

Small but not least changes: The Art of Creating Disruptive

Innovations

Running title: Minor Changes, Major Disruptions

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Abstract

In the ever-evolving landscape of technology, product innovation emerges through the replacement of outdated technologies with groundbreaking advancements or the creative fusion of diverse technologies. This pioneering study employs a genetic framework to represent products, extracting chromosomal data to construct a comprehensive phylogenetic network of automobiles. By highlighting the significance of technological features, we delve into the product phylogenetic network (Lee et al., 2022). By introducing the revolutionary ‘Product Disruption Index’—inspired by the D index (Wu et al., 2019)—to this network, we can measure a product’s disruptiveness. Our approach is validated against the well-documented trend of declining disruptiveness over time (Park et al., 2023) and substantiated through two compelling case studies. Statistical analysis reveals that disruptive innovations often stem from minor, yet pivotal, modifications. Furthermore, inheriting superior technologies from predecessors and making slight adjustments to key technologies are more effective in enhancing a product’s disruptiveness than extensive technological changes. Indeed, a small step on the shoulders of giants can lead to monumental strides in disruptive innovation.

Keywords: product phylogenetic network, technological importance, product-family triangle, disruptive innovation, product disruption index (PDI), disruptive ancestral effect

1. Introduction

Innovation is a powerful driver of economic development and offers a sustainable competitive edge in management (Damanpour and Wischnevsky, 2006; Nagano et al., 2014). The groundbreaking disruptive innovation theory by Christensen, introduced in ‘The Innovator’s Dilemma,’ has revolutionized our understanding of technological advancement (Christensen et al., 2018). This theory (Christensen and Clayton M., 2013) highlights how initially inferior technologies can evolve to surpass dominant ones, reshaping entire markets. Despite its profound impact, the definition of disruptive technological innovation within companies remains elusive (Roblek et al., 2021). Godart and Pistilli (2024) provide a comprehensive typology, categorizing disruption into technological and non-technological forms (e.g., Sull, 1999; Tripsas and Gavetti, 2000; Danneels et al., 2017; Pino et al., 2016). Market-based models, such as those by Linton (2002) and Schmidt and Druehl (2008), offer valuable insights into disruptiveness, yet often overlook the nuances within individual organizations (Paap and Katz, 2004; Myers, 2002; Nagy et al., 2016). Empirical studies validating the universality of disruptive innovation theory are scarce (Ben-Slimane, Diridollou, and Hamadache, 2020). While citation networks have been utilized to assess disruptive innovation (Dotsika et al., 2017; Wang et al., 2024), the potential of product information networks remains untapped. This study introduces a novel method leveraging a product network and the D index (Wu et al., 2019) to identify disruptive products, empowering enterprises to harness product information for innovation.

Our PDI was validated through several approaches. Park et al. (2023) noted a decline in disruptive innovation over time in scientific and technological fields. Similarly, early iterations within a product series often show greater disruption potential. This trend is due to the rapid growth of consolidated products outpacing disruptive ones. We verified the PDI for all car series, finding that earlier models are generally more disruptive. A case study comparing Tesla and Chevrolet models revealed that Tesla’s products, despite smaller changes, hold significant PDIs, while Chevrolet’s EVs, despite considerable changes, exhibit lower PDIs. This underscores the principle of ‘small but not least’ (SBNL) in promoting disruptiveness. Another case study comparing regular and luxury vehicles showed that luxury brands, with higher prices, exhibit less disruption, aligning with the theory that disruptive innovation often uses affordable, simpler technology to capture lower-end market share (Christensen, 2000; Christensen and Raynor, 2003; Govindarajan and Kopalle, 2006; Tellis, 2006).

This research focuses on the relationship between disruptive products and technological changes. Most analyses of disruptive innovation are market or business model-oriented (Benzidia et al., 2021; Christensen and Raynor, 2013). However, the design principle of ‘small but not least changes’ is technological. Literature on disruptive innovation supports this argument. Govindarajan and Kopalle (2006) distinguished between radicalness and disruptiveness. Adner (2002) classified disruptive innovation attributes into inherited and novel, arguing that competition occurs in these dimensions. Yu and Hang (2011) suggested strategies for disruptive innovation: miniaturization, simplification, augmentation, and exploitation. These studies provide insights and guidance for creating disruptive products. Section 1 introduces disruptive innovation theory and the objective of measuring product disruptiveness. Section 2 reviews research on product

phylogenetic networks (O'Brien et al., 2001; Khanafiah and Situngkir, 2006; Tëmkin and Eldredge, 2007) and the D index from bibliometrics, major methods for calculating product disruptiveness. Section 3 details the framework and methods for constructing a product phylogenetic network for automobile data and presents the PDI calculation, including validation and case studies. Section 4 discusses regression analysis results and robustness. Section 5 presents conclusions and study limitations.

2. Literature review

2.1 Disruptive innovation

Disruptive innovation, a key issue in innovation and strategic management, often sees incumbents surpassed by new entrants (Christensen, 1997). Defined as a market-level process (Levina, 2017), it poses challenges for quantitative research. Schmidt and van der Sijde (2022) classified disruptive business models but did not enable quantitative study. Quantitative forecasting of disruptive innovation remains difficult (Linton, 2002). Unlike business models, disruptive products should have quantifiable disruptiveness, yet current theories lack methods for this. Technologically, existing theories fail to explain the relationship between disruptive products and their ancestors. Some scholars have used technology diffusion to interpret disruptive innovation (Chen et al., 2016; Linton, 2002; Wang et al., 2024), but no measurement of product disruptiveness exists.

2.2 Technology recombination strategy

The technological invention is the constructive assimilation of pre-existing elements into a new synthesis (Usher, 1954). Scholars recognize technological novelty as driven by the recombination of existing knowledge and technology (Nelson and Winter, 1982; Weitzman, 1998; Arthur, 2009). Arts and Veugelers (2015) highlight this recombinant search process as key to useful inventions. Analyzing the early U.S. automobile industry, Argyres et al. (2015) found innovation shocks significantly alter industry dynamics, creating a follower's dilemma. Lee et al. (2012) categorized learning from previous products into imitation and creative adaptation, with the latter having a stronger positive effect on financial performance. Liao (2022) suggested SMEs improve skills through imitation, with adaptation leading to greater skill improvement. Dell'Era and Verganti (2007) proposed that imitation involves quickly adopting new product attributes and experimenting with multiple combinations. While imitation can promote innovation, selecting objects of imitation and extracting knowledge to develop disruptive products remains unaddressed. This paper fills this gap, proposing the principle of "small but significant changes" in product design to create more disruptive products.

