Laws, Models, and Theories in Biology Within a Unifying Structuralist Interpretation: A General Explication and an Account of the Case of Classical Genetics

Pablo Lorenzano[1]

1. Introduction

Three metascientific concepts subject to philosophical analysis are law, model and theory. Throughout the twentieth and twenty-first centuries, three general conceptions of scientific theories can be identified: the "classical (or received)" view, the "historical (or historicist)" view and the "semantic (or model-theoretic)" view.

For the *classical view*, in its most general approach, theories should be represented as sets of statements deductively or axiomatically organized. Laws, on the other hand, are an essential component of these: they constitute the axioms by means of which they are metatheoretically represented (Carnap 1939; 1956; 1966). In the beginnings of the classical view, models were conceived as marginal phenomena of science (Carnap 1939). Subsequent authors (Braithwaite 1953 and Nagel 1961) strive to incorporate the models, and recognize their importance, into the framework of this classical view.

Historicist philosophers of science, with their alternative notions to the classical concept of theory (*pattern of discovery* in Hanson (1958), *ideal of natural order* in Toulmin (1961), *paradigm* or *disciplinary-matrix* in Kuhn ([1962] 1970; 1970; 1974a), *research program* in Lakatos (1969; 1970; 1971) and *research tradition* in Laudan (1977)), shine light on a conception of the laws that

[1]National University of Quilmes; National Scientific and Technical Research Council. To contact the author, write to: pablo.lorenzano@gmail.com.

diverges from the classical one. In addition, at the same time alternative proposals to the classical one are developed, which highlight the function of models in scientific practice (Achinstein 1968; Hesse 1966; Harré 1970) and investigate the role analogies and metaphors play in the construction of models (Black 1962; Hesse 1966) or of other components, linked to these, raised by historicist philosophers, such as exemplars (Kuhn [1962] 1970; 1970; 1974a; 1979).

In the current day and age, where the importance of models in scientific practice(s) is emphasized, the "*semantic view*"—which deals with the subject matter of models within the framework of a general conception of scientific theories—has been imposed as an alternative to the classical and historicist views of scientific theories.[2] Meanwhile, the "*model views*" of science—which deal with questions of the relationship between models and experience and between models and general theories independently of a general metatheory of science (Cartwright, Shomar and Suárez 1995; Morrison 1998; 1999; Cartwright 1999; Suárez and Cartwright 2008)—have been developed. Even more recently, the "*model-based science*"—which grew out of the community of philosophers, epistemologists, logicians, cognitive scientists, computer scientists, and engineers, working in different aspects of what is known as "model-based reasoning", with special focus on hypothetical-abductive reasoning and its role in scientific rationality (Magnani, Nersessian and Thagard 1999; Magnani and Nersessian 2002; Magnani and Li 2007; Magnani, Carnielli and Pizzi 2010; Magnani 2013; Magnani and Casadio 2016; Magnani and Bertolotti 2017)—has been proposed.

According to the semantic view of theories concepts relative to models are much more fruitful for the philosophical analysis of theories, their nature and function, than concepts relative to statements. The nature, function, and structure of theories can be better understood when their metatheoretical characterization, analysis or reconstruction is centered on the models that they determine, and not on a particular set of axioms or linguistic resources through which they do it.[3] Therefore, the most fundamental component for the identity of a theory is a *class* (set, population, collection, family) *of models*, so thata theory can be characterized in the first place for defining/determining the class, set, population, collection or family of its models. That is to present/identify a theory means mostly presenting/identifying its characteristic models. With the emphasis on models, one might think that not only can the term, or the concept, of "law" be dispensed with,[4] but also that the issue of laws should not be discussed. However, models must be identified in some way. And in the "*semantic view*" this is usually done through the laws or principles or equations of the theory to which they belong (thus, models would constitute the semantic or model-theoretic counterpart of such laws or principles or equations). On the other hand, even though for "model views" models do not form part of, and/or are independent or "autonomous" with respect to, theories (in some usual, encompassing sense of the term), they

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[2]"Over the last four decades the semantic view of theories has become the orthodox view on models and theories" (Frigg 2006, p. 51).

[3]This idea has been developed in different particular ways, giving rise to different approaches, variants or versions, which despite their differences constitute a family, the *semantic family*. For a characterization of this family, and of some of its members as well as a reference to many of them, see Lorenzano (2013b), and Ariza, Lorenzano and Adúriz-Bravo (2016) and Section 4.1 below.

[4]For skeptical positions about any notion of law and the substitution of the term "law" by other notion, such as "(fundamental) equations" or "(basic) principles", see Cartwright (1983; 2005), Giere (1995) and van Fraassen (1989). In fact, Carnap himself had already considered the possibility of dispensing with the term "law" in physics (Carnap 1966, p. 207).

would also be represented, or would contain, or would be identified, by means of principles, equations or laws, although not universally.

The aim of this article is to present the explication of these concepts, and of their relationships, made within the framework of Sneedian or Metatheoretical Structuralism,[5] and of their application to a case from the realm of biology: Classical Genetics. The analysis carried out will make it possible to support, contrary to what some philosophers of science in general and of biology in particular hold, the following claims: a) there are "laws" in biological sciences, b) many of the heterogeneous and different "models" of biology can be accommodated under some "theory", and c) this is exactly what confers great unifying power to biological theories.

To begin with, the structuralist explication of the concepts of law, model and theory will be presented successively, which will be preceded by an introduction to the subject, followed by its application to Classical Genetics.[6]

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[5]See Balzer, Moulines and Sneed (1987) for a complete and technically precise presentation of this metatheory, and see Díez and Lorenzano (2002), Moulines (2002) or Kuipers (2007) for a concise presentation of it.

[6]The analysis of Classical Genetics is based on Lorenzano (1995; 2000; 2002). The expression "Classical Genetics" is ambiguous. Sometimes it refers to all that was done in genetics prior to the development of molecular genetics and in contrast to it, i.e. to what was done in the so-called "classical period", a period that would cover the period from 1900 to 1939 (Dunn 1965). Sometimes it refers to what was done in genetics, in a shorter period of time, namely from 1910 to the late 1920s or early 1930s, primarily by Thomas Munt Morgan and his disciples and collaborators Alfred Henry Sturtevant, Calvin Blackman Bridges and Hermann Joseph Muller—later known as "the *Drosophila* Group", "the *Drosophila* School" or "the Columbia School". And sometimes it refers to one of the theories developed in the larger or shorter "classical period", which, besides "Classical Genetics", is also known as "Mendelian Genetics", "Transmission Genetics", "Classical Transmission Genetics", the "Theory of Gene Transmission", "Formal Genetics", "Gene Theory" and the "Theory of the Gene". We use here the expression "Classical Genetics" in this last sense of one theory, which we make precise through our analysis. We believe that the designation of this theory as "Mendelian", as is customary, among other things, in many genetics' textbooks, is historically erroneous, since formulations—such as the so-called "Mendelian laws"—and developments never made by Gregor Mendel are thus attributed to him. (For an structuralist analysis of Mendel's "hybridism", see Lorenzano 2022; and for an analysis of these, as well as of other questions related to the history of genetics—such as that of the supposed "rediscovery" of Mendel at the beginning of the century—, see Lorenzano (1995), and the bibliography cited therein). On the other hand, we agree with Kitcher (1984), Weber (1998) and Waters (2004), who have argued that the expressions "Transmission Genetics", "Classical Transmission Genetics" or the "Theory of Gene Transmission" do not refer to all that was done in genetics in the "shorter" classical period, i.e. to all types of research carried out during that period, to all answers for all kinds of questions that classical geneticists asked, to all theories developed by classical geneticists. It refers rather to a theory of inheritance developed during that period, which was—and still is—accepted as providing explanations, even satisfactory ones, of some regularities or patterns of inheritance (inheritance patterns), i.e. answering one (still important) type of questions that were raised during that period, corresponding to one type of research carried out by classical geneticists. According to Kitcher (1984), the theory of *gene transmission*, which addresses the family of *pedigree problems*, constitutes the "heart" of "classical genetic theory", while out of this theory grow other "subtheories", like the theory of *gene mapping*, which addresses questions about the relative positions of loci on chromosomes, and the *theory of mutation*, which tackles the question of how to identify mutations. Another name that sometimes appears in the literature is "Chromosome Theory of Inheritance" (or "Chromosome Theory of Mendelian Inheritance"). This name refers both to the attempts made at the beginning of the 20th century by Sutton and Boveri and to those made by Morgan and his collaborators ten years later to link the theory of inheritance with cytology. Thus, the chromosome (Mendelian) theory of inheritance would form a theory that includes, together with a theory

Next, the relevance of the previous analysis to the issues of the existence of laws in biological sciences, the place of models in theories of biology, and the unifying power of biological theories will be stressed.

