Jurassic Park @ 35: Reflections on evolutionary genetics, de-extinction, and the science-society interface

C. Brandon Ogbunugafor[1,2] ✉

[1]Department of Ecology & Evolutionary Biology, Yale University, New Haven, CT 06520, USA
[2]Santa Fe Institute, Santa Fe, NM 87501, USA

✉CBO: brandon.ogbunu@yale.edu

Abstract | On the 35th anniversary of the release of Michael Crichton's *Jurassic Park*, I reflect on both technical and cultural themes of the novel that resonate in the current moment. First, I offer a concise review of three evolutionary concepts—*plasticity*, *pleiotropy*, and *epistasis*—that complicate our efforts to engineer organisms with desirable phenotypes. I show how these ideas play out in the fictional narrative of *Jurassic Park* and in real-world genome engineering projects such as the "de-extinction" of the dire wolf. I then consider the broader technical and social significance of the novel: its lessons for our quest to control biological systems, its cautionary critique of techno-optimism, and its rich portrayal of scientists. The perspective is organized around quotes from Ian Malcolm, a fictional mathematician who offers insightful commentary on the challenges of the biotechnological exploits in the story. I argue that the novel's lessons are especially valuable today, as we reassess the ambitions guiding scientific practices.

I Introduction

2025 marks the 35th year since the release of Michael Crichton's *Jurassic Park* (Knopf, 1990). It was an immediate commercial success, selling millions of copies within its first few years on the market. However, it is best known for inspiring the *Jurassic Park* films, which have grossed over USD 5 billion worldwide. The critical reception of the book was largely positive and scholars in multiple disciplines have analyzed its narrative and cinematic adaptations, exploring topics such as ancient DNA (*1*), bioethics (*2*), and beyond. Here, I use this anniversary to reflect on several themes from the novel in light of contemporary issues in evolutionary genetics and the interface between science and society. In addition to its scientific relevance, I propose that *Jurassic Park* was successful in demonstrating how scientific progress is a social practice, where our ambitions can become complicated by forces other than curiosity about the natural world.

The story of *Jurassic Park* focuses on the activities of a biotechnology company, InGen, founded by a wealthy investor/philanthropist named John Hammond, who is also a dinosaur enthusiast. InGen scientists developed a method to extract DNA from extinct dinosaurs via mosquitoes that had once fed on them (fossilized in amber). Using cutting-edge molecular techniques, InGen scientists constructed full-length genomes comprising extinct dinosaur DNA, with frog DNA used to fill in gaps introduced during fossilization. They then injected the engineered DNA into artificial eggs and grew embryos (all female by design) in the laboratory.

An evaluation of the feasibility of fictional methods in *Jurassic Park* would not be useful, as the impact of the story does not depend on the believability of the proposed science. One could even argue that the aspirational nature of the technology in *Jurassic Park* was part of its appeal. Furthermore, Crichton wrote much of this in the 1980s, predating the Human Genome Project (*3*), well before sequencing and cloning tools became affordable and widely available. When we consider this, *Jurassic Park* was successful in the main endeavor of many speculative fiction works: building a world based on an imaginative extrapolation of technology, one believable enough to avoid distracting the reader from the story.

However, I propose that *Jurassic Park* achieved a goal more ambitious than detailed world-building: it effectively articulated many issues, both technical and non-technical, that are pertinent to genome engineering. To anchor this discussion, I will highlight a recent breakthrough (in 2025) where *Jurassic Park* can be invoked for comparison: Colossal Biosciences' attempt at the de-extinction of *Aenocyon dirus*, better known as the dire wolf.

I begin with a brief survey of contemporary approaches to de-extinction. I then provide a mini-review of three concepts from evolutionary biology that complicate genome engineering efforts more broadly, and propose a framework for considering our attempts at controlling biological systems with the tools of bioengineering (Parts

II-V). Finally, I discuss several ethical and cultural matters that appear in both the book and in other real-world settings (Part VI). This article is structured around quotations from the most resonant character of the book, Ian Malcolm, a fictional mathematician who serves as the vehicle for the ethical messages in the story[1].

Note: I have constructed this perspective to be read by both experts and non-experts with a basic to moderate understanding of evolutionary concepts[2]. To do so, I minimized the use of mathematical and statistical formalisms. For those interested, some of these details are provided in Boxes 1–3.

"You create new life-forms, about which you know nothing at all." (pg. 342)

Several subfields of genetics have generated a large body of literature on ideas featured in *Jurassic Park*, many of which are similar to concepts central to modern de-extinction efforts. For example, practitioners in the fields of ancient DNA and paleobiology have long examined the science of resurrecting fossil species (*1*), and leaders have offered detailed summaries of the science of de-extinction, including the many challenges involved (*4*,*5*).

Recently, the science of de-extinction has received an unprecedented level of attention. The April 2025 announcement from Colossal Biosciences involving the engineering of genes from the extinct dire wolf (*Aenocyon dirus*) into the gray wolf (*Canis lupus*) was accompanied by widespread media coverage (*6*–*9*). In a press release, the Chief Executive Officer of Colossal Biosciences celebrated the event: "This massive milestone is the first of many coming examples demonstrating that our end-to-end de-extinction technology stack works (*9*)." This required the isolation of the dire wolf genome from ancient DNA extracted from subfossil remains, followed by the engineering of mutations from this extinct species into cells of a modern surrogate species, the gray wolf. The effort involved several technical innovations, including the use of advanced paleogenomics techniques, the assembly of a high-quality dire wolf genome, and the application of CRISPR-based multiplex genome editing of dire wolf-specific loci in viable embryos.