2.3 Product evolution and phylogenetic networks

Phylogenetic networks, used in biology to analyze species evolution, can also be applied to products, viewing technologies as product genes (Arthur, 2007). Product evolution mirrors biological evolution, adhering to the survival of the fittest and continuous learning (Yoon et al., 2024; Lee et al., 2021; Tellis et al., 1981; Massey, 1999; Utterback and Abernathy, 1975). Products form lineages over time, with technology genes spreading across brands. Phylogenetic networks based on product similarity (O'Brien et al., 2001; Khanafiah and Situngkir, 2006; Tëmkin and

Eldredge, 2007) help examine technology life cycles and dynamics (Jeong et al., 2023; Lee et al., 2023; Jeong and Lee, 2024; Park et al., 2024).

Lee et al. (2022) introduced a method for constructing phylogenetic product networks. These networks differ from biological ones, focusing on technology life cycles and product lineages. For instance, Lee et al. (2022) used phylogenetic network analysis on smartphones to predict future types. In the power sector, these networks show how institutional inertia and ecological pressure affect evolution (Lee et al., 2023). Park et al. (2024) demonstrated that diversity and technology integration are crucial for photovoltaic technology evolution. Jeong and Lee (2024) highlighted the importance of maintaining niche markets for feature phones. Additionally, phylogenetic networks have been used to explore financial AI technology evolution (Jeong et al., 2023). This framework systematically converts product information into chronologically sequenced citation networks, utilizing product evolution theory principles.

2.4 D index

Funk and Owen-Smith (2017) introduced a novel CD index to measure whether an invention consolidates or destabilizes existing technology paths, based on Schumpeter's (1976) theory of technological change. Park et al. (2023) found that the average CD index of papers and patents decreases over time, indicating their disruptiveness. Innovations can either improve existing knowledge or disrupt it, making it obsolete and steering technological development in new directions. The CD index characterizes this nature by analyzing citation networks (Funk and Owen-Smith, 2017). Wu et al. (2019) simplified the CD index with a D index in equation (1) to evaluate academic papers, categorizing nodes into developing or disruptive based on their citation patterns (Figure 1). They found that large teams tend to develop, while small teams disrupt science and technology. Park et al. (2023) and Lin et al. (2023) used the CD index to show that papers and patents are becoming less disruptive over time and that remote collaboration results in fewer breakthrough ideas.

$$D = \frac{n_i - n_j}{n_i + n_j + n_k} \quad (1)$$

Where:

n_i : the number of i type nodes that cite the focal paper but not the ancestors of the focal node.

n_j : the number of j type nodes that cite both the focal node and any of its ancestors.

n_k : the number of k type nodes that cite an ancestor of the focal node but not the focal node.

Although the D index is not limited to patent and paper citation networks, it has not been used to measure product disruptiveness due to the lack of explicit citation networks in the product space. However, the D index offers a method for measuring disruptiveness through a citation network that accounts for the chronological sequence of innovations.

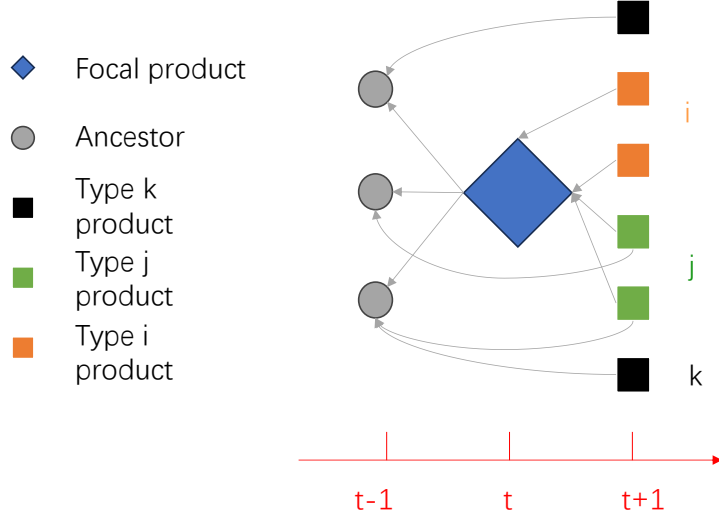


Figure 1. Part of product phylogenetic network. This network contains the focal product in the center. At time $t + 1$, type i , j , and k products are present.

3. Methods

3.1 Data

We conducted an empirical case study using automotive industry data from Edmunds, which includes comprehensive consumer evaluation scores for passenger cars sold in the US market. The dataset spans model years 2013 to 2024, covering cars listed from 2012 to 2023. After cleaning, we analyzed 4,496 car models featuring 38,127 technologies, ranging from continuous variables like cruising range to binary variables like engine type. All technologies were normalized to the interval $[0,1]$ using l1 normalization (Albon and Chris, 2018), ensuring the sum of gene values for each product equaled 1. This resulted in a matrix with 38,127 columns (technologies) and 4,496 rows (car models), known as the chromosome matrix of products. Due to the lack of ancestors for 2013 models, our analysis started with 2014 products, excluding 2024 data. Thus, we analyzed 4,114 products from 2014 to 2023.

3.2 Conceptual framework

The construction of a phylogenetic network involves several key steps (Figure 2). First, products are represented as chromosomes. Next, a product similarity adjacency matrix is calculated using chromosome and gene weight matrices. This matrix is then used to construct a product phylogenetic network. The Product Disruption Index (PDI) is detected through these networks for each focal product. Finally, a statistical analysis of variables such as lost gene rate, inherited gene rate, and new gene rate is performed. The lost gene rate measures the gene values present in ancestors but not passed to the focal product, while the new gene rate measures gene values in the focal product but not in ancestors. The inherited gene rate is the ratio of gene values inherited from ancestors. Detailed mathematical definitions are provided in the following sections.

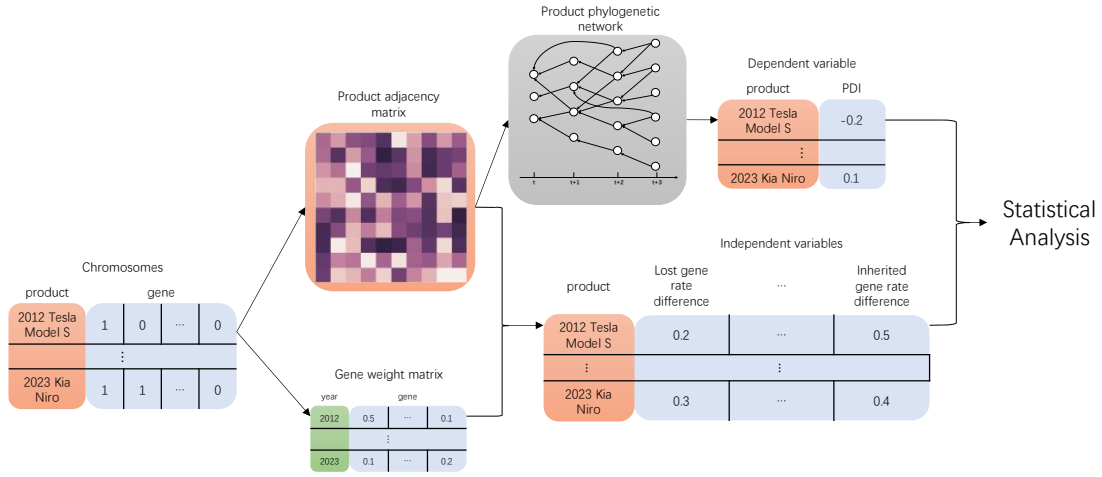


Figure 2. Conceptual framework

3.3 Methodology

The traditional D index, based on citations, isn't directly applicable to products due to inherent similarities rather than citations. To address this, we enhanced the D index for product phylogenetic networks by redefining product similarities as citations and incorporating disruptiveness into the PDI calculation. In the product space, edge weights represent cosine similarity between products, ranging from [0,1]. We converted implicit similarities into explicit citations using a threshold, retaining edges with similarities above this threshold.

