow from the quiver of possible causes of actions for aggrieved genomic data holders. And that, in turn, would largely deprive the holders of such data of the ability to bring their case in federal court, absent diversity jurisdiction or a particular wonky set of facts involving either supplemental jurisdiction or the Computer Fraud and Abuse Act.[225] If the typical case—like those presented above—involved a former employee or confident copying genomic data and giving it to another, there doesn't seem to be any other private, civil federal cause of action that neatly fits.

Relatedly, a no-go on misappropriation also preempts the possibility of litigating the dispute in the International Trade Commission under its authority to ban the importation of articles derived through the misappropriation of a trade secret.[226] The importation of data, alone—data not being an "article"—is already not a viable cause of action for complainants in the ITC.[227] So an absence of trade secret protection would seemingly also stymie cases where the genomic data is tied up in the germplasm of some organism. This happens now and then, like in *In re Certain Botulinum Toxin Products, Processes for Manufacturing or Relating to Same and Certain Products Containing Same*, where the complainant alleged that a former employee stole a trade secret bacterial strain useful in manufacturing Botox (onabotulinumtoxinA).[228]

Without a federal hook, disputes between genomic data holders and their unwanted possessors would need to be brought into state court. But because the DTSA's definition of trade secret subject matter mirrors the state-level UTSA's definition, state court trade secrecy claims would similarly be duds. So genomic data holders wishing to police their wares would likely need to rely on other sorts of claims—breaches of confidence or fiduciary duties, unjust enrichment, tortious interferences, violation of a bailment—the bread-and-butter of state-court business disputes. But—and unlike trade secrets law—these state-law causes of action are far from harmonized. They turn—hard—on which state they are filed, which state's law governs, and, whether personal jurisdiction is even available over the accused tortfeasor. In some instances, the success of such cases is subject to even smaller technicalities: which county or courthouse the complaint gets assigned to, the makeup of the jury pool, or the presiding judge

225. 28 U.S.C. §§ 1332(a) (establishing diversity jurisdiction), 1367(a) (establishing supplemental jurisdiction); 18 U.S.C. § 1030(g) (establishing the Computer Fraud and Abuse Act's private cause of action).

226. 19 U.S.C. § 1337(a)(1)(A).

227. ClearCorrect Operating, LLC v. Int'l Trade Comm'n, 810 F.3d 1283, 1290–91 (Fed. Cir. 2015).

228. *See, e.g.*, Verified Complaint of Medytox and Allergan Under Section 337 of the Tariff Act of 1930, As Amended at 2, 5–6, *In re.* Certain Botulinum Toxin Prods., Processes for Mfg. or Relating to Same & Certain Prods. Containing Same, Inv. No. 337-TA-1145, USITC Pub. 5301 (Jan. 30, 2019) (seeking to enjoin the importation of a genetically modified bacteria used in pharmaceutical manufacturing).

To be clear, this is not a criticism—"laboratories of democracy" and all that.[229] Perhaps these disputes are indeed more aptly resolved as disputes surrounding the violations of business confidences than the nature of genomic data itself. But given that federal fora are the preferred venue of choice for sophisticated litigants, this may be a significant drawback for some of the most well-heeled genomic data holders. Some—without trade secrecy protection—may prefer not litigating their breach of confidence cases at all, rather than suffer the vagaries of whichever state court in which they can hale the accused.

B. STATE-LEVEL VARIABILITY ON ENFORCING NON-TRADE SECRET CONFIDENTIALITY AGREEMENTS

Even apart from the lack of harmonization of employment or fiduciary disputes in state-court, there's a wide variability on whether and to what extent courts will enforce data confidentiality provisions in NDAs.[230] This is potentially significant to DNA database holders because—again—absent trade secrecy protection, and without an employer-employee relationship between the genomic data holder and the accused, the most likely place for a claim to arise would be under an NDA. This is, in fact, a popular legal mechanism for genomic data sharing between commercial entities.

Recent data on NDAs from Camilla A. Hrdy and Christopher B. Seaman shows that of a large subset of NDAs disclosed in trade secrets lawsuits, 97%—431 NDAs out of a sample of 446—prohibited the disclosure or use of confidential information even beyond information kept as a trade secret.[231] Compare this to the number of NDAs centered on nondisclosure of trade secrets alone: 77%, or 343 of the sample of 446.[232] These confidentiality provisions are wide-ranging, protecting confidential business information, technical information, research results, data, and, of course, trade secrets.[233]

Perhaps, then, DNA database owners wishing to police the disclosure of "their" sequences could use such confidentiality restrictions to do what trade secrecy could not. But the problem with that approach is enforceability: Courts do not always enforce such broad confidentiality provisions, especially where the information sought to be protected is not a trade secret.[234] California in particular—home to many biotech companies with loads of DNA sequence data—has famously upended overbroad confidentiality agreements as

229. *Cf.* New State Ice Co. v. Liebmann, 285 U.S. 262, 311 (1932) (Brandeis, J., dissenting) ("[A] single courageous State may, if its citizens choose, serve as a laboratory; and try novel social and economic experiments without risk to the rest of the country.").