The project targeted 20 mutation edits across 14 gray wolf genes, all focusing on physical traits (morphology, bone structure, coat color, etc.). Of these 20 mutations, 15 were from the extinct dire wolf genome, and the other five mutations were derived from other gray wolves. This is because direct engineering of select dire wolf mutations has conferred unexpected defects in other canids (e.g. blindness, deafness) (*9*,*10*). To avoid these defects, Colossal Biosciences engineered gray wolves in a manner that recapitulated some physical traits of dire wolves while avoiding the deleterious effects. Photographs and videos of beautiful animals shared around the world highlighted the final result: a successful genome engineering effort that generated an animal with physical attributes of two different species.

For illustrative purposes, one can compare the ambitions and activities of InGen (the fictional company in *Jurassic Park*) to those of Colossal Biosciences. Both aim to bring extinct species back using modern molecular techniques. Colossal Biosciences does not intend to build a theme park, and their genetically modified organisms are reared in controlled settings, sharing little in common with the world in which dinosaurs are engineered in *Jurassic Park*. But the technical errors from InGen in *Jurassic Park* reflect a lack of clarity around several important evolutionary concepts that may complicate our real-world genome engineering excursions, including de-extinction.

In the next several main sections (Parts II-V), I survey three (of the many) theoretical concepts that apply to the challenge of bioengineering a phenotype of interest through genomic modification: plasticity, pleiotropy, and epistasis. We will discuss the relevance of these topics in toy examples inspired by *Jurassic Park*, and in real-world settings.

II "It isn't adapted to our world... Everything is different." (pg. 178)

Plasticity

Plasticity is a central idea in evolutionary biology, describing the ability of a genotype to produce different phenotypes across environmental contexts (Box 1). Its roots can be traced to Richard Woltereck's experiments in 1909 on water fleas, where he coined the term "Reaktionsnorm (reaction norm)" to communicate how trait expression depended on the environment (*11*,*12*).

The literature on plasticity is vast, and several treatments have rigorously examined its large implications across the biosphere (*13*–*19*). There are various types of plasticity, including discrete, categorical, develop-

[1] Quotes are mostly co-opted for the purpose of the article, are used outside of their context in the novel.

[2] For example, I do not explain concepts like *genotype*, *phenotype*, or *mutation*.

mental, and behavioral (12,16–18). For example, *phenotypic plasticity* often involves reversible changes in phenotype across environments. In contrast, *developmental plasticity* refers to traits that are plastic with respect to the environment during development, potentially leading to fixed phenotypes during adulthood.

Box 1: Plasticity

Plasticity is the ability of a genotype or organism to produce different phenotypes across environmental contexts (12–18). It can be defined in several ways, two of which are presented below.
The first definition describes plasticity as the variance in phenotype across environmental contexts (20):

$$\text{Plasticity} = \text{Var}(P_1, P_2, \dots, P_n) \tag{1}$$

where $P_1, P_2, \dots, P_n$ are phenotype values measured in n distinct environments.
The second definition expresses plasticity as a linear function relating phenotype to an environmental variable (15):

$$P(E) = a + bE \tag{2}$$

where $P(E)$ is the phenotype expressed in environment E, a is the intercept, and b is the slope representing the rate of phenotypic change per unit change in E. The linear function in Equation 2 only applies to the simplest, most circumscribed cases. Plasticity is more often the result of nonlinear relationships between the phenotype and the environment.

The *reaction norm* (sometimes referred to as the *norm of reaction*) is widely used in ecology and quantitative genetics to visualize how the trait values of genotypes vary across environments (12,21–25). Not only does it highlight the environmental dependence of phenotypes, but also how genotypic performance interacts with the environment, a phenomenon called a *gene-by-environment interaction* (G×E) (Figure 1) (26,27). G×E interactions have been extensively studied and are now a part of the standard canon of evolutionary and population genetics. They complicate simple interpretations of performance and fitness, especially when comparing genotypes of a species, strain, or breed. For example: Which population of *Mimulus guttatus* grows the fastest? Which strain of *Escherichia coli* can break down sugar the most efficiently? Which variant of SARS-CoV-2 is the most transmissible? Plasticity proposes that the answer may depend on the environment, making our attempts to link genotype to phenotype more challenging.

The flexibility of phenotype is a property of many complex biological systems and has important implications for bioengineering. Robustness across a range of real-world environments is the goal of engineering a modified phenotype. For example, let us consider a hypothetical bioengineer interested in generating plants with a certain leaf morphology. Leaf shape is a well-known plastic trait that varies depending on environmental factors such as temperature and light intensity (28). Consequently, a scientist seeking to engineer a specific leaf shape must consider how environmental conditions influence its development.

Similarly, plasticity is evident both in the fictional ambitions of InGen and in the very real aims of modern biotechnology companies. The scientists in *Jurassic Park* sought to breed *Tyrannosaurus rex* so that they would look and behave as they presumably had in the late Cretaceous period: large, intimidating, and apex predators. But, as the Ian Malcolm quote that forms the title of this section suggests, the challenge is that the Jurassic ecosystem is vastly different from that of the early 1990s (or of 2025). Consequently, a scientist attempting the de-extinction of *T. rex* must consider how phenotypes of interest, such as pigmentation or body mass, might be sensitive to the environment in which the organism exists.