Finally, the article will conclude with a discussion of the presented analysis.

2. The Concept of Law from the Point of View of Metatheoretical Structuralism

2.1. Introduction

In English the term "law" (in Old English *lagu*, in Medieval English *lawe*; in Latin *lex, legis*, in French *loi*) has an old Teutonic root *lag*, "lie", what lies fixed or evenly. It is usually used either alone, in the singular or plural form, "law(s)", or in the phrases "law(s) of nature", "natural law(s)", "law(s) of science" and "scientific law(s)". Although in Western culture the ideas of natural law, in the juridical (legal) and ethical (*ius naturale*, *lex naturalis*) sense—i.e., laws or moral precepts, in the approximate sense of those that are held to be either a divine mandate or intuitively obvious to all or with the ability to arrive at them by reasoning from obvious and indisputable premises, i.e., not based on legislated law, but on reason, divine command or moral instinct, and which are common to all nations—, and of *law of nature*, in the sense of the natural sciences, they go back to a common root, here we will only consider laws of nature in the scientific sense.

Despite having a long history going back to a time when people thought of nature as obeying the laws of its Creator in a similar way as individuals obeyed the laws imposed by their monarch, the expression "law(s) of nature" in the latter sense has only very rarely been used in the philosophical discussions of classical antiquity, as well as in theological discussions throughout the Middle Ages and the Renaissance. However, it is frequently used in the natural philosophy of the seventeenth century and by the end of that century it became common currency in scientific discussion and has remained so ever since.

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of inheritance, its interrelations with another body of biological knowledge, namely cytology. According to Darden and Maull (1977) and Darden (1980; 1991), the chromosome (Mendelian) theory of inheritance would be an example of an "interfield theory", whereas the theory of inheritance would be an example of an "intrafield theory". The expressions "Transmission Genetics" and "Classical Transmission Genetics" have an ambiguous meaning, since it is sometimes used in the sense of an intrafield theory and sometimes in the sense of an interfield theory. We might call the theory discussed here "Theory of Gene Transmission" (following Kitcher 1984), but also "Theory of the Gene"—following Morgan's (1917; 1926) usage—, although, and according to Vicedo's (1990a; 1990b; 1991) suggestion to distinguish between the formal concept of gene (which lacks any specification about its nature) and the biological concept of gene (which interprets the formal concept in cytological terms), the expressions "Formal Gene Theory" or "Formal Genetics" could also be used. By this we refer to the theory of inheritance developed by Morgan and his collaborators, without including the essential links that this theory has with other theories, especially with cell theory. We also believe that it is methodologically more appropriate to first reconstruct both theories—gene theory and cell theory—as two distinct and separate theories and then to investigate their intertheoretical relations or links. As a final note, for the first systematic exposition in a book of the theory referred to here, see Morgan *et al.* (1915); while Sinnott and Dunn (1925) may be considered the *first textbook of genetics in the Kuhnian sense*, inasmuch as it contains, with pedagogical goals, a clear and actualized—in comparison with Morgan *et al.* (1915)—exposition of the principles of genetics, paradigmatic applications of them (or 'exemplars'), as well as problems to be solved by the student.

In addition, the following two aspects should be taken into account. On the one hand, natural philosophers of early modernity, and especially mathematicians, had at their disposal an alternative, well-established and highly differentiated terminology, which they could and often did use to refer to natural regularities. Among these expressions, we find following: *regula*, *axioma*, *hypothesis*, *ratio*, *proportio*. On the other hand, the expression "law(s) of nature" does not necessarily denote a single concept or a concept with precise limits. Moreover, the concept of law of nature, like many of our concepts—whether they are everyday, scientific or metascientific—, may be considered as an "open" concept—both extensionally, i.e. as an open set, and intensionally, i.e. that doesn't possess conditions that are jointly necessary and sufficient for its application; or whose conditions are necessary but not sufficient; or sufficient but not necessary; or that they constitute a disjunction of conditions neither necessary nor sufficient, but whose instances of application share a certain "family resemblance" (Wittgenstein)—or as a "cluster" concept—having associated with it a cluster of criteria, of which only *the majority* must be satisfied by any instance (prototype theory)—, even though these conditions or criteria may change historically.

Thus, in the uses already established in the 17th century of the concept of law of nature, such as those of Descartes and Newton, the connection between laws of nature and God, as creator and lawgiver, was explicit. The secularization of the concept of the law of nature occurred at different times in Europe. In France, towards the end of the 18th century, with the French Revolution, Laplace was already able to argue that God was "an unnecessary hypothesis". In the German-speaking countries, Kant thought he could base the universality and necessity of Newton's laws no longer on God or nature, but on the constitution of human reason. While in Britain, despite the legacy of Hume, discussions continued as to whether the laws of nature were expressions of divinity until the Darwinian Revolution, but the secular interpretation of Darwin's "law of natural selection" finally prevailed there. This secularized version of the laws of nature has dominated the philosophical understanding of science ever since.

In scientific as well as in philosophical literature many authors speak not just plainly about *laws*, but about *natural* laws, or laws *of nature*, on one hand, and about *scientific* laws, or laws *of science*, on the other hand, too. Such expressions, besides, are commonly used as if the expressions belonging to one pair were interchangeable with the expressions belonging to the other pair, i.e. as if they were synonymous or had the same meaning. However, we consider it convenient to distinguish the first pair from the second one, since they correspond to different approaches or perspectives (e.g., Weinert 1995). The first pair corresponds to an approach of an *ontological* kind—corresponding to how things themselves are—, while the second one corresponds to an approach of an *epistemic* kind—centered in what we know.

Some philosophers have argued that a philosophical treatment of laws should be given only for the laws of nature and not for the laws of science. While others consider it more appropriate to refer to the laws of science than (only) to the laws of nature, because, in any case, it is the laws of science that would provide important keys to understanding what a law of nature is.

In what follows when we speak about laws, we will be talking about *scientific* laws, or laws *of science*, and not about *natural* laws, or laws *of nature*.[7]

At least as of 1930 the problem of what a law—i.e. the problem of finding the necessary and

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[7]For a more extensive discussion about the nature of laws as well as an analysis of natural laws, within the framework of Metatheoretical Structuralism, see Forge (1986; 1999) and Lorenzano (2014-2015).

sufficient criteria or conditions which a statement should satisfy in order to be considered or in order to function as a law—is discussed.

According to the classical view (Hempel and Oppenheim 1948), a *law* is a true *lawlike* statement that has the following properties: it is universal, with an unlimited or at least unrestricted scope of application; it does not refer explicitly or implicitly to particular objects, places, or specific moments; it does not use proper names; and it only uses "purely universal in character" (Popper 1935, Section 14-15) or "purely qualitative" predicates (Hempel and Oppenheim 1948, p. 156).

Despite successive and renewed efforts there is not a satisfactory adequate set of precise necessary and sufficient conditions as a criterion for a statement to be considered a "(scientific) law".[8]

The discussions in the field of general philosophy of science have also been held, and have taken place, in the special field of philosophical reflection on biology and its different areas such as classical genetics, population genetics, evolutionary theory and ecology, among others.

Some philosophers of science and of biology—partly based on, and partly supported by, evolutionists like Mayr (1982; 1985) and Gould (1970; 1989)—deny the existence of laws in biology in general, and in genetics in particular. Two main arguments have been put forward against the existence of laws in biology. The first one is based on the alleged locality or non-universality of generalizations in biology (Smart 1963); the second one is based on the alleged (evolutionary) contingency of biological generalizations (Beatty 1995).