230. *See* Camilla A. Hrdy & Christopher B. Seaman, *Beyond Trade Secrecy: Confidentiality Agreements that Act Like Noncompetes*, 133 YALE L.J. 669, 706–21 (2024).

231. *Id.* at 730.

232. *Id.*

233. *Id.* at 685–86.

234. *Id.* at 707–21.

impermissible restrictive covenants under state law.[235] Wisconsin, too, seems to be pretty antipathic to confidentiality provisions for non-trade secret data.[236] To be clear, some jurisdictions have no problem enforcing NDAs on *confidential* but not *trade secret* information,[237] something akin to allowing NDAs to sequester de facto secrets regardless of their de jure status. But the point here is that assessing whether a confidentiality agreement can protect genomic data is widely variable from state-to-state and from case-to-case. The existence of an NDA provides no great assurance that its confidentiality provisions will extend to information that is *not* a trade secret. Not only that, but the answer seems to be rapidly changing, with several states amending their laws to specifically address enforcement of confidentiality provisions covering non-trade secret but nonetheless confidential information.[238]

And yet, even getting over these hurdles—that is, assuming that an NDA could prohibit the disclosure of readily ascertainable DNA sequence information—there are still significant choice of law problems with enforcing such an agreement. Sure, an NDA could simply site its choice-of-law provision to a protectionist state, for example, *not* California. But it's not clear such a choice-of-law provision would itself be enforceable. Generally, an NDA's state choice-of-law controls.[239] But that dissolves if the state of the law chosen has no relationship to the transaction or otherwise "would be contrary to a fundamental policy of a state which has a materially greater interest than the chosen state."[240] In such cases, choosing the correct state's law to apply turns on factors such as where the substance of the transaction takes place or the location of the "property," if any.[241]

What do these factors mean for genomic data? Does it pertain to where the data is located? Where—or from whom—it was sequenced? Where the use takes place? Or the transfer? None of these questions have clear answers in the way a garden variety trade secrets claim would have—the action, and consequently, jurisdiction, tends to occur where the misappropriation took place. But they're especially more problematic for DNA sequence data, which—like the data in *North American Deer Registry*—may exist in a variety of locations and, increasingly today, in the nebulous "cloud." This "deterritorialization" of complex data means that using a particular state's geographic borders as the locus of harm makes enforcement an ever-moving target.[242]

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235. *Id.* at 714–18.

236. *Id.* at 718–19.

237. *Id.* at 708, 710.

238. *Id.* at 708–10, 713–14, 721–23.

239. RESTATEMENT (SECOND) OF CONFLICT OF L. § 187(1) (AM. L. INST., amended 1988).

240. *Id.* § 187(2)(b).

241. *Id.* § 188.

242. *See* Paul Schiff Berman, *Legal Jurisdiction and the Deterritorialization of Data*, 71 VAND. L. REV. EN BANC 11, 17 (2018) ("[S]uch [jurisdiction and choice-of-law] principles are themselves always in flux, often precisely because of the pressures placed on such principles by new communications technologies such as the internet and new ways in which social lives become deterritorialized.").

C. RELATIVE DECREASE IN DAMAGES

Damages in trade secret misappropriation cases can be both large and wide-ranging. They include compensatory damages for the diminishment in value of the underlying information; damages related to the act of misappropriation itself; lost profits of the trade secret holder; unjust enrichment of the misappropriator; ancillary damages—such as those stemming from reputational or competitive harms—to the trade secret holder; and, in some cases, attorneys' fees.[243] As this list suggests, whatever trade secrecy law is missing for causes of action, it makes up for in the wide-ranging types and quantity of remedies available. Put them together, and it's not surprising that some trade secret misappropriation verdicts net hundreds of millions of dollars.[244] One recent dispute, concerning the misappropriation of trade secret software by a former employee, yielded a two billion dollar verdict—not including twenty-three million dollars' worth of attorneys' fees.[245]

But damages for similar disputes—*without* a cognizable trade secret claim—are likely to be far less. This is true because damages for, say, a breach of fiduciary duty with confidential information or the violation of an NDA on similar grounds tend to turn on whether the complainant incurred a direct harm as a result of the *breach*—not, say, the diminishment in the value of the information, if any.[246] Courts routinely award nominal damages for breach of confidentiality claims where the plaintiff can't demonstrate an actual, commercial harm from the breach.[247]

Whether aggrieved data holders really would be compensated less, all else equal, is, in some ways an empirical question. And it's conceded that data on this point are hard to come by, not the least of which is because the analysis is a true apples-to-oranges comparison. The harm giving rise such claims is necessarily different—the violation of trust versus the diminishment in value of a piece of intellectual property—so one should expect damages calculations to be different. But recognizing that the value of damages in such cases goes to the

243. SPRANKLING & SPRANKLING, *supra* note 38, § 7.01.

244. *See* Elizabeth Rowe, *Unpacking Trade Secret Damages*, 55 HOUS. L. REV. 155, 178–79 (2017); Randall Kahnke, Anna Sallstrom & Bryan Washburn, *Developments to Watch in Trade Secret Practice This Year*, LAW360 (Jan. 23, 2023, 5:33 PM EST), https://www.law360.com/articles/1568251 [https://perma.cc/4L4A-HER5] (discussing the trend toward increased damages in trade secrets cases).