Each product is a node, with ancestors being nodes from previous years and descendants from subsequent years. Figure 3 illustrates the product similarity space, showing the relationships among a focal product, its ancestors, and descendants. We converted product similarities into citations using a threshold, a common method in constructing phylogenetic networks (Jeong and Lee, 2024; Jeong et al., 2023; Park et al., 2024). The threshold is the minimum of two averages: the average cosine similarities within the product family triangle and across all product-family triangles. Details on converting the product similarity space into a product phylogenetic network can be found in the appendix A.

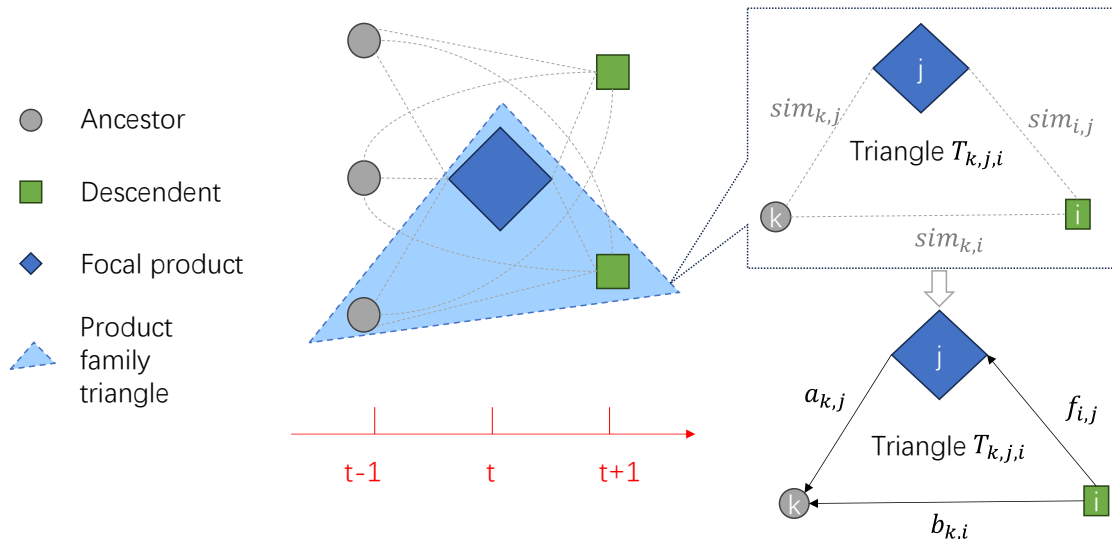


Figure 3. Product similarity space, including focal product, its ancestors, and descendants, and

product-family triangle. In product-family triangle, we can transfer similarities between products into citations. $sim_{k,j}$ is similarity between product k and j , $sim_{i,j}$ is similarity between product i and j , and $sim_{k,i}$ is similarity between product k and i . $a_{k,j}$ is citation from node j to node k , $f_{i,j}$ is citation from node i to node j , and $b_{k,i}$ is the citation from node i to node k .

3.4 Product genetic variables

Technological importance can be represented by the weight of a gene. The weight of a gene can be determined through various methods. For instance, Lee et al. (2023) utilized normalized entropy weight, while Lee et al. (2022) and Jeong et al. (2023) applied the Term Frequency – Inverse Document Frequency (TF–IDF) method to calculate gene weight. In this study, the weight of a gene increases with the number of products it is found in. Therefore, we used frequency weight to calculate the gene’s weight. We explore the role of technology genes as catalysts for technological advancements through three distinct search patterns (Park et al., 2024): vertical inheritance (VI) (Lawrence, 2005), horizontal gene transfer (HGT) (Carignani et al., 2019), and mutation (MT) (Kardong, 2008). Vertical Inheritance (VI): Descendants inherit genetic information from direct ancestors, using them as benchmarks for evolution (Lawrence, 2005; Carignani et al., 2019; Wagner and Rosen, 2014). This gradual evolutionary process is guided by inherited genetic traits (Anderson and Tushman, 1990; Tellis and Crawford, 1981). The inherited gene rate is the ratio of all inherited gene values in the focal product to the sum of all gene values in the focal product. The weighted inherited gene rate is the ratio of all weighted inherited gene values to the sum of all weighted gene values in the focal product. The inherited gene rate difference represents the degree of genetic importance inherited from ancestors. In appendix B, we provide the mathematical definitions of all the product genetic variables. The inherited gene rate measures the degree of VI, while the weighted inherited gene rate quantifies the extent of VI for significant genes. By examining the inherited gene rate difference, we can determine whether a product has inherited more crucial or less important genes.

The lost gene rate measures the rate of gene loss during the VI process, while the weighted lost gene rate assesses the extent of loss for significant genes. By examining the lost gene rate difference, we can determine whether more crucial or less important genes have been lost. The lost gene rate is the ratio of all lost gene values in the focal product to the sum of all gene values in the ancestors. The weighted lost gene rate is the ratio of all weighted lost gene values in the focal product to the sum of all weighted gene values in the ancestors. The lost gene rate difference represents the degree of genetic importance lost from its ancestor. During Horizontal Gene Transfer (HGT), descendants acquire new genetic information from neighboring ancestors of different lineages, rather than direct ancestors (Lawrence, 2005; Smets and Barkay, 2005). Mutation (MT) introduces new traits do not present in previous generations, facilitating the emergence of novel genetic configurations (Kardong, 2008). The new gene rate measures the proportion of new genes acquired during MT and HGT processes. The weighted new gene rate assesses the significance of these new genes, while the new gene rate difference indicates whether the product has obtained more important or less important new genes. The new gene rate is the ratio of all new gene values in the focal product to the sum of all gene values in the focal product. The weighted new gene rate is the ratio of all weighted new gene values to the sum of all weighted gene values in the focal product. The new gene rate difference represents the degree of genetic

importance of the new genes in a product. The brand-new gene rate measures the proportion of new genes obtained solely during the MT process. The brand-new gene rate is the ratio of the brand-new gene count in the focal product to the total gene count in the focal product.