At least three responses to these arguments can be found. The first one consists in submitting them to a critical analysis. This approach is chosen by Ruse (1970), Munson (1975), and Carrier (1995), among others. The second one is to defend the existence of laws, or principles, in biology but arguing that they are non-empirical, a priori. This strategy is followed by Brandon (1978; 1981; 1997), Sober (1984; 1993; 1997) and Elgin (2003). The third one is to defend the existence of empirical laws, or principles, in biology but arguing for a different explication of the concept of law or of non-accidental, counterfactual supporting, generalizations (Schaffner 1993; Carrier 1995; Mitchell 1997; Lange 1995; 2000; Dorato 2005; 2012; Craver and Kaiser 2013). Our proposal will be of this third kind. But in such a manner that it will allow us to consider "theoretical pluralism", "relative significance" controversies and some kind of contingency as not exclusive of biology (agreeing with Carrier (1995) on this) and to better understand the role played by different laws or lawlike statements of different degrees of generality in biology (capturing some of the points made by Ruse (1970) and Munson (1975)) as well as the "a priori" component pointed out by Brandon, Sober and Elgin.[9]

With respect the existence of laws in genetics in particular—and taking into account the classical proposal of differentiating between two types of genuine laws: on the one hand, laws of unlimited, unrestricted scope or *fundamental laws* and on the other, laws of limited, restricted scope or *derivative laws* that would *follow* from more fundamental laws (Hempel and Oppenheim 1948, p. 154)—, we must distinguish the claim that there are no laws in genetics at all, which is hardly tenable given at least the so-called "Mendel's *laws*", and the more asserted and discussed claim that there are no fundamental and/or general nomological principles in genetics. And, in a similar way as we did in the case of laws in biology in general, our position with respect to the denial of the

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[8]See Stegmüller (1983) and Salmon (1989) for an analysis of the difficulties of the classical explication of the notion of scientific law.

[9]For a more detailed discussion of the two first kinds of responses, see Lorenzano (2006b; 2007b; 2007c; 2014-2015) and Díez and Lorenzano (2013; 2015).

existence of fundamental laws in genetics will be of replacing the classical understanding of such laws and of the more restricted laws by a different one, which will allow us to better understand the role played by different laws or lawlike statements of different degrees of generality in genetics.

For their part, the historicist philosophers of science, on the way to conform and/or expound, or expand on, their conceptions about the development of science, with their correlative alternative notions to the classical concept of theory (such as *patterns of discovery* in Hanson (1958), *paradigm* or *ideal of natural order* in Toulmin (1961), *paradigm* and *discipline-matrix* in Kuhn ([1962] 1970; 1974a; 1977), or *research program* in Lakatos (1969; 1970; 1971), or *research tradition* in Laudan (1977), or *field* in Shapere (1974; 1984)), let emerge a certain conception about laws different from the classical concept of law, either with the same terminology (Toulmin 1953; Hanson 1958, Lakatos 1969; 1970; 1971; [1974] 1978; Shapere 1984c) or with a different one (Kuhn ([1962] 1970; 1974a; 1976; 1977; 1981; 1983a; 1983b; 1989; 1990), who, besides speaking of "laws", speaks of "symbolic generalizations").

One of the aspects shared in their stance related to the classical concept of law is that universality is a too demanding condition. This is a point already made many years ago by Toulmin for physics:

> Any one branch of physics, and more particularly any one theory or law, has only limited scope: that is to say, only a limited range of phenomena can be explained using that theory, and a great deal of what a physicist must learn in the course of his training is connected with the scopes of different theories and laws. It always has to be remembered that the scope of a law or principle is not itself written into it, but is something which is learnt by scientists in coming to understand the theory in which it figures. Indeed, this scope is something which further research is always liable to, and continually does modify. (Toulmin 1953, p. 31)

And what is valid for physics may also be valid for biology. This means that the alleged critique to biological generalizations for their non-universality doesn't even hold for the generalizations of physics. Therefore, biological generalizations should not be "doomed" because they lack of universality. What matters is not strict universality but rather the existence at least of non-accidental, counterfactual supporting, generalizations, which we take as uncontroversial present in biology, though generally more domain restricted and *ceteris paribus* than in other areas of science such as mechanics or thermodynamics.

A second aspect shared by the historicist philosophers of science is the acceptance of "laws"—or whatever they are called—of different degrees of generality within a "theory"—or whatever they are called. Thus, e.g., we have in Lakatos the most general "laws" as part of the *hard core* of the *research programme*, while the less general ones constitute the "'protective belt' of auxiliary hypothesis" (Lakatos [1974] 1978, p. 4); and what Kuhn calls "symbolic generalizations"—but also "generalization-sketches" (Kuhn 1974a), "schematic forms" (Kuhn 1974a), "law sketches" (Kuhn [1962] 1970; 1970; 1974a; 1974b; 1983a) or "law-schema" (Kuhn [1962] 1970)—and their "particular symbolic forms" (Kuhn [1962] 1970, 1970; 1974a; 1974b) adopted for application to particular problems in a detailed way. In both cases, the most general "laws" have a sort of a-priori (or analytical) "flavor" inasmuch as they are *irrefutable* by a methodological decision for Lakatos and because they are not directly tested (or applicable) for Kuhn. And in Kuhn more clearly than in Lakatos the relation between the two types of "laws" is not of a deductive kind—even though he does not delve into the analysis of the nature of the logical relationship between them.

As many philosophers of biology and of physics, we also accept a broader sense of lawhood that does not require non-accidental generalizations to be universal and with no exceptions in order to qualify as laws.[10]

This minimal characterization of laws as counterfactual-supporting facts is similar to the one defended in Dorato (2012), and it is also compatible with some proposals about laws in biology in particular, such as the "paradigmatic" (Carrier 1995) and "pragmatic" (Mitchell 1997) ones.

Whether one wants to call these non-accidental, domain restricted, generalizations "laws" is a terminological issue we will not enter here. What matters is, tagged as one wills, that these non-accidental generalizations play a key role in biology in general and in genetics in particular. We will show that in the case of Classical Genetics (**CG**). But, before that, we will present in the next subsection the structuralist explication of the concept of law. In particular, we will present the structuralist explication of the two kinds of laws, of the most general ones—even though without universality and with modal import—and of the less general ones within a theory, and of the type of relationship between them.

2.2. The Structuralist Concept(s) of Law

Within the structuralist tradition, when dealing with the subject of laws, discussions, even from their beginnings with Sneed (1971), though not with that terminology, focus on those scientific laws which, starting with Stegmüller (1973), are called "fundamental laws" of a theory.

However, accepting the problems for finding a *definition* of the concept of a law, when the criteria for a statement to be considered a fundamental law of a theory are discussed within the framework of Metatheoretical Structuralism, one tends to speak rather of "necessary conditions" (Stegmüller 1986, p. 93), of "*weak* necessary conditions" (Balzer, Moulines and Sneed 1987, p. 93), or, better still, only of "symptoms", some even formalizable (Moulines 1991, p. 233), although

> in each particular case of reconstruction of a given theory, it seems, as a general rule, to be relatively easy to agree, on the basis of informal or semi-formal considerations (for example, on its systematizing role or its quasi-vacuous character), that a given statement should be taken as the fundamental law of the theory in question. (Moulines 1991, p. 233)

On the other hand, Metatheoretical Structuralism draws a distinction between the so-called *fundamental laws* (or *guiding principles*) and the so-called *special laws*. This distinction, which will be developed later, elaborates the classical distinction between two kinds of laws with different degrees of generality in a different way as well as the Kuhnian distinction between the symbolic generalizations and their "particular symbolic forms" adopted for application to particular problems in a detailed way.[11]

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[10]Some philosophers of biology admit this, i.e. the existence of laws or some sort of non-universal and non-exceptionless lawlike generalizations, at least in some areas of biology, such as ecology (Weber 1999; Cooper 1998; 2003; Colyvan 2004; Colyvan and Ginzburg 2003; Lange 2005), evolutionary theory and classical genetics (Weber 2004).

[11]On the other hand, the expressions 'fundamental law' and 'special law' are not used here in Fodor's sense (Fodor 1974; 1991)—the former for laws of basic or fundamental sciences, the latter for laws of special sciences—but rather in the sense used by structuralists, i.e. for different kinds of laws within a theory.