245. *See* Final Judgment Ord. at 1–2, Appian Corp. v. Pegasystems Inc., No. 2020-07216 (Va. Cir. Ct. Sept. 15, 2022).

246. *See, e.g.*, Vojdani v. Pharmsan Labs, Inc., 741 F.3d 777, 786 (7th Cir. 2013) (concluding that no damages were available for a breach of confidentiality agreement where there was no harm to the plaintiff); Recif Res., LLC v. Juniper Cap. Advisors, L.P., No. H-19-2953, 2020 WL 6748049, at *11, *13 (S.D. Tex. Nov. 17, 2020) (denying damages for a breach of confidentiality agreement on an oil and gas development project where no harm was proven); The Toledo Grp., Inc. v. Benton Indus., Inc., 623 N.E.2d 205, 211 (Ohio Ct. App. 1993) (decreasing damages award to only nominal damages where no harm from a breach of confidentiality agreement was presented).

247. *See* Murphy, *supra* note 129, at 567 ("[I]n the absence of a misappropriation claim, the damages available may not be economically significant because the plaintiff may not be able to show that the taking of the information caused any actual damages.").

breach—the act, itself, of using or disclosing the nontrade trade secret confidential information—not the *commercial value* of the information does suggest they won't be in the same ballpark as what are routinely becoming multimillion dollar trade secrets cases.[248]

So too for "DNA theft" cases, or so we should assume. Without trade secrets protection, damages are likely to be diminished there because the economic harm—a touchstone of damages calculations in similar cases—would be more difficult if not impossible to prove. Figure it this way: If raw DNA sequence data, as discussed above, doesn't derive independent economic value from its secrecy, what economic value does it have? Or, to put it more granularly for cases litigated in the post-genomic trade secrets context, could the aggrieved data holder demonstrate a real, economic harm resulting from the breach? Perhaps—and it's a stretch—complainants in such cases could allege that absconding with such data deprived them of the fruits of their paid-for sequencing efforts; that is, the economic harm comes from competitors freeriding on sequencing they paid for. But this means such harm would be valued at the cost of sequencing—again, one cent per *million bases* of DNA.[249] Getting from there to the multi-million verdicts of larger trade secret disputes is a practical impossibility.[250]

D. RESTRICTIONS ON INJUNCTIONS

But that's not all! The rump causes of action left for genomic data complainants in the absence of trade secrecy protection come with weak, difficult-to-obtain, or nonsensical equitable remedies. Take *North American Deer Registry*'s claim for violation of a constructive trust. The typical remedy for the demonstrated violation of a constructive trust is the return of the property to the original holder.[251] But—and just like *North American Deer Registry*—this makes little sense when the property is data, which can exist in multiple hands simultaneously. Not only that, but some jurisdictions go out of their way to sever the traditional suite of equitable remedies—namely, injunctions—from those pertaining to constructive trusts. As but one example, the Minnesota Supreme Court noted that the imposition of a constructive trust "does not create an injunction," is not "equivalent to injunctions," and is generally "unrelated to the

248. Kahnke et al., *supra* note 244.

249. *See* Pennisi, *supra* note 77, at 1258.

250. If a court were to calculate competitive harm based on the cost of sequencing, could there be, say, a ten-million-dollar case? At a cost of one cent per million bases, the defendant would have needed to disclose one quadrillion bases. That's roughly 312,500 complete human genomes—almost 50% more genomes than the largest whole genome biobank currently in existence, the U.K. Biobank. Alison Cranage, *How Do You Sequence over 240,000 Whole Human Genomes?*, WELLCOME SANGER INST.: BLOG (Sept. 26, 2022), https://sangerinstitute.blog/2022/09/26/how-do-you-sequence-over-240000-whole-human-genomes [https://perma.cc/VX85-T8ZZ].

251. *E.g.*, *In re* Est. of Figliuzzi, 979 N.W.2d 225, 232 (Minn. 2022) ("A constructive trust requires the holder of the title to property to convey that property to another that has a superior equitable ownership claim.").

preservation or restoration of the status quo."[252] This suggests that aggrieved genomic data holders—without trade secrecy protection—seeking to impose a constructive trust on those who "wrongfully" hold their data may have difficulty obtaining permanent injunctions to do so.

Beyond constructive trusts, there are also possible claims centering on covenants of good faith and fair dealing, especially when dealing with former employees or those operating under an NDA. But injunctions are not automatic even where the implied covenant is violated. Courts still balance a host of factors in assessing the applicability of a permanent injunction in such cases, including whether the defendant has suffered an irreparable harm, the balance of hardships between the parties, and whether the public interest would be best served by an injunction. And even then, permanent injunctions may not in fact be *permanent*; they may be time-limited to prevent the harm found at trial, but not beyond it. Contrast this with permanent injunctions in trade secrets cases: In one recent empirical analysis of 150 federal trade secrets, Elizabeth A. Rowe found that permanent injunctions were awarded in almost every case where the plaintiff requested them, and damages were also awarded.[253]