3.5 Descriptive Statistics and Correlations

We calculated the product adjacency similarity matrix (4496×4496) using the chromosome matrix, representing the similarity between product pairs. Using this matrix, we built a product phylogenetic network and calculated the 1-year Product Disruption Index (PDI) for each product using equation (1). The average 1-year PDI was -0.296, indicating that products with a one-year generational interval generally did not exhibit disruptiveness. In contrast, the average CD index for patents and papers (Park et al., 2023) was above zero, indicating disruptiveness. This discrepancy is due to the presence of ‘multiples’—highly similar innovations developed independently (Merton, 1936; Merton, 1968; Wagner and Rosen, 2014). In explicit citation networks, a focal node may lack citation links with closely related ancestors, leading to the omission of some ancestors (Heneberg, 2013) which might be ‘multiples’. Such omissions can result in an overestimation of the focal node’s D index. However, this issue does not arise within the phylogenetic network, as our methodology involves calculating a citation network post-assessment of all ancestors’ similarity to the focal product. Therefore, the D index may overestimate disruptiveness compared to the PDI. Figure 4.a shows the distribution of the 1-year PDI, revealing that disruptive products are much fewer than developing products. Figure 4.b shows the average 1-year PDI trend by year, with a clear downward trend from 2015 to 2023. The increase in PDI in 2015 is attributed to the large influx of electric vehicles and the emergence of various new technologies.

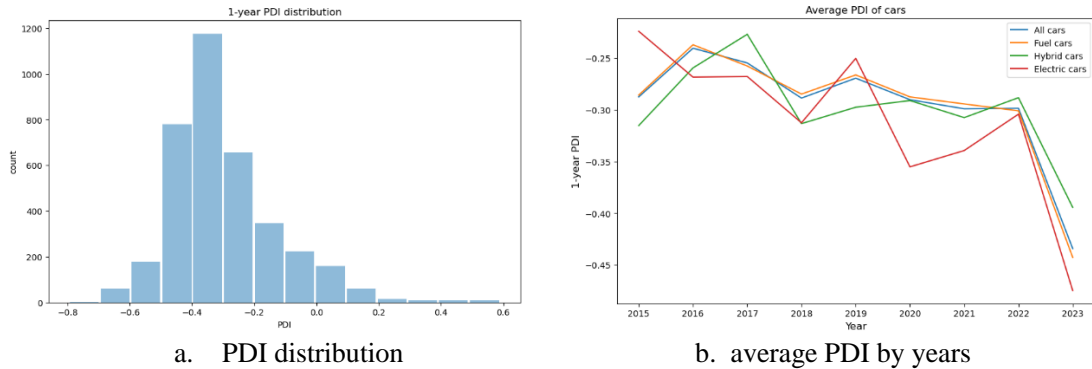
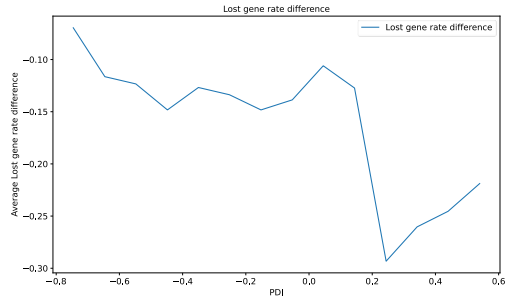


Figure 4. One-year PDI distribution

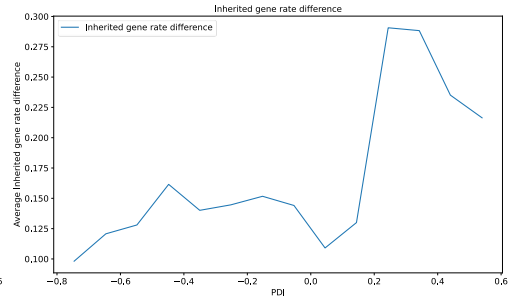
Table 2 summarizes the descriptive statistics of the variables. The PDI is positively correlated with the lost gene rate difference, inherited gene rate difference, brand-new gene rate, and ancestor PDI, and negatively correlated with the new gene rate difference. The ancestor PDI is the average PDI value of the focal product’s ancestors, chosen as the three most similar products that appeared earlier. These relationships are presented in Table 2 and Figure 5, showing that disruptive products tend to have disruptive ancestors, likely due to the one-year intergenerational phylogenetic network and one-year PDI.

Table 2. Descriptive Statistics and Correlations

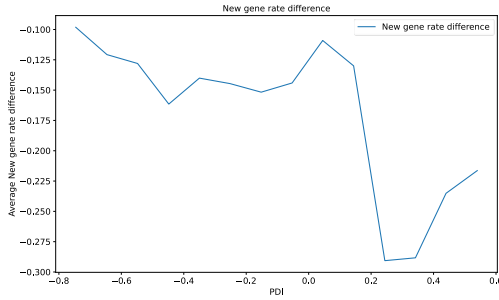
Variable	Mean	SD	Max	Min	1	2	3	4	5
1. PDI	-0.296	0.173	0.589	-0.795	1				
2. Weighted lost gene rate	0.061	0.052	0.543	0	-0.073	1			
3. Unweighted lost gene rate	0.197	0.122	0.853	0.009	0.004	0.83	1		
4. Lost gene rate difference	-0.136	0.084	0.03	-0.701	-0.052	-0.585	-0.938	1	
5. Weighted inherited gene rate	0.935	0.05	1	0.551	0.009	-0.737	-0.744	0.623	1
6. Unweighted inherited gene rate	0.789	0.125	0.991	0.118	-0.01	-0.802	-0.979	0.924	0.776
7. Inherited gene rate difference	0.146	0.092	0.761	-0.195	0.019	0.69	0.928	-0.919	-0.512
8. Weighted new gene rate	0.065	0.05	0.449	0	-0.009	0.737	0.744	-0.623	-1
9. Unweighted new gene rate	0.211	0.125	0.882	0.009	0.01	0.802	0.979	-0.924	-0.776
10. New gene rate difference	-0.146	0.092	0.195	-0.761	-0.019	-0.69	-0.928	0.919	0.512
11. Price(log)	10.74	0.687	14.164	9.392	-0.039	-0.009	-0.014	0.015	0.005
12. Review rate	4.624	0.362	5	1	0.051	0	-0.01	0.014	0.009
13. Brand-new gene rate	0.083	0.089	0.633	0	0.35	0.151	0.289	-0.327	-0.064
14. Ancestor PDI	-0.34	0.234	0.763	-0.832	0.551	-0.102	0.058	-0.147	0.019
Variable	6	7	8	9	10	11	12	13	14
6. Unweighted inherited gene rate	1								
7. Inherited gene rate difference	-0.939	1							
8. Weighted new gene rate	-0.776	0.512	1						
9. Unweighted new gene rate	-1	0.939	0.776	1					
10. New gene rate difference	0.939	-1	-0.512	-0.939	1				
11. Price(log)	0.014	-0.016	-0.005	-0.014	0.016	1			
12. Review rate	0.004	-0.001	-0.009	-0.004	0.001	-0.012	1		
13. Brand-new gene rate	-0.279	0.344	0.064	0.279	-0.344	-0.07	0.009	1	
14. Ancestor PDI	-0.077	0.115	-0.019	0.077	-0.115	0.018	0.045	0.364	1