In Figure 1, we present a fictional scenario in which two traits are expressed in different environments. Relatedly, the success of de-extinction is connected to the degree of plasticity in traits associated with fitness, and the specific environment that the animal lives in. The book addresses this directly, noting that the engineered dinosaurs suffer from several defects, including susceptibility to disease, which are likely the result of attempting to survive in a foreign (modern, human-constructed) ecosystem. To quote Henry Loomis, a scientist in 2025's *Jurassic World Rebirth*: "The fitness landscape of the Earth no longer suits them[3] (33).

[3]The *fitness landscape* (often called the *adaptive landscape*) is a depiction of genotype-space that analogizes the process of evolution to a physical landscape, where evolution moves populations "towards fitness peaks" or "down fitness valleys." The concept was introduced by Sewell Wright in 1932 (29) and has since become a foundation of modern population and evolutionary genetics (30–32).

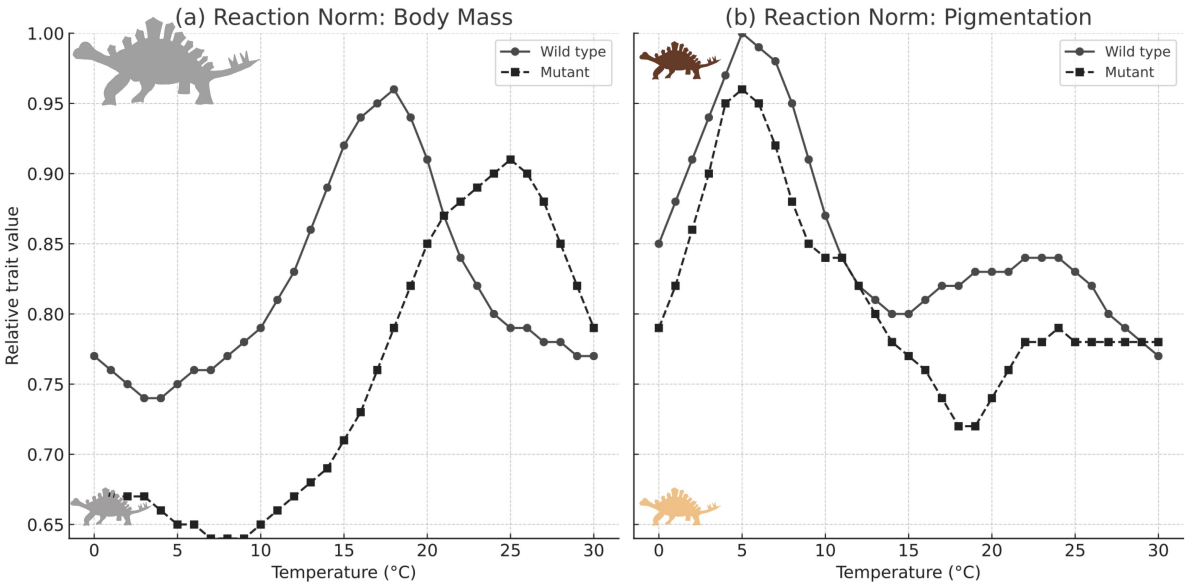

Fig. 1. Plasticity and pleiotropy. Fictional reaction norms illustrate how trait values vary across environmental contexts (*21*,*22*). Here we compare wild type and mutant variants of a single gene that affects two developmental traits in a genetically modified animal: (a) pigmentation and (b) body mass. The x-axis is temperature; the y-axis is trait value relative to a standard. Lines connect genotype mean values from measurements of individuals at selected developmental temperatures, with trait values fixed in adulthood (developmental plasticity). Plasticity is reflected in how genotypes differ across environments for a given trait (pigmentation, body mass). Crossing reaction norms indicate a gene-by-environment (G×E) interaction, where genotype performance depends on environment (*26*,*27*). Here, temperature is the environmental gradient, but environments may be continuous (e.g., pH) or categorical (e.g., location, resource presence). Pleiotropy is observed when a single genotype differs across traits: the fictional gene affects both pigmentation and body mass, so changes in one trait accompany changes in the other. *Technical notes:* This example suggests that pigmentation and body size are significantly influenced by a single locus, though both traits are polygenic in most known animal species. Fictional animals are engineered homozygotes, avoiding dominance effects. Pigmentation peaks at cooler temperatures are inspired by literature on plasticity in thermal melanism (*34*,*35*).

III “Such isolation is impossible. It simply cannot be done.” (pg. 101)

Pleiotropy

Plasticity refers to the way measurable traits are expressed in different environmental contexts. Pleiotropy, on the other hand, is the propensity for a single gene to affect multiple (often unrelated) phenotypes (*36*–*39*) (Box 2). While the term pleiotropy was introduced by German geneticist Ludwig Plate in 1910 (*38*), the concept appeared in Gregor Mendel’s pea plant (*Pisum sativum*) experiments. In it, Mendel discovered that the same genes that dictated the white and purple colors of flowers also influence the color of seed coats (*40*,*41*). Even Charles Darwin discussed phenomena related to pleiotropy under the guise of “correlated variation” between traits, offering that “Colour and constitutional peculiarities go together, of which many remarkable examples could be given amongst animals and plants[4]” (*42*). That pleiotropy appeared from the very beginnings of evolutionary biology and genetics is a testament to its fundamental status.

Many examples of pleiotropy also exist in complex organisms such as humans. A classical case involves Marfan syndrome, an autosomal dominant condition caused by mutations in the *FBN1* (fibrillin-1) gene. These mutations are associated with a variety of clinical symptoms, including an increased risk of aortic dissection, long limbs, myopia, hypermobile joints, and several others (*43*). This diversity of outcomes highlights the interconnectedness of genes and functions in humans. This becomes easier to understand when we learn that *FBN1* encodes a protein that contributes to the structure of connective tissue. Pleiotropy often appears when alterations occur in genes that contribute to basic components of the morphology or physiology of the organism.