These difficulties in fitting the equitable remedy peg in the stolen-but-not-trade-secret DNA data hole aren't counterintuitive. They make sense when considering the principal purpose of many equitable remedies: maintenance of the status quo. If the status quo sought to be preserved is to maintain the data's secrecy—that ship has likely sailed by the time the litigants have found themselves in court. If, instead, it's an effort simply to preserve the competitive status quo—that is, to prevent one party from using DNA sequence information it now knows—it's not entirely clear how that can be achieved. If, for example, the competitor has used the purloined genomic data in conducting its own genomic analyses—must those be rerun now without the data in question? And even if that were the case, once the source of the genomic information is known, what's stopping the defendant from simply rerunning—or even computationally inferring—the data? Equitable remedies, here, seem less like efforts to preserve the status quo than quixotic attempts to unring a bell. Indeed, courts have been antipathetic to issuing injunctions that seek to impose secrecy provisions on information that has lapsed into the public domain.[254]

252. *Id.* at 233.

253. Elizabeth A. Rowe, eBay*, Permanent Injunctions, and Trade Secrets*, 77 WASH. & LEE L. REV. 553, 578–79 (2020).

254. *E.g.*, Nite Glow Indus. Inc. v. Cent. Garden & Pet Co., Nos. 2020-1897, -1983, 2021 WL 2945556, at *6 (Fed. Cir. July 14, 2021) (affirming denial of an injunction where "there is a claim for misappropriation of idea and the idea at issue becomes public after it has been misappropriated through no fault of the defendant"); Shapiro v. Hasbro, Inc., 653 F. App'x 568, 568–69 (9th Cir. 2016) (affirming denial of preliminary injunction where information was in the "public domain"); Luccous v. J. C. Kinley Co., 376 S.W.2d 336, 340 (Tex. 1964) (refusing to enjoin defendant from making use of information a trade secret holder otherwise publicly disclosed in a patent application).

Of course, perhaps the plaintiff isn't interested in injunctive relief—as seems to be the case, oddly enough, in most trade secrets disputes.[255] That's a fair assessment. But it's important to recognize that injunctions do work beyond simply expanding remedies available to aggrieved plaintiffs. Injunctions are also a powerful form of leverage toward settlement, a cudgel used to scare a defendant to sitting at the negotiation table.[256] The absence of injunctive relief, by contrast, makes damages and settlement more of an economic affair—a problem for DNA sequence data cases where damages, in the absence of trade secrecy protection, are likely to be low.

IV. LESSONS FROM THE MYTH FOR TRADE SECRETS LAW

Beyond these litigation practicalities, this entire enterprise of understanding the DNA trade secrecy as a myth uncovers some deeper insights about the nature of technology and trade secrets, generally. It provides an example of trade secrecy protection terminating for an entire class of information due to changing technological conditions, something yet to recognized anywhere in the trade secrecy literature. It also suggests that various elements and defenses of trade secrets claims—ready accessibility, independent derivation, and reverse engineering—can, in some circumstances, be closer to one another than perhaps previously appreciated. And it demonstrates, à la the comedy of the commons, that removing trade secret protection may benefit both the former trade secret holder and the public at large. These are both wide and deep lessons for trade secrets law from a somewhat narrow example. But taken together, they suggest that technological advances independent of the trade secret holder may do much to upend the protectability of the underlying information.

A. TRADE SECRET TERMINATION DUE TO CHANGED TECHNOLOGICAL CONDITIONS

The crux of this Article is that advances in and the democratization of DNA sequencing technology, independent of any act on the part of DNA sequence data owners, have diminished the trade secret protectability of DNA sequence information. This is a novel claim, not just for its substance, but also due to its broader underlying assumption: That trade secrets can be extinguished for reasons other than the *specific* information at issue otherwise becoming publicly known. This isn't typically how trade secrets work. Trade secrets, unlike other forms of intellectual property, are immortal: They last forever, so long as their holders maintain their secrecy and the information does not otherwise become known. Ancillary technological advances—the possibility of obtaining *other*

255. Rowe, *supra* note 253, at 578–79.

256. *Cf.* eBay Inc. v. MercExchange, L.L.C., 547 U.S. 388, 396 (2006) (Kennedy, J., concurring) (commenting that in some patent cases, "the threat of an injunction is employed simply for undue leverage in negotiations").

secret information—haven't readily figured into that equation, at least, until now.[257] At its core, this Article proposes that they should.

This is less radical than it may seem. Start with perhaps the most famous trade secret in American history: the formula for Coca-Cola. It (supposedly) has never been made public, despite countless attempts to uncover it. Now, imagine the invention of a device meant to assist home cooks—say, a tabletop artificial intelligence-powered gas chromatograph—that can take a small sample of any liquid and not only identify its individual ingredients but faithfully spit out a recipe for how to make it. And say, further, that this invention becomes widely democratized: It becomes cheap and widespread, given as gifts, and goes viral on TikTok. At that point, it seems silly to suggest that the formula for Coke—or really, any other liquid—can be reasonably kept secret. For the price of our tabletop device—and one can of Coke—we could (finally) uncover Coke's trade secret formula. And this is true even though Coke had no hand in the development of this ancillary technology and did nothing—by omission or commission—to let its closely guarded formula lapse into the public domain.