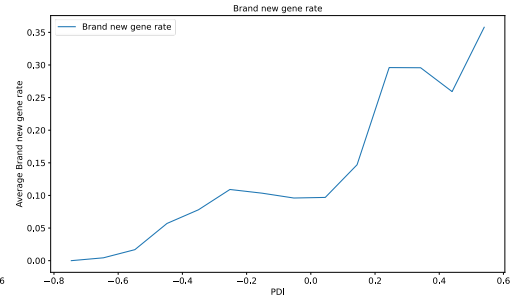
a. Average PDI plots of lost gene rate difference



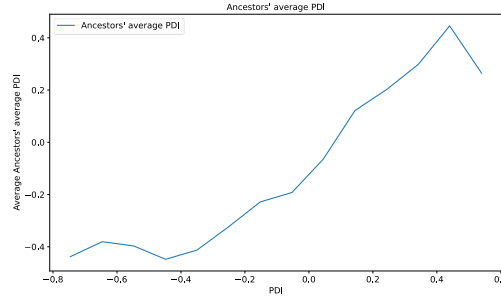
b. Average PDI plots of inherited gene rate difference



c. Average PDI plots of new gene rate difference



d. Average PDI plots of brand-new gene rate



e. Average PDI plots of ancestor PDI

Figure 5. Trends of independent variables with PDI

3.6 Validation with car series

Validating the PDI was challenging due to the lack of real disruption data for products. Even previous validations of the D Index couldn't guarantee absolute correctness (Bornmann et al., 2020; Ruan et al., 2021). However, the PDI is based on the validated D index (Wu et al., 2019). Our validation relied on the widely accepted notion that automobile models are innovations. According to Park et al. (2023), technology and science are becoming less disruptive over time, suggesting that earlier car models in a series are more likely to be disruptive. This principle was used to validate our PDI results, showing a decreasing trend in average PDI (Figure 4.b). For car products, many series exist, such as Tesla's 'Model S'. Later products in a series are expected to be less disruptive than earlier ones. Different series have varying PDI means and variances, so we used a normalized PDI to compare disruption within series. We employed percentiles in ascending order to denote chronological order within each series. For example, products from 2012, 2013, 2014, and 2015 would have percentiles of 0, 0.33, 0.66, and 1, respectively. Averaging all series, Figure 6 shows that normalized PDI decreases as products appear later in the series, indicating earlier products are more disruptive. This aligns with Park et al. (2023), which observed a decline in disruptiveness over time in paper and patent data.

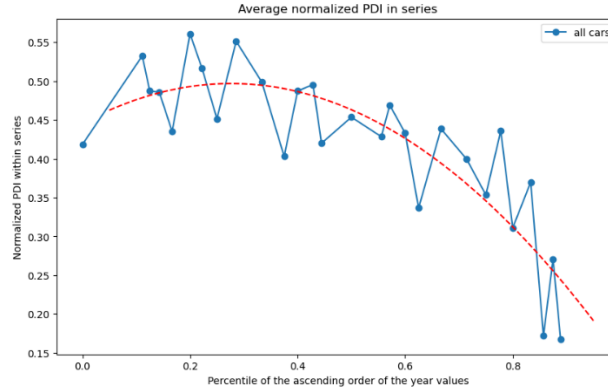


Figure 6. Average normalized PDI in series

3.7 A Case Study of Tesla and Chevrolet

We compared the 2014 Tesla Model S (third generation) and the 2014 Chevrolet Spark EV (first generation) as early-stage electric vehicles. Table 3 details their gene counts, with significant genes identified using the median weight threshold. The first ancestor is the most similar product from the previous year, from which inherited genes are derived. New genes are those present in the product but not in the first ancestor. The review rate, based on consumer surveys, ranges from

0 to 5, with higher scores indicating better performance. Figure 7 shows the PDI positions of both products.

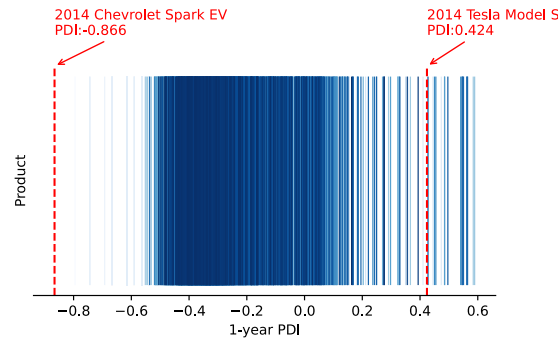


Figure 7. Positions of the two car models in the PDI distributions

In Table 3, the 2014 Tesla Model S has a positive PDI, much higher than the Chevrolet Spark EV, aligning with consumer review rates. Tesla's Model S is more similar to its ancestor, inheriting more genes, while Chevrolet's Spark EV has adopted many new genes, indicating new technology development but a lower disruption rate. Tesla maintains design consistency with few critical changes, while Chevrolet modifies more key elements. This supports Dell'Era and Verganti's (2007) theory that innovators have less heterogeneity in product language, while imitators show more variation.

Table 3. Details of two electric vehicles

	2014 Tesla Model S	2014 Chevrolet Spark EV
Gene count	147	152
Weight threshold	0.003	
Important genes	97	119
Unimportant genes	50	33
New important genes	7	86
New unimportant genes	0	2
Inherited important genes	90	33
Inherited unimportant genes	50	31
First ancestor	2013 Mercedes-Benz CL-Class	2013 GMC Savana 3500
Similarity	0.918	0.310
PDI	0.424	-0.866
Review rate	4.8	4.5
Price	69900	26685

3.8 A Case Study of Luxury and Regular Cars

We analyzed three pairs of luxury and regular brands from three companies, measuring the average values of the lost gene rate difference, inherited gene rate difference, new gene rate difference, and PDIs for six brands (Table 4). Regular brands exhibited higher PDI, lower lost gene rate difference, higher inherited gene rate difference, and higher brand-new gene rate compared to luxury brands.

Table 4. Average values of Luxury cars and Regular cars

Company	Toyota Motor Corporation	Hyundai Motor Group	Volkswagen AG
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Brands	Toyota	Lexus	Hyundai	Genesis	Volkswagen	Audi
Type	Regular	Luxury	Regular	Luxury	Regular	Luxury
PDI	-0.322	-0.348	-0.327	-0.356	-0.306	-0.321
Price	32807.991	53901.930	27206.361	53927.407	28665.450	64392.913
Review rate	4.646	4.628	4.591	4.519	4.588	4.629
Lost gene rate difference	-0.183	-0.178	-0.182	-0.128	-0.198	-0.165
Inherited gene rate difference	0.160	0.155	0.149	0.112	0.161	0.149
Brand-new gene rate	0.087	0.078	0.087	0.036	0.110	0.080

Luxury brands, with higher prices, showed less disruption than regular brands. Regular brands, with positive and higher inherited gene rate differences, inherit more important genes, which constitute the majority of their total genes. They also have negative and lower lost gene rate differences, indicating they lose more important genes, which are a smaller portion of the total genes. This suggests that small but significant changes drive disruption. Additionally, regular brands have a higher brand-new gene rate, adopting many new technologies for innovation.