Very briefly, five criteria can be mentioned as necessary conditions, *weak* necessary conditions or "symptoms" for a statement to be considered a fundamental law/guiding principle in the structuralist sense:

1) *Cluster or synoptic character*. This means that a fundamental law should include "*all* the relational terms (and implicitly also all the basic sets) and, therefore, at the end, *every fundamental concept* that characterize such a theory" (Moulines 1991), "several of the magnitudes", "diverse functions", "possibly many theoretical and non-theoretical concepts" (Stegmüller 1986), "almost all" (Balzer, Moulines and Sneed 1987), "at least two" (Stegmüller 1986).[12]

2) *Applicability to every intended application.*. According to this, it is not necessary that fundamental laws have an unlimited scope, apply every time and everywhere and possess as universe of discourse something like a "big application", which constitutes an only one or "cosmic" model, but it rather suffices that they apply to partial and well-delimited empirical systems: the set of intended applications of the theory (Stegmüller 1986).[13]

3) *Quasi-vacuous character*. This means that they are highly abstract, schematic, and contain essential occurrences of T-theoretical terms, which in structuralist sense are terms whose extension can only be determined through the application of a theory's fundamental law(s)[14] so that they can resist possible refutations, but which nevertheless acquire specific empirical content through a non-deductive process known as "specialization" (Moulines 1984).

4) *Systematizing or unifying role*. Fundamental laws allow including diverse applications within the same theory since they provide a guide to and a conceptual framework for the formulation of other laws (the so-called "special laws"), which are introduced to impose restrictions on the fundamental laws and thus apply to particular empirical systems (Moulines 1984).[15] It is clear that the distinction between fundamental and special laws is relative to the considered theory.

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[12]It is clear that the consideration of this criterion, in any of its versions, must take into account that it is strongly dependent on the respective language used, i.e. on the respective formulation of a theory, since it is only in relation to it that a term can be considered primitive, basic or fundamental. On the other hand, it is interesting to note a difference in this criterion between the classical conception of laws and theories and the structuralist metatheory. According to the former, the descriptive (non-logico-mathematical) concepts occurring in laws, as axioms or postulates of a formal axiomatic system (Hilbertian or Frege-Hilbert type), are, typically, theoretical concepts (in the classical sense) and, thus, fundamental laws are *theoretical laws*, formulated by means of pure theoretical statements, containing only theoretical terms (or concepts). Whereas here, typically, but not necessarily—as in the case of reversible thermodynamics (see Moulines 1984)—fundamental laws contain both **T**-theoretical and **T**-non-theoretical (in the structuralist sense) terms (or concepts), and if described classically, they would be described as *mixed* statements.

[13]The validity of laws can be regarded as *exact*—and thus as *strict* or non-interferable laws—or, rather, to the extent that they usually contain not only *abstractions*, but also various *idealizations*, as *approximate*, as already pointed out by Scriven (1959) and more extensively by Cartwright (1983)—and so as non-strict or *interferable* laws, and compatible with various specific treatments of this situation, such as those referring to ceteris paribus clauses (Cartwright 1983), "provisos" (Coffa 1973 and Hempel 1988) or "normicity" (Schurz 2009).

[14]For more on the structuralist **T**-theoretical/**T**-non-theoretical distinction, see Section 3.2.

[15]By saying it in a model-theoretic way, fundamental laws determine the whole class of models of a theory, while special laws determine only some of them, which constitute a subclass of the class of models.

5) *Modal import*. Fundamental laws express non-accidental regularities, are able to give support to counter-factual statements (if they are taken "together-with-their-specializations" within a theory, in the sense that we will introduce later of theory-net), even when they are context-sensitive and with a domain of local application, and that, in its minimal sense, instead of attributing *natural necessity*, *necessity of the laws* is attributed, and, in that sense, they should be considered as *necessary in their area of application*, even when outside such an area it doesn't need to be that way (Lorenzano 2014-2015; 2019; Díez and Lorenzano 2013; Moulines 2019).

Fundamental laws/guiding principles are "programmatic" or heuristic in the sense that they tell us *the kind of things* we should look for when we want to explain a specific phenomenon. But, as said before, taken in isolation, without their specializations, they say empirically very little. They can be considered, when considered alone, "empirically non-restrict". In order to be tested/applied, fundamental laws/guiding principles have to be specialized ("concretized" or "specified"). These specific forms adopted by the fundamental laws are the so-called "special laws".

It is worth emphasizing that the top-bottom relationship established between laws of different levels of generality is *not* one of implication or derivation, but of *specialization* in the structuralist sense (Balzer, Moulines and Sneed 1987, Chapter IV): bottom laws are specific versions of top ones, i.e. they specify some functional dependencies (concepts) that are left partially open in the laws above. That is the reason why they are called "*special* laws" instead of "*derivative* laws" like in the classical view of laws, according to which the laws with a more restricted or limited scope are assumed to be logically derived or deduced from the fundamental laws. Actually, "special laws" *are not derived* or *deduced literally* from the fundamental laws (at least are not derived or deduced *only* from them) without considering some additional premises. Formally speaking, the specialization relation is reflexive, antisymmetric and transitive, and does not meet the condition of monotonicity.

When the highest degree of concretization or specificity has been reached, i.e. when all functional dependencies (concepts) are completely concretized or specified, "*terminal* special laws" are obtained. This kind of special laws, proposed to account for particular empirical situations, can be seen as particular, testable and, eventually, refutable hypotheses to which to direct "the arrow of *modus tollens*" (Lakatos 1970, p. 102).

2.3. Laws in Classical Genetics (CG)

Classical Genetics (**CG**) is a theory about the hereditary transmission, in which the transmission of several traits or characteristics is followed from generation to generation of individuals. It talks about *individuals*—sets of individuals or populations that make up "families", that is, populations connected by bonds of marriage, parentage or common descendent—, and of certain *traits* or *characteristics possessed by them* (their "appearance")—what is called their "phenotype"—, individuals that *mate* and produce *progeny*, which also possess certain *traits* or *characteristics* (phenotype) and where numerical ratios, proportions or relative frequencies (r_j's) in the *distribution* of those characteristics in the progeny are distinguished.

The connections between its different components, i.e. its different objects and functions, can be graphically represented in the following way (see Figure 1), where the objects are represented by rectangles and the functions by arrows:
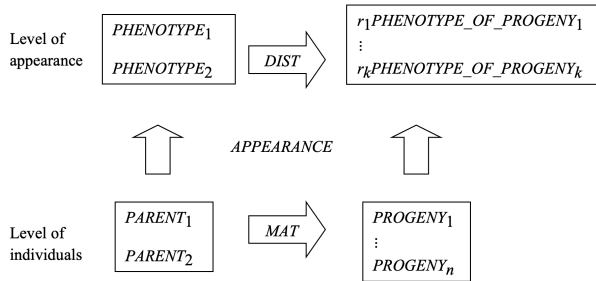
Figure 1

Classical Genetics (**CG**) intends to account for *biological systems*—constituted by *individuals* (that make up "families") *possessing* certain *traits* or *characteristics* (their phenotype) that *mate* and produce *progeny*—that show certain *patterns of inheritance*, which **CG** conceptualizes as *distribution of characteristics* from parental individuals toprogeny, expressed by certain proportions, numerical ratios or relative frequencies.

Examples of *cases* of characteristics *distributions* in *specific biological systems* are the following:

1) For the case of the color of pea seed albumen: Pea plants belonging to the first filial generation, with yellow seed coats, which are self-fertilized and produce offspring having a proportion 3:1 of yellow seed coat (¾) and green seed coat (¼).

2) For the case of the color of four o'clock flowers: Four o'clock plants belonging to the first filial generation,with pink flowers, which are self-fertilized and produce offspring having a proportion 1:2:1 of red, pink and white color flowers.

3) For the case of the color of pea seed albumen together with the form of pea seeds: Pea plants belonging to the first filial generation, with yellow seed coat and round seed form,which are self-fertilized and produce offspring having a proportion 9:3:3:1 of yellow seed coats and round seed form ($\frac{9}{16}$), of yellow seed coats and angular seed form ($\frac{3}{16}$), of green seed coats and round seed form ($\frac{3}{16}$), and of green seed coats and angular seed form ($\frac{1}{16}$).

4) For the case of the color of pea seed albumen together with the form of pea seeds and the color of pea flowers: Pea plants belonging to the first filial generation, with yellow seed coat, colored flowers and round seed form, which are self-fertilized and produce offspring having a proportion 27:9:9:9:3:3:3:1 of yellow seed coats, colored flowers and round seed form ($\frac{27}{64}$), ofyellow seed coats, colored flowers and angular seed form ($\frac{9}{64}$), of yellow seed coats, white flowers and angular seed form ($\frac{9}{64}$), of green seed coats, colored flowers and angular seed form ($\frac{9}{64}$), of yellow seed coats, white flowers and angular seed form ($\frac{3}{64}$), and of green seed coats, white flowers and angular seed form ($\frac{1}{64}$).