Such an idea—that changes in the surrounding world may have an effect on individual property rights—isn't cut from whole cloth. The law of servitudes has a readily analogous situation: the termination of covenants due to changed conditions.[258] Generally, servitudes—like trade secrets—last until their beneficial owners do some act to affirmatively extinguish them, for example, abandonment, release, estoppel, etc. But servitudes can also be terminated—independent of any act on the part of the beneficiary—if "a change has taken place since the creation of a servitude that makes it impossible as a practical matter to accomplish the purpose for which the servitude was created."[259] This generally involves an assessment of development surrounding the burdened parcel, for example, whether commercial uses have since engulfed a once-residential neighborhood.[260] If the changes are so "radical . . . that perpetuation of the servitude would be of no substantial benefit to the dominant estate," courts will, on occasion, terminate the servitude entirely.[261]

Extending this general principle suggests that trade secrets can be terminated by changed conditions in the surrounding informational landscape; call it, trade secret termination due to changed technological conditions. If the

257. Or perhaps it has: We now readily assume that much non-secret information is "readily ascertainable" from the Internet in a way that was simply not true—even *if* the same information was non-secret—before the Internet's advance. Perhaps this has, in fact, changed the scope of trade secrecy protection in the same manner. *See* Elizabeth A. Rowe, *Saving Trade Secret Disclosures on the Internet Through Sequential Preservation*, 42 WAKE FOREST L. REV. 1, 20 (2007) ("The very nature of the Internet—that it allows equal access to anyone with a computer, irrespective of certain traditional limitations to accessing information, like geography and cost—means that it makes information at least readily discoverable, if not ascertainable.").

258. RESTATEMENT (THIRD) OF PROP.: SERVITUDES § 7.10 (AM. L. INST. 2000) (establishing that a servitude may be terminated upon "changed conditions").

259. *Id.*

260. *Id.* Application, cmt. c, Covenants.

261. *Id.* cmt. c.

development of ancillary technology yields a radical shift in the availability of information such that it can be easily uncovered by the public at large, then it seems fair to say that the perpetuation of trade secrecy protection for that class of information gives little substantial benefit to the information holder—or, for that matter, the public. Taking a cue from the law of servitudes, courts should terminate the protectability of such information as a trade secret, even if the possessor of the secret has continued to keep it so.

This finding extends the nascent literature on other novel forms of trade secret extinguishment, namely, abandonment.[262] Trade secret abandonment occurs when the trade secret holder no longer derives economic value from the secret information by, for example, replacing a product that embodies the secret information with a new one that doesn't.[263] As described by Camilla A. Hrdy and Mark A. Lemley, however, this generally centers on the conduct of the trade secret holder—whether the holder replaces the product with an updated version, or exits the market, or doesn't enter at all.[264] Secret DNA sequence information, by contrast, may no longer derive economic value from its secrecy for reasons having nothing to do with the trade secret holder. It may cease to be valuable simply because of changing technical and social circumstances on the ground. Nonetheless, understanding termination as a sister form of extinguishment to abandonment, termination due to changed technological conditions fits well within the parameters of trade secret law. And the rise of NGS technologies for DNA provides a sterling example. As other forms of information uncovering technology become radically democratized—drones, artificial intelligence, 3D scanning—they too may change the technological landscape enough to terminate entire classes of trade secrets.

B. TECHNOLOGICAL BLURRING OF TRADE SECRET DEFENSES

There are a variety of defenses to trade secret misappropriation claims, three of which center on how and how easily the accused came to possess the information in question: ready accessibility, independent derivation, and reverse engineering. At the same time, these three defenses operate quite differently from one another. Asserting that information is "readily accessible" is a defense to whether the underlying information is trade secret subject matter in the first instance. No subject matter, no trade secret, and consequently no misappropriation claim regardless of how the defendant came into possession of the information. Independent development, by contrast, is a defense to the accusation of misappropriation; that while the information is nonetheless a trade secret, the defendant came to possess the information by doing its own independent research.[265] Similarly, reverse engineering arises by "starting with

262. Camilla A. Hrdy & Mark A. Lemley, *Abandoning Trade Secrets*, 73 STAN. L. REV. 1, 1, 5 (2021).
263. *Id.* at 4–6.
264. *Id.* at 5–6.
265. TRADE SECRETS LAW, *supra* note 2, § 5:10; MILGRIM ON TRADE SECRETS, *supra* note 2, § 7.02[1][a].

the known product and working backward to find the method by which it was developed,"[266] and is a defense to a claim of misappropriation even if the underlying information is otherwise protectable as a trade secret.

Conceptually, the separation of these defenses makes some sense according to the object of their inquiry. Ready accessibility turns on how widely available the information is, potentially, to the public, even if the defendant obtained the information from the plaintiff. In its purest form, determining ready accessibility turns on "the how" and how easily the public, writ large, *could* obtain the same information. Independent development turns on the efforts of the accused *independent* of the trade secret holder; whether the defendant actually invested enough of its own efforts to develop the same underlying information. And reverse engineering turns on the efforts of both the trade secret holder and the accused: a reward for the defendant who expended its own effort to understand the underlying secret, and punishment for the plaintiff who did not do enough to protect the same. The public, the defendant, or both the trade secret holder and the defendant; the defenses seem to protect different activity by different actors.