Figures 8a and 8b show scatter plots of the sums of log prices and PDI grouped by series and brands, respectively. Both figures reveal a similar decreasing trend: as the total price increases, the sum of the PDI decreases, indicating that more luxurious brands are less disruptive. Luxury brands focus more on quality development rather than disruption. Thus, a product's innovation cannot be solely determined by its price. These calculations, based on sums rather than averages, reflect overall values rather than individual values.

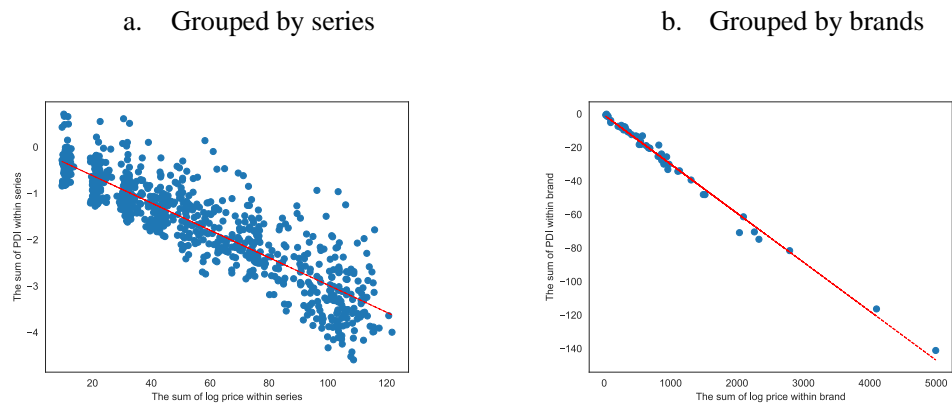


Figure 8. Scatters of the sum of grouped PDI and log price. X-axis represents sum of log price and Y-axis is sum of PDI.

4. Results

4.1 Regression analysis

We conducted regression analysis using the 1-year PDI as the dependent variable and various gene rates, product price, review rate, and the average PDI of the three most similar ancestors as

independent variables. Due to incomplete ratings, the model with the rating variable had fewer observations (3694) compared to the original dataset (4496). We performed six regression analyses, summarized in Table 5, using pooled OLS regression due to the cross-sectional nature of the data.

Table 5. Multiple regression results from years 2014 to 2023

	(1)	(2)	(3)	(4)	(5)	(6)
Unweighted lost gene rate	-0.038** (0.019)					
Lost gene rate difference				0.064** (0.029)		
Unweighted inherited gene rate			0.045** (0.019)			
Inherited gene rate difference						-0.087*** (0.026)
Unweighted new gene rate		-0.045** (0.019)				
New gene rate difference					0.087*** (0.026)	
Price(log)				-0.013*** (0.029)	-0.013*** (0.026)	-0.013*** (0.026)
Review rate	0.013* (0.019)	0.013* (0.019)				
Ancestor PDI	0.408*** (0.019)	0.409*** (0.019)	0.409*** (0.019)	0.412*** (0.029)	0.412*** (0.026)	0.412*** (0.026)
const	-0.208*** (0.007)	-0.206*** (0.007)	-0.193*** (0.010)	-0.013 (0.004)	-0.008 (0.004)	-0.008 (0.004)
N	3694	3694	3694	3694	3694	3694
R2	0.306	0.306	0.305	0.307	0.309	0.309
R2 Adj.	0.305	0.305	0.305	0.307	0.308	0.308
F-statistic	541.197	541.967	810.49	546.019	549.039	549.039
Log-Likelihood	1911.598	1912.401	1910.538	1916.62	1919.758	1919.758
VIF	5.739	6.084	3.056	6.339	6.056	6.056

Notes: This table evaluates the relationship between different measures of the use of product genetic information, survey data from website, price and 1-year PDI. Estimates are from ordinary-least-squares regressions. Each coefficient is tested against the null hypothesis of being equal to 0 using a two-sided t-test. We do not adjust for multiple hypothesis testing. Robust standard errors are shown in parentheses.

+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001.

Our models confirmed the absence of multicollinearity, with all Variance Inflation Factor (VIF) values below 7. The Product Disruption Index (PDI) of ancestral products positively correlated with the PDI of the focal product across all models, highlighting the benefits of aligning with disruptive predecessors. This positive coefficient of the ancestral PDI provides compelling evidence of the ‘disruptive ancestral effect,’ suggesting that insights from a disruptive predecessor can significantly boost innovation in subsequent products. This aligns with the wisdom that excellence begets excellence, akin to ‘like father, like son.’ However, the presence of a disruptive ancestor does not guarantee that the focal product will surpass its predecessor in disruptiveness. Instead, it indicates a higher likelihood of disruptiveness compared to products without such an

ancestor, emphasizing the advantage of ‘standing on the shoulders of giants.’ Additionally, the ‘review rate’ variable, derived from website review scores, showed a positive association with the PDI in models 1 and 2, indicating that this rating can partly reflect a car’s disruptiveness.

In model 1, the unweighted lost gene rate was negative; in model 2, the unweighted new gene rate was negative; and in model 3, the unweighted inherited gene rate was positive. These results imply that inheriting technology from predecessors enhances disruptiveness more than introducing new technologies. Conversely, the inherited gene rate difference negatively associated with PDI in model 6, the lost gene rate difference positively in model 4, and the new gene rate difference negatively in model 5. This suggests that discarding significant genes, inheriting non-significant genes, and introducing crucial new genes are beneficial for disruptiveness. Thus, altering key technologies is more conducive to enhancing disruptiveness than changing non-essential ones.

In summary, the SBNL (Small But Not Least Changes) principle helps innovative products become more disruptive by building on disruptive ancestors, making minor key technology changes, and maintaining reasonable prices. This aligns with the MAYA (Most Advanced, Yet Acceptable) principle by Silvennoinen and Mononen (2023), emphasizing critical enhancements within a reasonable scope.

4.2 Robustness check

To mitigate the potential fixed effects of time and brand on the product’s 1-year PDI, we implemented multidimensional regression analyses accounting for both year and brand fixed effects, ensuring robustness. Additionally, we conducted regressions on product gene data computed with both frequency weight and TF-IDF weight, reinforcing our results’ credibility. In Table 6, models 1, 2, and 3 use frequency weight, while models 4, 5, and 6 leverage TF-IDF weight. TF-IDF, a statistical measure, transforms a document into a vector, highlighting significant keywords (Salton and McGill, 1983). Each year is treated as an individual document for TF-IDF computation, a method widely applied in phylogenetic networks to evaluate technological significance (Lee et al., 2022; Jeong et al., 2023).