5) For the case of the length of corn ear: Corn plants belonging to the first filial generation, with neither short nor long ear length, which are self-fertilized and produce offspring with corn ear length that ranges from very short to very long in a transitional continuous way.

6) For the case of the form of fowl combs: Fowls belonging to the first filial generation, with walnut comb form, are crossed among them and produce offspring having a proportion 9:3:3:1of walnut comb form ($^9/_{16}$), of rose comb form ($^3/_{16}$), of pea comb form ($^3/_{16}$), and of single comb form ($^1/_{16}$).

7) For the case of the color of pea flowers together with the length of pea pollen grain: Pea plants belonging to the first filial generation, with purple flower color and long pollen grain length, which are self-fertilized and produce offspring having a proportion 7:1:1:7 of purple flower-color and long pollen grains ($^7/_{16}$), of purple flower-color and round pollen grains ($^1/_{16}$), of red flower-color and long pollen grains ($^1/_{16}$), and of red flower-color and long pollen grains ($^7/_{16}$).

For every specific case geneticists have to postulate *specific* (pairs of) factors/genes of the (parental) individuals—what is called their "genotype"—and the *specific* manner of their *combination* in reproduction (genotype-distribution) that accounts for the *specific* distribution of characteristics (phenotype-distribution) in the progeny.

This means that, in order to account for the distributions of characteristics in the progeny (i.e., for the ratios, proportions or relative frequencies), the following parameters have to be theoretically postulated:

(i) appropriate types and numbers of (pairs of) factors or genes—the genotype—(either one or more),

(ii) the way in which they are distributed in the progeny (as expected or theoretical probabilities, with combinations of factors or genes with the same probability or not),

(iii) the specific relationship in which they are with the characteristics of the individuals—their phenotype—(with complete or incomplete dominance, codominance or epistasis).

Thus, geneticists propose *special laws*, which contain these three types of specifications, plus the assumption (iv) that, given specifications (i) and (iii), the genotype distributions, given by specification (ii), *match* or *fit* (exactly or approximately) the phenotype distributions in the progeny.

The following are the specifications introduced to account for the above examples:

1) (i) these pea plants are heterozygous with respect to factors for seed coat color, (ii) combinations of their factors in offspring are equiprobable, and (iii) factors for yellow seed coat are dominant over factors for green seed coat (Sinnott and Dunn 1925, pp. 40-41, 45-50).

2) (i) these four o'clock plants are heterozygous with respect to factors for flower color, (ii) combinations of their factors in offspring are equiprobable, and (iii) factors for red flower color are incomplete dominant over factors for white flower color (Morgan 1926, pp. 5-7).

3) (i) these pea plants are heterozygous with respect to factors for seed coat color and for seed form, (ii) combinations of their factors in offspring are equiprobable, and (iii) factors for yellow seed coats are dominant over factors for green seed coat and factors for round seed form are dominant over factors for angular seed form (Morgan 1926, pp. 7-10).

4) (i) these pea plants are heterozygous with respect to factors for seed coat color, for flower color and for seed form, (ii) combinations of their factors in offspring are equiprobable, and (iii) factors for yellow seed coats are dominant over factors for green seed coat, factors

for colored flowers are dominant over factors for white flowers and factors for round seed form are dominant over factors for angular seed form (Sinnott and Dunn 1925, pp. 72-73).

5) (i) these corn plants are heterozygous with respect to factors for ear length, (ii) combinations of their factors in offspring are equiprobable, and (iii) the three pairs of factors are for ear length in corn with a cumulative effect (Sinnott and Dunn 1939, pp. 125, 127-129).

6) (i) these fowls are heterozygous with respect to both pairs of factors for comb form, (ii) combinations of their factors in offspring are equiprobable, and (iii) the walnut comb depends on the presence of two dominant factors, one of these genes alone produces the rose comb, the other alone produces the pea comb, the combination of the recessive alleles of these factors produces the single type of comb (Sinnott and Dunn 1925, pp. 91-92).

7) (i) these pea plants are heterozygous with respect to factors for flower color and for pollen grain length, (ii) combinations of their factors in offspring are not equiprobable (purple flower-color and long pollen grains that go in together come out together more frequently than expected for independent assortment of purple-red and round-long), and (iii) factors for purple flower-color are dominant over factors for red-color and factors for long pollen grain are dominant over factors for round pollen grain (Sinnott and Dunn 1925, p. 151; 1939, pp. 192-193).

In the terminology of Metatheoretical Structuralism the result of specifying (i), (ii) and (iii), plus the specific form adopted by the match or fit (iv), should be considered a *special law*; moreover, to the extent that all concepts are completely concretized or specified, each special law should be seen as a *terminal* special law. And such kind of special laws are what are intended to apply to particular cases.

In all of the above cases, it turns out that the postulated distributions in the progeny of parental pairs of factors or genes involved (specification (ii)) *matches* or fits (exactly or approximately) the characteristics distributions in the progeny (assumption (iv)), given the type and number of factors involved (specification (i)) and the postulated relationships between pairs of factors (genes) and characteristics ((specification (iii))). This means that the proposed special laws are *successfully applied* in the respective cases presented.

So far, we have identified some of the different special laws that have been proposed in classical genetics.

In order to try to identify some fundamental law/guiding principle in classical genetics, the strategy we will use is to ask what all the different special laws of **CG** have in common.

It is worth noting that the key metatheoretical question is not "from what fundamental laws or general principles or equations are all specific special laws of **CG** deduced?", but "what do all special laws of **CG** have in common?"

Answering this question is not only a feasible task; it will also shed light on the relationship between laws of **CG**, and moreover, as we shall see later, on the relationship between models of **CG**, and **CG** as a theory, in the sense of a theory-net, and on the unifying power of **CG** in particular and of theories in general.

One might respond to this question by denying that there is one particular feature (or set of features) that all special laws of **CG** share and argue that the case of genetical laws is analogous to Wittgenstein's games (1953, § 66 and ff.): what ties different special laws together and what makes

them belong to **CG** is some kind of family resemblance between them rather than the existence of a fixed set of shared features, providing necessary and sufficient conditions for membership to them.

However, this answer begs another question because we still want to know in what sense the different special laws of **CG** are similar to each other.

It seems unlikely that the desired similarities can be read off from the mere appearance of them, and this is all that the Wittgensteinians can appeal to. Moreover, what matters is not that they are similar to each other in appearance but rather that they share certain structural features: the special laws of **CG** possess the same structure (of the same logical type), meaning that they all are specifications/specializations of one and the same fundamental law/guiding principle of **CG**, respectively. And thus, as we shall see later, they form a theory, or, better, a theory-net, the theory-net to which they all belong.

In specific **CG** applications only specific laws appear, and that is all what we have in standard text-books. However, we would like to suggest that they are specific versions of a general, fundamental law or guiding principle for the application in point. Nevertheless, in contrast to other empirical theories like those that belong to physics such as classical particle mechanics or thermodynamics,[16] the fundamental law/guiding principle of **CG** is not "observed" in the standard literature, but it is only "implicit" there. The Fundamental Law/Guiding Principle of Classical Genetics, implicitly presupposed in specific **CG** applications, reads in an intuitive way as follows:

CGGP: The statistical communality of characteristics/phenotypes between parents and progeny (given by characteristics/phenotypes distributions in the progeny) is due to (i) the presence in parents of factors/genes, (ii) the factors distribution from parents to progeny, and (iii) a determining relation between specific factors and specific characteristics, so that (iv) factors distributions "match"/"fit" (in specific manner to be specified) characteristics distributions.