[4] *Linkage disequilibrium*, where genes are inherited together due to their physical proximity on a chromosome, is another force that can underlie trait correlation in a manner that Darwin described.

Box 2: Pleiotropy

Pleiotropy refers to the tendency of a single gene or locus to influence multiple, often distinct, phenotypic traits (*36*–*38*,*44*). A simplified way to represent this is as a property of the genotype–phenotype map, where a genotype contributes to more than one trait. In quantitative genetics, this can be illustrated with a linear model (*45*):

$$P = \mu + BG + \epsilon \tag{3}$$

where P is a vector of phenotypic trait values, μ is the baseline (population) mean, G is the genotype, B is a vector or matrix of regression coefficients describing pleiotropic effects, and ϵ captures residual variation due to environment, noise, or unmeasured loci. While this form highlights the basic idea, the genetic architecture of pleiotropy is often more complex, involving nonlinear and context-dependent effects.

Pleiotropy arises from a feature of complex systems in which the number of possible functions exceeds the number of elements that construct them. In biology, this means that there are far fewer genes (in *Homo sapiens*, roughly 20,000 protein-coding genes) than discrete phenotypes (an unknown but larger number, depending on how we define a phenotype). This disparity is reconciled through the recombination and reorganization of genetic information through many mechanisms (e.g., variable gene expression, alternative splicing), allowing each genetic element to contribute to multiple phenotypes (*37*,*46*). This represents an important feature of genome evolution: biological information is engineered to be wired and re-wired, and this feature underlies the evolutionary potential of new functions (*39*).

This is related to an idea in evolution called the *cost of complexity*, where widespread pleiotropy in complex organisms constrains evolution, because it is challenging to modify genes (through mutation, as occurs during molecular evolution) without affecting other functions (*47*,*48*). However, this cost can be mitigated through a feature called *modularity*, the tendency for biological information to be organized into functional units (*47*,*49*,*50*). This means that tweaking certain genes will not always perturb functions throughout an organism, but mainly those within a module. This can limit the negative consequences of altering genes that contribute to multiple phenotypes.

How does pleiotropy appear in genome engineering efforts such as those depicted in *Jurassic Park* and in the dire wolf project? The genetic contribution to multiple phenotypes presents a significant complication because it implies (often unpredictable) "off-target" effects of modifying genes, where altering one part of a system can influence others (*51*). As in Marfan syndrome, changes in a gene can have multiple phenotypic consequences, many of which are difficult to predict. This uncertainty is magnified when we engineer genomes in organisms with which we are unfamiliar, as was the case in *Jurassic Park*, and in modern de-extinction efforts. Like the *FBN1* gene in *Homo sapiens*, the dire wolf mutations, when expressed in the genomic background of another animal, can affect more phenotypes than the intended physical traits. This might explain why Colossal Biosciences had to use molecular tricks to engineer dire wolf features into the gray wolf while avoiding defects in unrelated phenotypes.

Figure 1 demonstrates a fictional scenario using a gene that plays a role in two phenotypes and a range of environments (temperature). Even if we have a rigorous understanding of how environmental context shapes our phenotype of interest (e.g., coat color in an animal and temperature), the gene of interest can influence multiple phenotypes.

IV "It is inherently unpredictable, just as the weather is." (pg. 178)

Epistasis

The source of unpredictability in pleiotropy is the fact that genes can participate in more than one function. But what are other major sources of unpredictability? One involves questions about the very nature of mutation effects. In theoretical population genetics, this has been studied with regard to the distribution of fitness effects, a statistical picture of mutations in terms of being neutral, beneficial, or deleterious (*52*,*53*). But another concept illustrates how the phenotypic effects of mutations depend on genomic context, a phenomenon known as *epistasis*.

There is a colloquial definition of epistasis that I have found useful: The "surprise at the phenotype when mutations are combined, given the constituent mutations' individual effects (*54*)." Or, I know what mutation [A] does to a phenotype, and I know what mutation [B] does to a phenotype. But when I combine them, I get a

phenotype that I could not have predicted from their individual contributions. More formally, epistasis refers to non-additive interactions between genes or mutations (*55*–*57*) (Box 3). It was conceptualized by William Bateson in 1909 to describe how the effects of some genes could mask the effects of others (*58*).

As in pleiotropy, we can invoke examples from human disease. Cystic fibrosis is a well-characterized Mendelian[5] disease that follows an autosomal recessive pattern (*59*,*60*). Symptoms present in multiple systems (e.g., respiratory, digestive), which also reflects the pleiotropic effects of the affected gene (not unlike the mutations in *FBN1* responsible for Marfan syndrome). Patients generally carry two copies (one from each biological parent) of a mutated cystic fibrosis transmembrane conductance regulator (*CFTR*) gene (often ΔF508), which encodes a protein responsible for the regulation of chloride and other electrolytes. Despite the purported simplicity of the cystic fibrosis disease phenotype[6], studies have shown that its severity is influenced by mutations in other genes, such as *TGFB1*, which encodes transforming growth factor β-1 (TGFβ-1). *TGFB1*-specific mutations can worsen the severity of cystic fibrosis (*62*,*63*), suggesting that the genetic effects of *CFTR* mutations are modified—through epistasis—by mutations in the *TGFB1* gene.