We applied both weighted and unweighted gene rates as explanatory variables. The results show consistency across most explanatory variables when comparing frequency weight and TF-IDF weight groups. The positive relationship between Ancestor PDI and 1-year PDI suggests that building on the groundwork laid by giants facilitates disruptive product creation. Conversely, a negative correlation between product price and PDI indicates that disruptive products often emerge from the lower end of the market or possess a price advantage (Christensen, 2000; Christensen and Raynor, 2003; Govindarajan and Kopalle, 2006; Tellis, 2006). A negative brand-new gene rate suggests that introducing new technologies, as opposed to capitalizing on established key technologies, does not markedly increase disruptiveness when accounting for year and brand fixed effects. An overabundance of brand-new genes might reduce a product’s disruptiveness, as too many untested, market-unrecognized genes do not necessarily lead to increased technology adoption. However, as shown in Table 2, without accounting for year and brand fixed effects, the brand-new gene rate appears conducive to disruptiveness, indicating heterogeneity within years and brands.

The positive unweighted inherited gene rate, contrasted with the negative weighted inherited gene rate, indicates that inheriting predecessor technologies benefits product disruptiveness, but requires modification of key technologies for greater disruptiveness. A positive weighted lost gene rate versus a negative unweighted lost gene rate implies that discarding significant rather than inconsequential technologies yields more disruptiveness. Moreover, a positive weighted new gene rate, as opposed to a negative unweighted new gene rate, reveals that introducing new and significant technologies, rather than ordinary ones, enhances product disruptiveness. Finally, in all models, the R-squared values exceed 0.5, higher than those of pooled OLS models in Table 5, indicating a higher explanatory power of the product gene rates and other information for the 1-year PDI when accounting for year and brand fixed effects.

Table 6. Fixed effects regression results from years 2014 to 2023

	Frequency weight			TF-IDF weight		
	(1)	(2)	(3)	(4)	(5)	(6)
Unweighted inherited gene rate	0.247*** (0.046)			0.543*** (0.047)		
Weighted inherited gene rate	-0.209* (0.098)			-0.383*** (0.038)		
Ancestor PDI	0.581*** (0.024)	0.581*** (0.024)	0.581*** (0.024)	0.521*** (0.025)	0.524*** (0.024)	0.521*** (0.025)
Review rate	0.009+ (0.005)	0.009+ (0.005)	0.009+ (0.005)	0.010+ (0.005)	0.008 (0.005)	0.010+ (0.004)
Price(log)	-0.013* (0.006)	-0.013* (0.005)	-0.013* (0.006)	-0.013* (0.005)	-0.012* (0.005)	-0.013* (0.005)
Brand-new gene rate	-0.215*** (0.046)	-0.235*** (0.044)	-0.215*** (0.046)	-0.432*** (0.047)	-0.499*** (0.055)	-0.432*** (0.047)
Weighted lost gene rate		-0.020 (0.126)			0.456*** (0.046)	
Unweighted lost gene rate		-0.178*** (0.052)			-0.622*** (0.055)	
Weighted new gene rate			0.209* (0.098)			0.383*** (0.038)
Unweighted new gene rate			-0.247*** (0.046)			-0.543*** (0.047)
Year fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
Brand fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
N	3694	3694	3694	3694	3694	3694
R2	0.529	0.528	0.529	0.553	0.556	0.553

Notes: This table evaluates the relationship between different measures of the use of product genetic information, survey data from website, price and 1-year PDI. Estimates are from ordinary-least-squares regressions. Each coefficient is tested against the null hypothesis of being equal to 0 using a two-sided t-test. We do not adjust for multiple hypothesis testing. Robust standard errors are shown in parentheses.

+ p<0.1; * p<0.05; ** p<0.01; *** p<0.001.

5. Conclusion

Disruptive innovation is often seen as a market phenomenon, disrupting incumbents by introducing distinct technological paradigms (Christensen et al., 2004; Christensen and Raynor,

2003). While approaches like lean methodology (Brad et al., 2016; Tuli et al., 2015), MVP (Olsen, 2015; Di Guardo et al., 2022), and the S-curve model (Borgianni and Rotini, 2012; Bradley and O'Toole, 2016) have influenced disruptive product design, there's a lack of literature on design principles based on existing product information. This gap is due to the qualitative nature of previous research (Schmidt and van der Sijde, 2022; Nagy et al., 2016), making quantification challenging. The PDI method proposed here quantifies product disruptiveness using comprehensive product technology data, integrating the D index and product phylogenetic network concepts (Wu et al., 2019).

Our study offers three key contributions. Firstly, the PDI measures product disruptiveness, grounded in the D index and product phylogenetic network theories (Lee et al., 2022). It transforms product phylogenetic networks into citation networks, validated by the annual decline in innovation disruptiveness (Park et al., 2023). Case studies of the 2014 Tesla Model S and Chevrolet Spark EV, and comparisons of luxury and regular cars from Toyota, Hyundai, and Volkswagen, support the PDI's validity, showing regular cars are more disruptive (Christensen, 2000; Christensen and Raynor, 2003; Govindarajan and Kopalle, 2006; Tellis, 2006). Secondly, regression analysis on 3,694 car models from 2014 to 2023 revealed that the principles of SBNL (Small But Not Least Changes) are crucial for enhancing disruptiveness. Unweighted gene rates indicate that inheriting more genes from ancestors benefits disruptiveness, while weighted gene rates show that altering key technologies is necessary for greater disruptiveness. Lastly, our regression model consistently shows a positive Ancestor PDI, suggesting that inheriting traits from disruptive ancestors enhances a product's disruptiveness. This aligns with the idea of 'standing on the shoulders of giants' (Bower and Christensen, 1995; Rhéaume and Gardoni, 2017).

This study addresses the gap in existing theories by providing a technical approach to measuring product disruptiveness and deriving SBNL design principles. Products result from assimilating and recombining existing and new technologies (Arthur, 2007). SBNL offers a methodological approach to selecting and integrating technologies during product design, serving as a quantitative metric for enhancing design capabilities. For business managers, the disruptive ancestral effect provides a strategy for selecting the right predecessors to emulate, leveraging the PDI to choose appropriate models.

Our study calculated a 1-year PDI to reflect the short-term disruptiveness of car products, given the rapid update cycle in the automotive industry. This approach may not be necessary for other products, where a longer-term PDI could be more appropriate. Additionally, we focused on the three most similar ancestors to the focal product when computing various gene rates, but the number of ancestors can be adjusted based on research needs. Alternative methods could also be used to convert the phylogenetic network into a citation network. Future research could integrate market data with the technical data of the PDI for a more comprehensive study of disruption. The PDI is particularly useful in scenarios where market data is hard to obtain, but technical data is readily available. For example, while sales data for AI products may be difficult to acquire, technical data is often accessible from public sources. Moreover, the D index tends to overestimate disruptiveness due to uncited ancestors. Using the PDI method to reconstruct citation networks for patents and papers can provide a more accurate measure of disruptiveness.