All interconnected concepts of **CG** can be graphically depicted as follows (see Figure 2, where besides the components already present in Figure 1 symbolic representations appear at the new theoretical level on the top). Specifically, there is a symbolic representation of *factors* or genes—the genotype—, of (probability) *distributions* (α_j's) of those factors or genes in the progeny (*COMB*), and of the function of the way in which (pairs of) *factors* or genes *relate to characteristics* (*DETERMINER*)):

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[16]For an analysis of these theories from a structuralist point of view, see among others Balzer, Moulines and Sneed (1987).
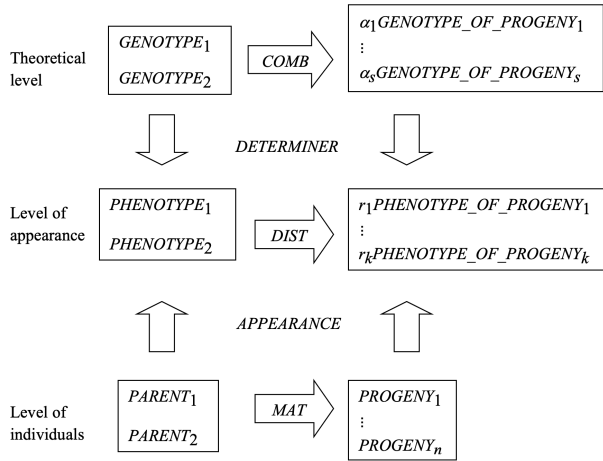
Theoretical level

$GENOTYPE_1$
$GENOTYPE_2$

COMB

$\alpha_1 GENOTYPE\_OF\_PROGENY_1$
⋮
$\alpha_s GENOTYPE\_OF\_PROGENY_s$

DETERMINER

Level of appearance

$PHENOTYPE_1$
$PHENOTYPE_2$

DIST

$r_1 PHENOTYPE\_OF\_PROGENY_1$
⋮
$r_k PHENOTYPE\_OF\_PROGENY_k$

APPEARANCE

Level of individuals

$PARENT_1$
$PARENT_2$

MAT

$PROGENY_1$
⋮
$PROGENY_n$

Figure 2

As mentioned before, fundamental laws/guiding principles are programmatic/heuristic in the sense that they tell us *the kind of things* we should look for when we want to apply the theory to a specific phenomenon. In the case of **CG** fundamental law/guiding principle, its heuristic character can be read as follows:

CGGP: When confronted with specific statistical distribution of specific parental characteristics (phenotype) in offspring, look for factors (genes) (genotype) responsible for the characteristics that combine in a specific manner in parents and "match"/"fit" the characteristics distribution in offspring.

As we already mentioned, in every specific case geneticists have to look for specific factors/genes (genotype) and discover the specific manner of their combination in reproduction (genotype-distribution) that accounts for the characteristics distribution (phenotype-distribution) in off-spring.

This means that **CG** fundamental law/guiding principle guides the process of specialization, since, as we saw before, in order to obtain special laws that account for the distributions of the parental characteristics in the progeny, (i) the number of pairs of factors or genes involved (either one or more), (ii) how the parental factors or genes are distributed in the progeny (with combinations of factors or genes with the same probability or not), and (iii) the way in which factors or genes are related to the characteristics (with complete or incomplete dominance, codominance or epistasis) have to be specified, and, in addition, (iv) the match/fit of the genotype-distribution with the phenotype-distribution is assumed.

3. The Concept of Model from the Point of View of Metatheoretical Structuralism

3.1. Introduction

The term "model", and its obsolete form "modell", in English, comes from the Middle French word "modelle" and the Old Italian word "modello", which arose during the Renaissance, in the 16th century, and is derived from the Latin term "modulus", which is a diminutive of "modus", meaning "manner" or "way", but also "measure" or "measurement". This term has since become customary in architecture and art, as well as its correspondingly derived terms "modelle" and "modèle" in French, "Modell" in German, and "modelo" in Spanish, through which the variety of meanings spread rapidly to the present abundance, in which it is used in all kinds of everyday situations (Müller 1983). In these situations, it is used both to refer to the thing "painted" or modeled and to the "painting" or model of some original.

In science it only began to be used towards the end of the 19th century, through the allusion to "mechanical models" or, with different terminology, "mechanical analogies", proposed and discussed, among others, by Maxwell (1855; 1861), Thomson (1842; 1884), Boltzmann (1902) and Duhem (1906). Similarly, in the context of German physics, the term "Bild", in singular, or "Bilder", in plural was usual (Helmholtz (1894), Hertz (1894) and Boltzmann (1905), who discussed the "models" and developed a "Bild conception" of physics in particular and of science in general).

Its use, however, was not limited to the field of physics, but extended to other domains of science, being of central importance in many scientific contexts. Thus, in biology, for instance, it is standard practice to speak about the Lotka-Volterra model of predator-prey interaction or the double helix model of DNA or models organisms or models "*in vivo*" or "*in vitro*". But neither in colloquial contexts nor in the diverse scientific contexts is the term "model" used in a non-unitary way, but rather it is an ambiguous, multivocal or polysemic expression that expresses more than one concept. As Nelson Goodman puts it: "Few terms are used in popular and scientific discourse more promiscuously than 'model' " (Goodman 1976, p. 171). At the same time, as we pointed out, it must be taken into account that different terms, such as the mentioned "analogy" or "Bild", have been used to refer to models. The term model applies to a bewildering set of objects from mathematical structures, graphical representations, computer simulations, to specific organisms or objects. Each of these objects seems so different that the idea has been firmly put forward that there is something that can be considered a model. And the means by which scientific models are expressed goes from sketches and diagrams to ordinary text, graphics and mathematical equations—just to name some of them.

In the face of such diversity, it is legitimate to raise the question of whether under the different uses of the term "model", not only in the empirical sciences, but also in the formal sciences, lies the same notion and/or there are systematic links between them. Suppes (1960) has argued for an affirmative answer to the question of the unity of notion, while Black (1962), Achinstein (1968) and McMullin (1968), among others, have supported a negative one. Falguera (1992; 1994) has proposed a sort of defense of Suppes' position, within the framework of structuralist metatheory, but doing so by assuming the *representational* perspective of Etchemendy (1988; 1990) in relation to models of formal semantics, rather than the standard *interpretational* one of Tarski (1936). He

has also discussed the relationships between some of the different types of models, such as the so-called "*scale* models", "*mathematical* models", "*analogical* models" and "*theoretical* models" (Falguera 1993; 1994).

Being models—in some of their meanings—for many scientists and philosophers of science of central importance in a multiplicity of scientific contexts, a diversity of functions is also attributed to them, such as: enabling the application and testing of theories, helping to construct theories, promoting the understanding of theories and abstract formalisms, contributing to the expansion and transformation of theories, mediating between theories and the world, serving as a pragmatic substitute for theories, enabling the description and preparation of data, being a component of explanations, helping to establish causal relationships between events, enabling the understanding of a concrete object or system, being useful in the classroom as pedagogical aids, helping to construct and evaluate experiments, and representing phenomena.

On the other hand, different authors have proposed different typologies and classifications (neither necessarily exhaustive nor, much less, exclusive) in order to analyze models and to understand their nature and function in science.

In fact, also the questions that have been discussed around the models have been of varied nature—e.g. ontological (what kind of entities are models?), semantic (what is the representational function that models perform?), epistemic (how do we learn with models?) and of general philosophy of science (how do models relate to theories?) (Frigg and Hartmann 2005; 2006; 2012). These questions, while varied in nature, are closely linked.

But although the literature in philosophy of science has concentrated mainly on the so-called "theoretical models" (Black 1962), not everyone agreed with the exact role that models played in the empirical sciences nor with their relevance for them. Neither does everyone agree on their relation with the laws and empirical theories and the eventual need to take them into consideration as components of the latter.

With respect to the philosophical discussion of such models, four temporally consecutive phases can be distinguished throughout the twentieth century (Hartmann 2010) and even so far in this century, since we can be considered to be still in the fourth of the phases. We may agree with Jim Bogen, when he states in the back cover of the book *Scientific Models in the Philosophy of Science* (Bailer-Jones 2009) that "The standard philosophical literature on the role of models in scientific reasoning is voluminous, disorganized, and confusing".[17] And we may also agree that one of the axes already mentioned that would enable the organization of at least part of such literature, and with which the book ends, is what is identified as one of the "contemporary philosophical issues: how theories and models relate each other" (Bailer-Jones 2009, p. 208).[18] Taking this into account, we can characterize the different phases referred to above as follows.

The *first phase* begins at the early 20th century with the analyses of the French physicist and philosopher of science P. Duhem (1906), who contrasts the role and meaning of mechanical models—conceived as graphic, illustrative, visible, tangible or palpable, and as characteristic of what he calls "the English spirit" and the "English school"—with the fundamental theories—which

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[17]To get an overview and delve deeper into various aspects of the philosophical debate on models and modeling, see also Morgan (2012), Weisberg (2013), Gelfert (2016) and Frigg (2023).