Box 3: Epistasis

Epistasis occurs when the combined phenotypic effect of two (or more) mutations is not equal to the sum of their individual effects, relative to a defined baseline (e.g., wild type) (*54*,*55*). In other words, the whole is not simply the sum of its parts.

$$\Delta P_{AB} \neq \Delta P_A + \Delta P_B \tag{4}$$

where ΔP_A and ΔP_B are the phenotypic effects of single mutations A and B relative to the wild type, and ΔP_{AB} is the effect of the double mutant. The second definition expresses epistasis in a statistical genetics framework, where the phenotype is modeled as the sum of additive and interaction effects (*64*):

$$P = \mu + \sum_i a_i x_i + \sum_{i<j} \epsilon_{ij} x_i x_j \tag{5}$$

where P is the phenotypic value, μ is the baseline phenotype, a_i are additive effects, x_i encodes the genotype at locus i, and ϵ_{ij} captures the epistatic interaction between loci i and j. Although epistasis can be described with simple forms such as Equations 4 and 5, it often involves complex, higher-order interactions.

In broader discussions, epistasis encompasses different definitions and use cases (*55*,*57*,*65*,*66*). It can be classified by the quantitative consequences of interactions between gene variants or mutations: *positive epistasis* occurs when two mutations produce a non-additive positive effect; *negative epistasis* when the effect is less than the additive combination; and *sign epistasis* when the direction of the effect (positive or negative) differs from that of the component mutations or genes—often the 'biggest surprise.' Figure 2 is a fictional depiction of how epistasis emerges between mutations in a gene that plays a role in pigmentation. When epistasis is present, we cannot predict the phenotypic consequences of combinations of mutations based on their individual contributions.

The notion that mutations can interact in a non-additive fashion complicates the relationship between genotype and phenotype and makes it difficult to predict the consequences of mutations, especially in complex organisms where many gene products and pathways interact. In the setting of *Jurassic Park*, epistasis helps explain why inserting foreign genes or mutations into a dinosaur genome could produce unexpected results. InGen scientists filled gaps in dinosaur DNA with frog DNA (due to breaks during fossilization). This frog DNA caused unexpected consequences, most notably the birth of males when all dinosaurs were designed to be female. Whatever the mechanism, this genetic 'surprise' can be attributed to epistasis between amphibian genes and the genomic background of dinosaurs (note that pleiotropy may also be at work here; perhaps the frog genes that InGen scientists thought participated in one function played an unforeseen role in sex determination).

The importance of epistasis is also evident in the dire wolf bioengineering exercise. As noted above, 20 mutations were engineered into 14 genes in the gray wolf. Fifteen of these mutations came from the reconstructed ancient genome of the extinct dire wolf. The other five were from extant genetic variants in gray wolves, engineered into two gray wolf loci—*MC1R* and *MFSD12*, both of which are associated with coat color (*69*). Recall

[5]By "Mendelian," I mean that it follows a pattern of inheritance where the phenotype—disease in this case—can be understood as the direct consequence of an allele passed down from each parent

[6]We commonly describe Mendelian traits as being "simple," as opposed to phenotypes that are "complex," as in, they are the product of multiple genes that contribute to a phenotype in a complicated manner (*61*).