Data Availability Statement:

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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Appendix A: Details on Converting the Product Similarity Space into a Product Phylogenetic Network

Using equations (3)-(5), we detected citations between the focal node, its ancestors, and descendants, converting the product similarity space into a product phylogenetic network. Each product family triangle's threshold was calculated using equation (2). Equations (6)-(8) determined the types of descendant nodes, ensuring no overlap in type classification. Finally, we calculated the PDI of the focal product using equation (1).

$$threshold_{k,j,i} = \min \left(\frac{sim_{k,j} + sim_{i,j}}{2}, \sum_{i=1}^n \sum_{k=1}^m \frac{sim_{k,j} + sim_{i,j}}{2mn} \right) \quad (2)$$

Where:

m : the count of ancestors

n : the count of descendants

k : the k -th ancestor

j : the focal product

i : the j -th descendant

$sim_{k,j}$: cosine similarity between nodes k and j

$$a_{k,j} = \begin{cases} 1 & sim_{k,j} > threshold \\ 0 & sim_{k,j} \leq threshold \end{cases} \quad (3)$$

$$f_{i,j} = \begin{cases} 1 & sim_{i,j} > threshold \\ 0 & sim_{i,j} \leq threshold \end{cases} \quad (4)$$

$$b_{k,i} = \begin{cases} 1 & sim_{k,i} > threshold \\ 0 & sim_{k,i} \leq threshold \end{cases} \quad (5)$$

Where:

$a_{k,j}$: the citation from the focal product and the k -th ancestor; 1: with citation and 0: no citation.

$f_{i,j}$: citation between the i -th descendant of the focal product and the focal product; 1: with citation and 0: no citation.

$b_{k,i}$: citation from the i -th descendant of the focal product and k -th ancestor; 1: with citation, 0: no citation.

$threshold_{k,j,i}$: the threshold in the product-family triangle formed by nodes i, j, k .

If p is the count of focal products, n the count of ancestors, and m the count of descendant products, there are $m * n$ product family triangles for one focal product. Since there is only one focal product, p equals 1. We obtained the values of $a_{k,j}$, $b_{k,i}$, and $f_{i,j}$ using equations (6)-(8). With all citations identified, we constructed a phylogenetic network centered around the focal node, spanning generations over a year. Using all triangles centered on focal node i , we determined the type of focal node i using equations (6)-(8). These equations classify descendant nodes into types i, j , and k . To avoid multiple classifications for the same node, we considered points in the order j, i, k . After identifying the number of descendants of each type for the focal node, we used equation (1) to calculate the PDI of the focal product.

$$\sum_{k \in anc, i \in des} (a_{k,j} = 1 \wedge b_{k,i} = 1 \wedge f_{i,j} = 1) > 0 \\ \Rightarrow node_i \in \{x \in X | type(x) = 'j'\} \quad (6)$$

$$(\sum_{k \in anc, i \in des} (b_{k,i} = 0 \wedge f_{i,j} = 1) > 0) \wedge (node_i \notin \{x \in X | type(x) = 'j'\})$$

$$\Rightarrow node_i \in \{x \in X | type(x) = 'i'\} \quad (7)$$

$$(\sum_{k \in anc, i \in des} (a_{k,j} = 1 \wedge b_{k,i} = 1 \wedge f_{i,j} = 0) > 0) \wedge (node_i \notin \{x \in X | type(x) \in \{j', i'\}\})$$

$$\Rightarrow node_i \in \{x \in X | type(x) = 'k'\} \quad (8)$$

Where:

$node_i$: i -th node of descendants of the focal node.

$type(x)$: Function used to obtain the type of node, which is a node following the focal node.

anc : Node set of the ancestors of the focal node.

des : Node set of descendants of the focal node.

Appendix B: Definition of Product genetic variables

B.1 Inherited gene rates:

$$inhr_j = \frac{\overline{\sum_{t \in anc(j) \cap foc(j)} x_{t,j}}}{\sum_{t \in foc(j)} x_{t,j}} \quad (9)$$

$$inhwr_j = \frac{\overline{\sum_{t \in anc(j) \cap foc(j)} x_{t,j} \cdot w_t^T}}{\sum_{t \in foc(j)} x_{t,j} \cdot w_t^T} \quad (10)$$

$$inhr_diff_j = inhwr_j - inhr_j \quad (11)$$

Where:

$inhr_j$: average inherited gene rate of the j -th product, $inhr_j \in [0,1]$.

$inhwr_j$: average weighted inherited gene rate of the j -th product, $inhwr_j \in [0,1]$.

$inhr_diff_j$: inherited gene rate difference of the j -th product.

$x_{t,j}$: i -th gene value of the j th product.

$anc(j)$: function for obtaining all the genes of the ancestors of the j -th product.

$foc(j)$: function for obtaining all the genes of the j -th product.

w_t^T : i -th gene weight in year T .

B.2 Lost gene rates:

$$lostr_j = \frac{\overline{\sum_{t \in anc(j) - foc(j)} x_{t,j}}}{\sum_{t \in anc(j)} x_{t,j}} \quad (12)$$

$$lostwr_j = \frac{\overline{\sum_{t \in anc(j) - foc(j)} x_{t,j} \cdot w_t^T}}{\sum_{t \in anc(j)} x_{t,j} \cdot w_t^T} \quad (13)$$

$$lostr_diff_j = lostwr_j - lostr_j \quad (14)$$

Where:

$lostr_j$: average lost gene rate the j -th product, $lostr_j \in [0,1]$.

$lostwr_j$: average weighted lost gene rate of the j -th product, $lostwr_j \in [0,1]$.

$lostr_diff_j$: gene lost rate difference of the j -th product.

B.3 New gene rates:

$$newr_j = \frac{\overline{\sum_{t \in anc(j) - foc(j)} x_{t,j}}}{\sum_{t \in foc(j)} x_{t,j}} \quad (15)$$

$$newwr_j = \frac{\overline{\sum_{t \in anc(j) - foc(j)} x_{t,j} \cdot w_t^T}}{\sum_{t \in foc(j)} x_{t,j} \cdot w_t^T} \quad (16)$$

$$newr_diff_j = newwr_j - newr_j \quad (17)$$

Where:

$newr_j$: average new gene rate of the j -th product, $newr_j \in [0,1]$.

$newwr_j$: average weighted new gene rate of the j -th product, $newwr_j \in [0,1]$.

$newr_diff_j$: new gene rate difference of the j -th product.

B.4 Brand-new gene rates:

$$X_t = \{x | x \text{ in the years earlier than } t\} \quad (18)$$

$$ngr_j = \frac{\sum_{x_{i,j} \in X_t} x_{i,j} \cdot I(x_{i,j} > 0)}{\sum x_{i,j} \cdot I(x_{i,j} > 0)} \quad (19)$$

Where:

X_t : set of the genes in years earlier than year t .

ngr_j : brand-new gene rate of the j -th product.

$I(x > 0)$: when $x > 0$, the value of the function is 1; otherwise, it is 0.