[18]For a different account of the relation between models and theories, though in a similar vein to the one presented here—in the sense of stressing the continuing importance of theories and the "partial" autonomy of models respect to theories—, see Morrison (2007; 2016).

he conceives as abstract and characteristic of what he calls "abstract", "imaginative spirits", and of the "French" and "German schools". Although he considers a physics that relies primarily on the use of models to be of lesser value and provisional, he nevertheless achieves a characterization of scientific models that set a course and allows him to assign an objective to the construction of models and a guiding function to models in the research process. However, in his view, physics ultimately aims at general, abstractly formulated principles and theories (Duhem 1906, Chapter 4). In contrast to this, Duhem's British antagonist, N. Campbell (1920), stresses precisely the necessity of analogies as essential parts of theories, even though he does not explicitly use the term "model".

In the *second phase*, corresponding to logical empiricism, models are conceived primarily as marginal phenomena of science. Thus, e.g., R. Carnap writes: "It is important to realize that the discovery of a model has no more than an aesthetic or didactic or, at best, heuristic value, but is not at all essential for a successful application of the physical theory" (Carnap 1939, p. 68). However, later authors, such as R. Braithwaite (1953) and E. Nagel (1961), strive to incorporate models, and to recognize their importance, within the framework of the *classical* (or received) view of scientific theories, even if a purely syntactic-formal treatment of the model concept is shown to be problematic (Psillos 1995).

In the 1960s and 1970s, the *third phase*, coinciding in time with the development of the *historical* (or historicist) conceptions of science (to which we will return later), a number of authors participated in this problematic (Achinstein 1968; Apostel 1961; Black 1962; Bunge 1973; Byerly 1969; Harré 1970; Hesse 1966; Hutten 1954; McMullin 1968; Suppes 1960; 1962). There originate, on the one hand, works that try to reconcile the most strongly formalist and model-theoretic proposals with the diversity of scientific practice (Apostel 1961; Bunge 1973) and, on the other hand, alternative proposals to the views of the logical empiricists are developed, which emphasize the role of models in scientific practice (Achinstein 1968; Hesse 1966; Harré 1970). In connection with this, it is also investigated what role analogies and metaphors play in the construction of models (Black 1962; Hesse 1966) or of other components, linked to these, put forward by historicist philosophers of science, like Kuhn's exemplars ([1962] 1970; 1970; 1974a; 1974b; 1979).

In the *fourth phase*, beginning around 1980, the importance of models in scientific practice (including conceptualization and theorizing) is emphasized. *Model* views of science and the so-called *model-based* science are developed—addressing, among others, the issues of the relationship between models and experience and between models and general theories independently of a general metatheory of science—as well as *semantic* (or model-theoretic) views of science—which address such issues within the framework of a general conception of scientific theories (and to which we will return later). But whether within model views, model-based science or semantic views, there is an attempt to understand not only what models are, but also how they work and even how they are constructed from detailed case studies belonging to different sciences. In addition, the consequences that model-building practice has for other philosophical questions are highlighted, such as realism—linked to the discussion of idealization, approximation and representation in science—,[19] reductionism—even in authors for whom there are no systematic

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[19]See Nowak (1979), van Fraassen (1980; 1987; 2008), Laudan (1981), Sneed (1983), Cartwright (1983; 1989), Laymon (1985), McMullin (1985), Mundy (1986), Stegmüller (1986), Balzer, Moulines and Sneed

relationships between models and theories—,[20] besides to the already mentioned laws of nature and laws of science,[21] and scientific explanation.[22]

In biology the term model is used in different ways, calling "models" different entities, whether equations (e.g. the Lotka-Volterra equations), idealized representations of empirical systems (e.g. as stated by the Hardy-Weinberg law), exemplars (e.g. "Mendelian" or classical account of the inheritance of colour seed peas), organisms (e.g. *Drosophila melanogaster*) or physical objects (e.g. the double helix model of DNA), among other things.

But whether in one sense or the other, there are authors who from the 1950s onwards emphasize the importance of models—especially mathematical or theoretical models—in the biological sciences and try to analyze them outside the framework of the semantic conceptions previously mentioned (Beckner 1959; Beament 1960; Holling 1964; Simon 1971; Schaffner 1980; 1986; Barigozzi 1980; Wimsatt 1987; Fox Keller 2000; Morrison 2002; 2004; Godfrey-Smith 2006; Winther 2006; Weisberg 2007; 2013; Knuuttila and Loettgers 2016). Levins (1966) occupies a central place in the discussion about models and model building in biology. Since then, his proposal about the existence of a three-way trade-off between generality, realism, and precision, such that a model builder cannot simultaneously maximize all of these *desiderata*, has been much discussed (e.g. Orzack and Sober 1993; Levins 1993; Orzack 2005; Odenbaugh 2003; Weisberg 2006; Matthewson and Weisberg 2009). And the role of Kuhnian-type exemplars has also been investigated in the field of biology (Schaffner 1980; 1986; Darden 1991; Lorenzano 2007a; 2008a; 2012; Skopek 2011). On the other hand, other types of models, different from the theoretical ones, such as material models of several kinds, have also been the object of analysis (see, e.g, Griesemer 1990 and Laublichler and Müller 2007, and for organisms in particular, the pioneer works of Burian 1993 and Kohler 1994, and, for an account and updated overview of this growing subject, Ankeny and Leonelli 2020, online/2021, print).

3.2. The Structuralist Concept(s) of Model

As would be expected, being a member of the semantic family, the structuralist view shares with all the other family members the fundamental thesis on the centrality of models for metatheoretical analysis. But, on the other hand, it sometimes differs from other members of the semantic family in its characterization of the precise nature of these entities that are called models, although occasionally it coincides.

(1987), Giere (1988; 1994; 2006), Suppe (1989), Worrall (1989), Swoyer (1991), Brzeziński and Nowak (1992), Mäki (1994), Ibarra and Mormann (1997; 2000), Díez and Falguera (1998), Ladyman (1998), Psillos (1999), Niiniluoto (2000), Chakravartty (2001; 2007), Suppes (2002), Casanueva and Benítez (2003), French and Ladyman (2003), Teller (2004), Morrison (2005), Rueger (2005), Frigg and Votsis (2011) and Frigg (2023).

[20]See Hacking (1983), Balzer, Pearce and Schmidt (1984), Moulines (1984), Balzer, Moulines and Sneed (1987), Bickle (1995; 1998; 2002; 2003), Falkenburg and Muschik (1998), Cartwright (1999), Hartmann (1999), Batterman (2002), Bokulich (2003) and Hartmann (2008).

[21]See, among others, Cartwright (1983; 1999), Giere (1999), van Fraassen (1989), Forge (1986; 1999), Lorenzano (2006b; 2007b; 2007c; 2008b; 2014; 2014-2015; 2019), Chakravartty (2007).

[22]See van Fraassen (1980), Cartwright (1983), Bartelborth (1996a; 1996b; 1999; 2002), Forge (1999; 2002), Elgin and Sober (2002), Díez (2002; 2014), Woodward (2003), Moulines (2005), Lorenzano (2005), Bokulich (2003; 2009; 2011; 2017), Kennedy (2012), Reiss (2012), Díez and Lorenzano (2013; 2015), Ginnobili and Carman (2016) and Lorenzano and Díez (2022).

A model, in its minimal informal meaning, is a system or structure which intends to represent, in a more or less approximative way, a "portion of reality", made up by entities of various kinds, which *makes* true a series of claims, in the sense that in this system "what the claims say occurs", or more precisely, the claims are true in this system.