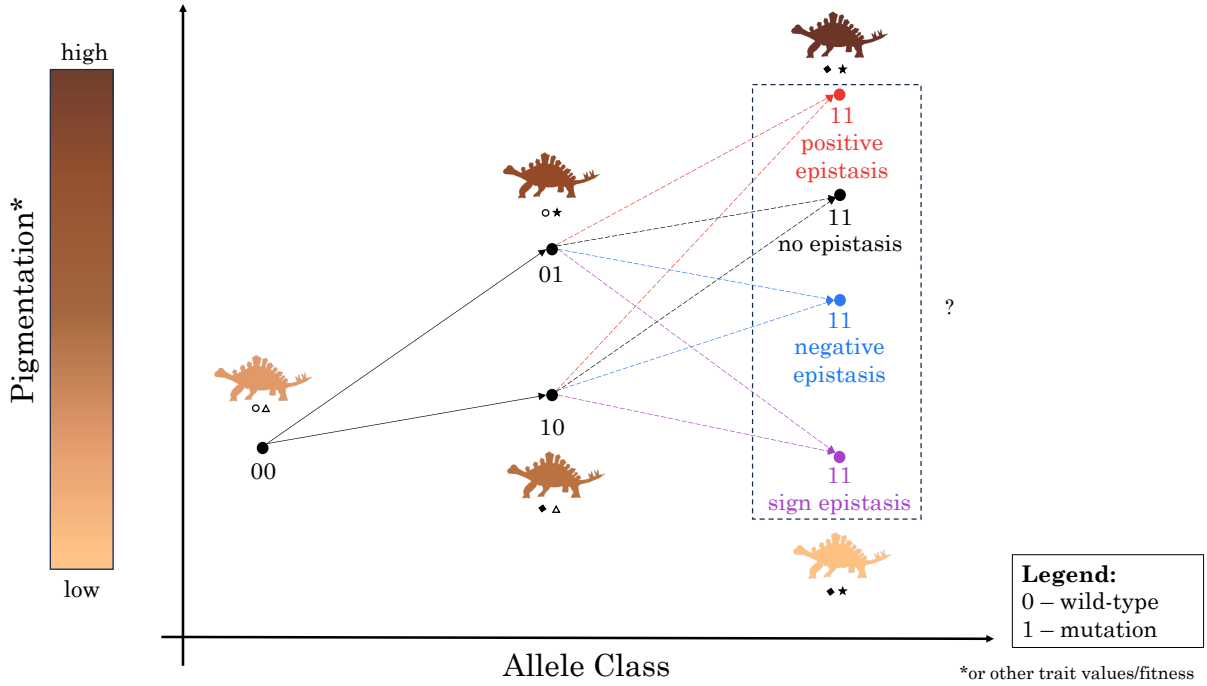

Fig. 2. Epistasis. In this fictional schematic, two engineered mutations in an extinct animal gene affect pigmentation at 25 ℃. Binary notation denotes genotypes: [0] is the wild type locus, [1] is a mutation. The x-axis shows pigmentation relative to a standard estimate. Combining mutations ([11]) produces a synergistic effect greater than the sum of their individual effects ([01], [10]). In evolutionary genetics, this reflects a G×G interaction, where a mutation's effect depends on genetic and genomic context. *Technical notes:* As in Figure 1, this example treats pigmentation as being influenced by a single locus. Studies have shown that pigmentation is polygenic (*67*) and we have no information about its genetic architecture in dinosaurs. Fictional animals are engineered homozygotes, avoiding dominance effects. Values are for schematic purposes only. This figure is adapted from a study on epistasis in viral pathogens (*68*).

that gray wolf mutations were used because several dire wolf mutations had deleterious effects in other canids, including blindness and deafness (*6*,*7*). Why is this so? Given the evolutionary history of the dire wolf (*70*,*71*), its genome differs sufficiently from that of existing canids to qualify as a meaningfully different genotypic background. Because of this, donor mutations from the dire wolf are engineered into the genome of another species. These mutations operate outside their evolved context, a substrate for epistatic surprise.

V "What we call 'nature' is in fact a complex system of far greater subtlety than we are willing to accept." (pg. 102)

Additional thoughts on plasticity, pleiotropy, and epistasis

In previous sections, we highlighted how plasticity, pleiotropy, and epistasis underlie many challenges with genome modification (Summarized in Box 4). But I am not arguing that they necessarily render these endeavors doomed to fail. Rather, I invoke them as concepts that should be considered in our broader applications. I should also emphasize that these concepts do not have strict boundaries and are not mutually exclusive. As shown in Figure 1, plasticity and pleiotropy can occur for the same gene variant. Epistatic interactions can also appear across multiple phenotypes through pleiotropy (*72*–*74*), a phenomenon that has been referred to as *epistatic pleiotropy* (*75*), or *pleiotropic epistasis* (*76*), though no single term is consistently used in the literature. In addition, there is overlap between plasticity and epistasis, when epistatic effects manifest differently across environments (*31*,*77*,*78*). This is called *environmental epistasis* (*78*), and can be depicted by the *mutation effect reaction norm*, which tracks mutation effects and epistasis across environments (*79*). Lastly, there are even examples where plasticity, pleiotropy, and epistasis can be examined within a single data set, when mutation effects differ for traits across environmental contexts[7].

[7]In one example, we observed how different mutations affect growth and resistance to an antimicrobial drug across varied cellular environments (*57*,*80*).

Box 4: Evolutionary concepts relevant for genome modification and de-extinction

Here we summarize three concepts that complicate de-extinction and genome engineering.

- *Plasticity*: The ability of a genotype to produce different phenotypes across environmental contexts (e.g., the fictional velociraptor, *Velociraptor mongoliensis*, of *Jurassic Park* evolved in an ecosystem vastly different from that of the proposed 1990s theme park. Such contextual differences would likely have phenotypic consequences).
- *Pleiotropy*: The propensity for a single gene or locus to influence multiple, often unrelated, phenotypes (e.g., in an animal de-extinction effort, modifying a gene for a desired trait could have unintended effects on other traits due to pleiotropy).
- *Epistasis*: The non-additive interaction between genes or mutations, where the effect of one depends on the presence of others (e.g., donor mutations from one species can interact with mutations and gene variants on a recipient species' genome, and have surprising, unforeseen phenotypic effects).

Though these concepts are relevant to today's biotechnological pursuits, they were all mentioned (not invented) by evolutionary theory luminary Sewall Wright in his landmark 1931 manuscript "Evolution in Mendelian Populations (*81*)." For plasticity, he wrote about "lability as a condition for evolution," referring to the need for plastic responses to environmental conditions. With regard to pleiotropy, he mentioned "A mutation, for example, may affect size, color, viability, fertility and many other characters at once." And he appealed to epistasis, stating that the "effects of a gene substitution often depend on the whole genetic system in which it occurs." I mention this to emphasize that these are not novel concepts, but are part of the standard canon of evolutionary and population genetics.

Notes on control in genome engineering and de-extinction

What makes de-extinction efforts, such as the one depicted in *Jurassic Park*, so provocative? The risk and reward (discovery) reside in the fact that we have never interacted with the target organisms and have limited knowledge of their genotype-phenotype maps and physiology.

Another distinguishing feature of bioengineering is that it does not rely on the typical tempo of adaptive evolution, which can take hundreds of generations (or more). Using modern molecular tools, we can introduce genetic novelties in minutes or hours, depending on the method and setting. But this is also a drawback. Pleiotropy and epistasis teach us that genomes are not like Lego bricks, where individual loci can be swapped in and out without consequences. Natural selection often works on entire genomes that function through the coordinated interaction between their component genes and gene products. For example, forces such as viral infection (*82*) and horizontal gene transfer (*83*) can introduce new parcels of genetic information into genomes, but they only persist in a population if they contribute to a fit and functional organism. But biotechnologists, as we learn in *Jurassic Park*), rarely move with the patience of natural selection. Instead, they focus on a phenotypic outcome without full knowledge of (or regard for) the gradual processes that produce functional organisms.