But obtaining genomic data challenges this neat little ordering. When it comes to human genomic data at least, the public is often the source of the data itself. In a world where sequencing is cheap, easy, accessible, and accurate, the public can—and routinely does—engage in DNA sequencing of themselves. A defendant, knowing the broader population used to build a confidential genomic database, can independently develop a close approximation of the same, even if the defendant did not expend its own efforts to conduct the sequencing. Is this ready accessibility—because the public *could* do the same, given the low economic barriers to sequencing—or independent development—because the accused actually crafted the database themselves? Tough to say. Or, perhaps, a defendant does perform the sequencing themselves, but only after learning of the sources for the underlying database and how the putative trade secret holder conducted its sequencing. Is *this* independent development—because the defendant engaged in its own independent research, much in the same way as did the trade secret holder—or reverse engineering—because the defendant started with information from the trade secret holder and worked backward? Again: tough to say.

This is, to be clear, more of a theoretical concern than a practical one; conflating the independent development and reverse engineering defenses works the same outcomes irrespective of how a court got there. But it suggests that for some technologies—especially where information is relatively cheap to obtain en masse, and the information is diffused among the public—the line among these defenses may be blurrier than appreciated. Where the broader public—not just the defendant—has easy access to reverse engineering tools, what *is* reverse

266. UNIF. TRADE SECRETS ACT § 1 (UNIF. L. COMM'N 1985).

engineering as opposed to ready accessibility is more of a matter of philosophy than legal formalism.

There are some policy implications to this line of thinking, too—specifically, as an extension to the (celebrated) literature on the law and economics of reverse engineering.[267] In a famous paper from 2002, *The Law and Economics of Reverse Engineering*, Pamela Samuelson and Suzanne Scotchmer explored reverse engineering as a policy lever to preserve the market of certain classes information. Eliminating reverse engineering—as proposed in some industries at the time—preserved the market for such information, even if otherwise readily accessible.[268] Making it more robust, by contrast, diminished the market for the same, and achieved perhaps other policy objectives—like interoperability for software.[269] Understood properly, Samuelson and Scotchmer demonstrated that the reverse engineering defense is not some inexorable command—say, a necessary incantation to some writ of trade secrets—but as a policy lever to tailor intellectual property incentives to achieve certain goals.[270]

This instruction could be readily applied to the DNA sequencing context, now, more than twenty years later.[271] One can easily imagine a regime where lowering the barriers to reverse engineering defenses—say, by allowing defendants to raise the defense simply by engaging in resequencing of some samples—is used to achieve specific policy goals. These may include encouraging more human genomic sequencing—an *explicit* policy goal of various governmental bodies, including the National Institutes of Health as a stepping-stone toward better precision medicine.[272] Indeed, an excellent way of pushing more sequence data into the public domain is to provide what is essentially a safe harbor to misappropriation through resequencing under a reverse engineering defense. Why pay for it when you copy it for free?

But why stop there? These same goals can be achieved just as well by recognizing that, in some contexts, ready accessibility, independent development, and reverse engineering are one and the same. If the ultimate policy goal is the sharing, and forcibly so, of genomic data—a goal that animated the Bermuda Principles—why cabin everything into reverse engineering? Why

267. *See generally* Samuelson & Scotchmer, *supra* note 134 (reviewing the law and economics of reverse engineering).

268. *Id.* at 1591–94.

269. *Id.* at 1621–26.

270. *Id.* at 1662–63.

271. It is worth pointing out that Samuelson and Scotchmer would have likely objected to expanding reverse engineering in the genomics context. Their paper ultimately concludes that "information-based" products are "more vulnerable than traditional manufactured goods to market-destructive appropriations," and this "may justify some limitations on reverse engineering or post-reverse-engineering activities." *Id.* Nonetheless, the authors do acknowledge that "[r]estrictions on reverse engineering ought to be imposed only if justified in terms of the specific characteristics of the industry," such as the economic necessity of trade secrecy—something not present in the genomics context. *Id.* at 1663.

272. *See, e.g.*, NAT'L INSTS. HEALTH, *supra* note 154.

not, instead, turn the policy knob "to 11"[273] and deny trade secrecy protection outright, when the information is, at least potentially, readily accessible to the public?

This, in fact, aligns with the practice in at least one state: Nebraska.[274] In Nebraska, the *potential* of independent development is a defense, even if the defendant did not themselves *actually* independently develop the secret information.[275] In that sense, the boundaries between independent development, reverse engineering, and ready accessibility have been wholly blurred. In the genomics context, one can imagine readily litigating an ideal DNA trade secrecy case presented here, with the rise in NGS technology taking the witness stand. Of course, Nebraska—here and in other ways—is unique: The same argument has been rejected in the other 49 other states (and, so it seems, the other US territories).[276] Nonetheless, states—interested in these defenses as policy levers—may want to revisit this as a categorical rule in all cases. This is especially true where—like genomics—there's been a radical shift in how the secret information can be obtained. Unlike one's genome, the law can always be changed.