Challenges notwithstanding, de-extinction, genome engineering, and synthetic biology constitute some of the most exciting technologies in all of the life sciences. They offer hope that we can translate our theoretical ideas into a means of controlling biological systems. Here, I propose a conceptual framework for our present and future attempts to control living systems.

$$Control = Prediction + Engineering \tag{6}$$

The desire to control complex biological systems predates modern science. For thousands of years, humans have controlled the genotype-phenotype maps of animals and crops through selective breeding (*84*,*85*). And controlling human populations was the goal of the eugenics movement[8] (*86*,*87*).

In recent times, scientists have taken steps to control how evolution works (*88*). Examples include steering cancer cell populations for more effective therapy (*89*), and the use of directed evolution to build new

[8] I am referring to the eugenics movement of the 20th century. Though it was based on bogus science, eugenic ideas remain embarrassingly popular in 2025, perhaps more so today than in recent decades.

biomolecules (*90*)[9]. Other modern technologies have similar control ambition, including embryo selection—where embryos are chosen for fertilization based on polygenic risk metrics for certain phenotypes (e.g., disease, physical traits) (*92*)—and the creation of "CRISPR babies," in which embryos are directly edited to confer specific phenotypic outcomes (*93*)[10].

Breakthroughs in gene editing (as with the dire wolf project) are central in our quest to control genotype-phenotype maps. Similarly, InGen scientists in *Jurassic Park* should be recognized for their triumphs: finding a way to isolate the DNA of an extinct animal, and building a functional genome and organism. But their predictive capacities were lacking—perhaps because of plasticity, pleiotropy, epistasis, and other forces—leading to the myriad problems experienced on Isla, Nublar, the fictional island, near Costa Rica, where the dinosaur park was built.

There is a subtle point to highlight in our efforts to control biological systems: As described in Equation 6, we must not mistake engineering achievements for effective control. It does not matter how well the engineer can tinker with the pieces of a complex system; if the target system's behavior cannot be reliably predicted, then whatever contraption is being built cannot be said to be effectively controlled. In 2025, I believe that we are much further along in engineering aspects than we are in predicting biological outcomes[11].

VI "But scientific power is like inherited wealth: attained without discipline." (pg. 343)

Relevance to science, society, and culture

In the preceding sections, we examined technical ideas in evolutionary genetics relevant to genome engineering efforts not unlike those portrayed in *Jurassic Park* 35 years ago. But there are other, less formal scientific ideas worth highlighting. Before exploring the social and cultural significance of *Jurassic Park,* it is important to note that a rigorous take on the bioethics of genomic modification is beyond the scope of this article. Bioethics is a large subfield, the product of scholarship from hundreds of scholars that spans many decades (or longer). Interestingly, ethical terrain is a pillar of speculative fiction and was the subject of many classics, including *Frankenstein* (Lackington, Hughes, Harding, Mavor, and Jones, 1818) and *Brave New World* (Chatto and Windus, 1952). I urge those interested in this issue to consult this rich literature[12]. In this section, we survey several broader themes that emerge from a close reading of *Jurassic Park*.

One of the storytelling features of *Jurassic Park* is that it lacks a single standard protagonist or antagonist[13]. Its characters are vehicles for a story about chaos, arrogance, greed, ethics, and unpredictability. Among its themes is an indictment of the tunnel vision of ambitious and powerful people. John Hammond, the wealthy benefactor most responsible for the Jurassic Park project, is not guilty of malice; rather, of toxic naïveté.

These lessons may be relevant in discourse surrounding today's de-extinction efforts. For example, the 2025 dire wolf project generated an initial wave of enthusiasm, followed by criticism and debate (*97*–*99*). Critics focused on the ethical implications of de-extinction for conservation and broader discussions on the technical and ethical aspects of genetic modification.

Regarding conservation, scholars have long argued that de-extinction diverts finite resources—financial, political, and intellectual—away from urgent conservation priorities for living species and vulnerable ecosystems (*100*). Moreover, because the dire wolf diverged from extant canids more than five million years ago (*70*,*71*), any engineered animal would exist outside its original ecological context (see discussion of plasticity above). This means that its introduction into natural environments could pose risks to existing species and ecological networks (*101*–*103*). But to my knowledge, Colossal Biosciences has no such plans, and their engineered gray wolves are raised under controlled conditions[14]

[9]The 2018 Nobel Prize in Chemistry was awarded to Frances Arnold for pioneering work on directed evolution (*90*,*91*).

[10]The ethical and technical dimensions to human genomic prediction and genome modification efforts were explored in a perspective article based on the film *Gattaca* (Niccol, 1997) (*94*).

[11]There are certain biological systems that we can control by many definitions. But on the molecular or cellular scale, the quest continues.

[12]One can even argue that we owe part of the modern science of de-extinction to speculative fiction. For example, the term de-extinction has been traced to the science fiction writer Piers Anthony (*5*,*95*) Even more, there has been a longstanding literature that has used *Brave New World* to discuss issues involved with cloning and genetic engineering (*96*).

[13]Alan Grant, a paleontologist in the book, could qualify as a protagonist by many standards. This point has been debated among fans.

[14]For a well-written, in-depth discussion of the greater issues, I point those interested to *How to Clone a Mammoth* (Princeton, 2020).