C. TRADE SECRECY AND THE COMEDY OF THE COMMONS

Last, appreciating the tenuous nature of trade secret protection for DNA sequence data furthers an understanding of the relationship between intellectual property and information production. Traditional accounts of the absence of protectability for research products suggests that they will accordingly be underproduced. That is, without a formal intellectual property right as an incentive, there will less DNA sequence data around to share.

There are, of course, myriad exceptions to this general understanding—so many, that even attempting to list them all would be a mountain of literature unto itself. Nonetheless, one particularly rich vein is the work on knowledge commons—areas of fruitful information production and efficient management even with diminished, and in some cases absent, intellectual property protection.[277] And one such commons resource identified in the literature is—

273. *Cf.* THIS IS SPINAL TAP (Embassy Pictures 1984) (demonstrating that the highest value on Nigel Tufnel's amplifier is 11, rather than the traditional 10, in order to give it that "extra push over the cliff").

274. MILGRIM ON TRADE SECRETS, *supra* note 2, § 7.02 n.3.

275. *Id.*; *see also* First Express Servs. Grp., Inc. v. Easter, 840 N.W.2d 465, 474–76 (Neb. 2013).

276. MILGRIM ON TRADE SECRETS, *supra* note 2, § 7.02 n.3.

277. "Commons theory" is largely ascribed to Elinor Ostrom, for which she won the 2009 Sveriges Riksbank Prize in Economic Sciences in Memory of Alfred Nobel (that is, the Nobel Prize in Economics). *Elinor Ostrom: Facts*, NOBEL PRIZE, https://www.nobelprize.org/prizes/economic-sciences/2009/ostrom/facts [https://perma.cc/3XZG-6WP5] (last visited Feb. 11, 2024). *See generally* Charlotte Hess & Elinor Ostrom, *Ideas, Artifacts, and Facilities: Information as a Common-Pool Resource*, 66 L. & CONTEMP. PROBS. 111 (2003). In the legal literature, Katherine J. Strandburg, Brett M. Frischmann, and Michael J. Madison have served as authors and editors on two magisterial volumes of commons case studies. GOVERNING KNOWLEDGE COMMONS (Brett M. Frischmann, Michael J. Madison & Katherine J. Strandburg eds. 2014); GOVERNING MEDICAL KNOWLEDGE COMMONS (Katherine J. Strandburg, Brett M. Frischmann & Michael J. Madison eds., 2017) [hereinafter GOVERNING MEDICAL KNOWLEDGE COMMONS].

you guessed it—DNA sequence data. As written about in detail in the 2017 volume, *Governing Medical Knowledge Commons*,[278] the volume's authors do much to explain the governance of early genomic data sharing paradigms, such as the Bermuda Principles, the sound of which continues to echo to this day.[279] Genomic data is produced by a diversity of actors in the larger DNA sequence data commons; widely shared; and used by a wide swath of the scientific public.[280] None of this diminishes the underlying resource; to the contrary, the larger resource is greatly improved by sharing because it allows researchers to engage in such value-enhancing activities like assembly correction and annotation.[281] Indeed, the primary challenge in DNA sequence commons isn't *creation*—it's storage, management, and access, the latter of which has become so complex it risks fragmenting the commons into private fiefdoms.[282]

But little of this otherwise detailed and useful analysis focuses on the connection between trade secrecy protection for DNA sequences and the meteoric rise of NGS.[283] To a certain degree, commons governance only works where the participants agree on the governance model. One could imagine that, as a community gets larger, the number of holdouts—namely, those interested in keeping the information they produce to themselves as trade secrets—increase, a problem as information production gets easier and the necessity to share information among one's peers goes down. Consequently, there's a risk that the willingness to be governed will diminish, along with larger incentives of information production. One way, of course, to police unruly fiefdoms is to enclose the meadow. This raises the question of whether the current system of genomic commons governance would continue to produce, even where sequencing is so cheap and thoroughly democratized that there are no real ways to govern its production.

Fortunately, perhaps, this does not seem to apply to genomic data—*yet*. We are *awash* in an explosion of genomic data, so much so that merely housing it—not producing it—seems to be the rate-limiting step.[284] It's difficult, frankly, to conceive of trade secrecy protection as encouraging the production of it any more of it in any practical circumstance, or its management once produced. If anything, the absence of such protection will likely encourage second-order innovations simply in managing it, thus improving the value of genomic data we

278. *See generally* GOVERNING MEDICAL KNOWLEDGE COMMONS, *supra* note 277.

279. *E.g.*, Peter Lee, *Centralization, Fragmentation, and Replication in the Genomic Data Commons*, *in* GOVERNING MEDICAL KNOWLEDGE COMMONS, *supra* note 277, at 46, 49–53.

280. *Id.* at 49–53.

281. *Id.*

282. *Id.* at 60.

283. In fairness, Michael Mattioli does acknowledge some of these issues—including some initial skepticism over whether clinical genomic information can actually be kept secret. Michael Mattioli, *Cancer: From a Kingdom to a Commons*, *in* GOVERNING MEDICAL KNOWLEDGE COMMONS, *supra* note 277, at 144, 148, 153–54.

284. Hernaez et al., *supra* note 18, at 20.

already have.[285] Put another way, if the genomic commons literature does a good job of explaining how the genomic commons have come to be *despite* the availability of intellectual property, it further suggests that the absence of intellectual property has follow-on benefits from experimentation in *using* the commons resource.