The dire wolf project also prompts the question of whether the products of these efforts are truly dire wolves. Colossal Biosciences' Chief Scientific Officer once remarked, "People are yelling at us that these aren't real dire wolves. But no one has ever questioned whether the dinosaurs in *Jurassic Park* are real dinosaurs (*104*)." The comment suggests that people were inconsistent in their critiques of the dire wolf project. Yet, this exact question arose in the *Jurassic* Park universe. During the third film, fictional paleontologist Alan Grant exclaims: "What John Hammond and InGen did at Jurassic Park is create genetically engineered theme park monsters. Nothing more and nothing less (*105*)." Colossal Biosciences recently acknowledged that their engineered animals are modified gray wolves, not dire wolves (*106*), ending this aspect of the dire wolf debate.

The disagreement surrounding whether an engineered animal is real or not could be charged to semantics. And a debate about whether the fictionally engineered *T. rex* in *Jurassic Park* was truly a *T. rex* feels less important than other technical and ethical concerns. But the question of what constitutes essential differences between individuals and populations is an old one in evolutionary biology, and has social implications. For example, suggesting that two humans of different geographical ancestry that differ by more than 20 mutations (fewer than many biological siblings) are truly different animals would be absurd[15]. No, we cannot compare the marketing campaign of a de-extinction company to debates around the genetics of human differences, or imply that the former carries any of the historical (and contemporary) baggage of the latter. But anyone who talks about essential genetic differences between two animals should consult a large body of literature and lessons learned from over a century of broken thinking in this realm. As Colossal Biosciences' scientific leadership includes some of the world's most respected geneticists, care in navigating this topic is a reasonable expectation, as it is for anyone working in this area.

"Scientists...are focused on whether they can do something. They never stop to ask if they should do something." (pg. 318)

There is an old idiom for situations where our ambitions outweigh our capacities: "Your eyes are bigger than your stomach." It describes the goals of InGen in *Jurassic Park* and should be considered in our modern genome engineering efforts. The eyes-stomach analogy also applies to the tech "overlords" of our era, who aim to improve society through artificial general intelligence, bioengineering to prolong life, and technology to terraform other planets (*107*). These perspectives highlight the true villains of *Jurassic Park*: (i) unbridled techno-optimism and (ii) the use of abundant resources as a shield from having to justify their scientific ambition. The story teaches us the dangers of naïveté and the need for transparency and ethical care in our biotechnological pursuits.

These ideas are especially worth reflecting on in light of perilous attacks on science infrastructure in the USA in 2025. The changes compel us to rethink how science will be conducted in the present and future. One prediction is that there will be an increase in privately funded research. There is no denying that the biotechnology sector has played a central role in some of the most important discoveries in recent years, including the COVID-19 mRNA vaccine and AlphaFold (each awarded the Nobel Prize in Physiology or Medicine and Chemistry, respectively) (*108*,*109*). But this model comes with its own limitations. Profit-driven research funded by investors can oversell achievements and ignore relevant technical and ethical shortcomings[16]. Whatever the future holds for how science functions, it should adhere to the lessons of *Jurassic Park* and to the advice from the fictional Ian Malcolm and generations of real-life scholars: we must be mindful of what we are doing and ask difficult questions about why we are doing it.

"I didn't imagine it. I calculated it." (pg. 392)

I end with a short discussion of Ian Malcolm[17], who has emerged as a cult figure in science fiction lore. There are several reasons why he serves as an effective vehicle for the core messages of *Jurassic Park*. Malcolm is a mathematician brought to the island by John Hammond because of his work on chaos theory and his understanding of disorder and unpredictability[18]. He is employed at the University of Texas at Austin and in the sequel, *Jurassic Park: The Lost World* (Knopf, 1995), is a professor at the Santa Fe Institute, an institution known

[15]There is a large literature surrounding the issue of biological essentialism and genetic determinism, from scholars and scientists of many kinds. In terms of race specifically, I point the reader to *Backdoor to Eugenics* (Routledge, 2004) and *The Nature of Difference* (MIT Press, 2009).

[16]Surely other research models can be guilty of the same.

[17]I note that I am discussing his depiction in the novel, not the 1993 film.

[18]We can even applaud Hammond and the InGen scientists for including a potentially contrarian view.

for research in chaos theory (Malcolm's research focus) and other areas of complexity science[19].

Malcolm's lasting appeal stems from his iconoclastic nature. He is a theoretician unafraid to apply his expertise to real-world problems, and his fears about the park's inevitable failure are realized. Even if Crichton did not intend to provide an appealing portrait of a renegade scientist, Malcolm offers a memorable example of someone with a strong ethical foundation who communicates ideas with clarity. This matters because it may encourage aspiring mathematicians to see themselves in science, dispelling the notion that there is a single archetype that they must adhere to.

These may be unusual lessons to emphasize in a technical perspective, but they underscore a crucial need for science in an age of significant threats to its infrastructure. We need better front-facing images of scientists to build trust in a world where public perception can change rapidly (*111*). This is especially true for fields like theoretical and population biology, where visible truth-telling can help counter the negative consequences of misinterpretations of knowledge in fields like evolutionary biology, genetics, ecology, and public health.

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Data availability

There are no biological data in this manuscript. All of the figures are built using fully simulated data and are intended to be fictional. However, we have provided tables of the simulated data used to generate Figure 1 on Github: https://github.com/OgPlexus/JP1

Author Contributions

CBO conceived the project, generated and analyzed the fictional data, and wrote the original and revised versions of the manuscript.

Conflict of interest

None to report.

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[19] I am currently a resident professor at the Santa Fe Institute. I mention this because the institute, once described as a "Justice League of renegade geeks" by *Rolling Stone Magazine* (*110*), fashions itself as a space for intrepid scientists, not unlike the fictional Ian Malcolm.

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