Depending on how one reads the work of Elinor Ostrom and Carol M. Rose, this may not be a revolutionary insight.[286] It's one more example of the benefits of commons resources heaped on a pile of them charmingly referred to as the "comedy of the commons."[287] This is the observation—in contrast to the more well-known tragedy of the commons—that diminishing private property in a shared resource may increase, rather than destroy, public welfare. Here, the value increase comes perhaps not just from production, but from allowing users freedom to experiment in managing it, making DNA sequence data live up to its promise of being useful to everyone.

CONCLUSION

It's time to bust the myth that DNA sequence data is subject to trade secrecy protection. DNA sequencing has undergone such a revolution since the Human Genome Project that human genomic sequence data, which once took billions of dollars, more than a dozen research institutions, and multiple federal agencies to birth, is now cheap and easy enough for an indigent art student to obtain. Today, sharing—not secrecy—garners genomic data its value. Even if kept secret, the information is likely readily ascertainable given the ease and ubiquity of DNA sequencing today. And even if these observations are wrong and genomic data otherwise meets the threshold to be trade secret subject matter, anyone interested in obtaining a suite of genomic information has a good shot at independently developing or reverse engineering a representative dataset from another. There's certainly no explicit statutory authority to the contrary. And courts faced with trade secrecy claims on genomic data have either purchased such skepticisms or have weakly rejected them in idiosyncratic industries, such as deer or shrimp breeding. So, what should we say to scholars who have long assumed that DNA sequences fall within the framework of trade secrecy? Perhaps that it's time to come along and "see the revolution of the times"[288]—or, at a minimum, subject their assumptions to serious reexamination.

This was fun. But beyond the sport of upending scholarly assumptions, understanding DNA sequences and genomic data as *not* being protectable by trade secret law has a host of both practical and theoretical consequences. Practically, it places limits—if not entirely negates—genomic data

285. *See* Jacob S. Sherkow, *Cancer's IP*, *supra* note 145, at 358 (discussing this concept in the context of Hetionet, a database of biomedical knowledge).

286. *E.g.*, Hess & Ostrom, *supra* note 277; Rose, *supra* note 43.

287. Rose, *supra* note 43, at 723.

288. WILLIAM SHAKESPEARE, HENRY IV, PART 2, act 3, sc. 1, l. 46.

misappropriation claims. This means some difficulties in litigating related claims in federal court. And state court litigation of the same is likely to yield variable results, decreased damages, and few equitable remedies. For scholars? It suggests another, yet-to-be articulated form of trade secret extinguishment: termination by changing technological conditions. It unveils some particularly fuzzy lines among the trade secrets defenses of ready accessibility, independent development, and reverse engineering. And it augments the data commons literature by bolstering examples of increased production despite the loss of private protection.

So: What's next? What should the courts or policymakers *do* about all of this? Well—perhaps nothing. It's not entirely clear that the state of affairs now is so terrible, regardless of our recognition of genomic data as susceptible to trade secret protection or not. We are, in many ways, living in the "golden age" of genomics. And the evidence that trade secrets litigation is threatening the burgeoning genomic data commons is—as this paper documents—borderline nonexistent. Perhaps, instead, this understanding of the lack of protectability of DNA sequence data suggests we should *avoid* doing anything lest we tear open the golden goose. This seems an anodyne prescription, but is an important finding precisely because changes are afoot to do just that—to increase intellectual property protections around DNA sequence data.[289] Instead, this Article suggests that if one were to take seriously trade secrecy in DNA sequences, policymakers should *not* specifically statutorily enumerate it as subject to trade secrecy protection.[290] By extension, they similarly should not use these findings regarding the difficulties in trade secrecy for DNA sequence data as a call to develop "database rights," as currently exist in Europe, for genomics.[291] Nor should policymakers use this Article's descriptive account to advocate for patent protection for genomic data, as some current proposals to the patent statute seek.[292]

Rather, the prescriptive solutions here are, perhaps, much smaller. Practitioners should rethink their reflexive assumptions about genomic data and trade secrecy and, if presented with a trade secrecy claim over DNA sequence data, litigate vigorously. Courts should, of course, take such findings into account and engage in actual, factual determinations as to whether genomic data are really independently valuable or readily ascertainable. But, perhaps mostly importantly of all, scholars should abandon the myth that DNA sequences are protectable by trade secrets—or, if they disagree, bring the receipts.

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289. *See, e.g.*, Patent Eligibility Restoration Act of 2022, S. 4734, 117th Cong. (2022).

290. *Cf.* Directive 2016/679, of the European Parliament and of the Council of 27 Apr. 2016 on the Protection of Natural Persons with Regard to the Processing of Personal Data and on the Free Movement of Such Data, and Repealing Directive 95/46/EC (General Data Protection Regulation), 2016 O.J. (L 119) 6 (enumerating a genetic data as a special class of information under the GDPR).

291. Directive 96/9/EC, of the European Parliament and of the Council of 11 March 1996 on the Legal Protection of Databases, 1996 O.J. (L 77).

292. S. 4734.