Models are conceived as systems or structures, i.e. mathematical structures. In the standard version of metatheoretical structuralism, these structures are set-theoretical or relational structures of a certain kind,[23] constituted by a series of basic domains (sets of objects) and of relations (or functions) over them, i.e. as entities of the form: $\langle D_1,..., D_k, R_1,..., R_n \rangle$, where $R_j \subseteq D_{i1} \times ... \times D_{ik}$ (the D_i's represent the so-called "base sets", i.e. the "objects" the theory refers to, its ontology, whereas the R_j's are relationships or functions set-theoretically constructed out of the base sets).[24]

In order to provide a more detailed analysis of empirical science, Metatheoretical Structuralism distinguishes three kinds of (classes, sets, populations, collections or families of) models. Besides what are usually called (the class, set, population, collection or family of) "*theoretical* models"

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[23]In trying to be as precise as possible, Metatheoretical Structuralism prefers the use of (elementary) set theory—whenever possible—as the most important formal tool for metatheoretical analysis. However, this formal tool is not essential for the main tenets and procedures of the structuralist representation of science (other formal tools, such as logic, model theory, category theory, and topology, as well as informal ways of analysis, are also used). Besides, there are also uses of a slight variant of Bourbaki notion of "structure species" in order to provide a formal basis of characterizing classes of models by means of set-theoretic predicates (Balzer, Moulines and Sneed 1987, Chapter I), and of a version of the von Neumann-Bernays-Gödel-type of language including urelements for providing a purely set-theoretical formulation of the fundamental parts of the structuralist view of theories (Hinst 1996). There is even a "categorial" version of Metatheoretical Structuralism that casts the structuralist approach in the framework of category theory, rather than within the usual framework of set theory (see Balzer, Moulines and Sneed 1986; Sneed 1984; Mormann 1996). The choice of one formal tool or another or of a more informal way of analysis is a pragmatic one, depending on the context which includes the aim or aims of the analysis and the target audience. Nonetheless, in standard expositions of Metatheoretical Structuralism, as well as in what is presented here, models are conceived of as *set-theoretical structures* (or models in the sense of *formal semantics*), and their *class* is identified by defining (or introducing) a *set-theoretical predicate*, just as in the *set-theoretical* approach of Patrick Suppes (1957; 1967; 1970; 2002; McKinsey, Sugar and Suppes 1953).

[24]In a complete presentation, we should include, besides the collection of so-called *principal base sets* $D_1,...,$ D_j or $D_1,..., D_k$, also a second kind of base sets, namely, the so-called *auxiliary base sets* $A_1,..., A_m$. The difference between them is the difference between base sets that are empirically interpreted (the principal ones) and base sets that have a purely mathematical interpretation, like the set $\mathbb{N}$ of natural numbers, or the set $\mathbb{R}$ of real numbers (the auxiliary ones). Here, auxiliary (purely mathematical) base sets are treated as "antecedently available" and interpreted, and only the proper empirical part of the models is stated in an explicit way.

On the other hand, in philosophy of logic, mathematics, and empirical science, there have intense discussion about what would be a better way of understanding the nature of sets occurring in the relational structures, and of the models themselves. In relation to sets, according to the standard interpretation of 'sets-as-one' (Russell 1903) or 'the highbrow view of sets' (Black 1971) or 'sets-as-things' (Stenius 1974) sets themselves, though not necessarily their elements which may refer to concrete entities, should be considered as abstract entities, while according to the interpretation of 'sets-as-many' (Russell 1903) or 'the lowbrow view of sets as collections (aggregates, groups, multitudes)' (Black 1971) or 'sets-of' (Stenius 1974) sets do not have to be interpreted that way. For theoretical models, even though they are usually considered as abstract entities, there is no agreement about what kind of abstract entities they are, i.e. what is the best way of conceive them—either as interpretations (Tarski 1935; 1936) or as representations (Etchemendy 1988; 1990), or as fictional (Godfrey-Smith 2006; Frigg 2010) or as abstract physical entities (Psillos 2011). However, due to space limitations, we will not delve into these issues.

or simply (the class, set, population, collection or family of) "*models*"—also called (the class of) "*actual* models" in structuralist terminology—, the so-called (class of) "*potential* models" and (class of) "*partial* potential models" are taken into account.

To characterize these structuralist notions, two distinctions are to be considered: the distinction between two kinds of 'conditions of definition' (or 'axioms', as they are also called) of a set-theoretical predicate, and the distinction between the **T**-theoretical/**T**-non-theoretical terms (or concepts) of a theory **T**. According to the first distinction, the two kinds of conditions of definition of a set-theoretical predicate are: 1. those that constitute the 'frame conditions' of the theory and that "do not say anything about the world (or are not expected to do so) but just settle the formal properties" (Moulines 2002, p. 5) of the theory's concepts; and 2. those that constitute the 'substantial laws' of the theory and that "do say something about the world by means of the concepts previously determined" (Moulines 2002, p. 5).

According to the second distinction, which replaces the traditional, positivistic theoretical/observational distinction, it is possible to establish, in (almost) any analysed theory, two kinds of terms or concepts, in the sense delineated in an intuitive formulation by Hempel (1966; 1969; 1970) and Lewis (1970): the terms that are specific or distinctive to the theory in question and that are introduced by the theory **T**—the so-called '**T**-theoretical terms or concepts'—and those terms that are already available and constitute its relative "empirical basis" for testing—the so-called '**T**-non-theoretical terms or concepts', which are usually theoretical for other presupposed theories **T**', **T**'', etc.

In accordance with the standard structuralist criterion of **T**-theoreticity (originated in Sneed 1971 and further elaborated in detail in the Structuralist program; see Balzer, Moulines and Sneed 1987, Chapter II), a term is **T**-theoretical (i.e. theoretical relative to a theory **T**) if *every* method of determination (of the extension of the concept expressed by the term) depend on **T**, i.e. if they are **T**-dependent, if they presuppose or make use some law of **T**; otherwise, a term is **T**-non-theoretical, i.e. if at least *some* method of determination (of the extension of the concept expressed by the term) *doesn't* presupposes or make use of some law of **T**, if it is **T**-independent.

Now we are in position to characterize these structuralist basic notions:

1) The class of *potential models* of the theory $\mathbf{M_p}$ is the total class of structures that satisfy the "frame conditions" (or "*improper* axioms") that just settle the formal properties of the theory's concepts, but not necessarily the 'substantial laws' of the theory as well.

2) The class of (actual) *models* of the theory **M** is the total class of structures that satisfy the "frame conditions", and, in addition, the "substantial laws" of the theory. If $A_1,..., A_s$ are certain formulas ("*proper* axioms" or simply "axioms") that represent the laws of the theory, *models* of the theory are structures of the form $\langle D_1,..., D_k, R_1,..., R_n \rangle$ that satisfy the axioms $A_1,..., A_s$. (And that is the reason why, as it was mentioned before, models may be considered the model-theoretic counterpart of theory's laws.)

3) The class of *partial potential models* $\mathbf{M_{pp}}$ are obtained by "cutting off" the **T**-theoretical concepts from the potential models $\mathbf{M_p}(\mathbf{M_{pp}}:= \mathbf{r}(\mathbf{M_p}))$, where **r**, the "restriction" function, is a many-one function such that $\mathbf{M_p} \rightarrow \mathbf{M_{pp}}$). If potential models are structures of type x ($x = \langle D_1,..., D_k, R_1,..., R_n \rangle$), *partial potential models* $\mathbf{M_{pp}}$ are structures of type y ($y = \langle D'_1,...,$

$D'_j, R'_1,..., R'_m\rangle$), where each structure of type y is a *partial substructure* of a structure x.[25] (And let's call a specific structure of type y, with specific instances of the **T**-non-theoretical concepts, a "*data model*" of **T**).[26]

Now, let us identify all these kinds of models in Classical Genetics, starting with data models, and then moving on to potential models first and then to theoretical models that result in a successful application—exemplified with a detailed analysis of the first case of Section 2.1—to end with the classes of potential models, models and partial potential models.

3.3. Models in Classical Genetics (CG)

If the examples of hereditary transmission given above (in Section 2.1) are to be represented in the structuralist format, they should be conceived as *data models* of **CG**. That is, they should be conceived as structures of type y of partial potential models: $y = \langle I, P, APP, MAT, DIST \rangle$, with specific values adopted by the concepts that occur therein each given example:

– the set of *individuals* ($I = \{i_1,...,i_n\}$) that can be proper individuals as well as populations, i.e. individuals that make up "families", that is, populations connected by bonds of marriage, parentage or common descendent; we write $i \in J$ to express that any individual i is in the model;[27]

– the set of *phenotypes* ($P = \{\pi_1,...,\pi_k\}$), where each phenotype $\pi \in P$ has the form $\langle c_1,..., c_k \rangle$, where $c_1 \in C_1,..., c_k \in C_k$ are characteristics of different types and $(C_i)_{i \leq k}$ symbolizes the whole set of *types of characteristics*. As can be easily seen, the actual primitive concept is this set of *types of characteristics*, while the set of phenotypes is a defined one);

– the function of *appearance* that assigns *their characteristics (phenotype)* to individuals—being parental ($APP(i_1) = \pi_1, APP(i_2) = \pi_2$) or progeny ($APP(i_n) = \pi_j$);

– the function of *mating* that assigns their progeny to pairs of individuals ($MAT(i_1, i_2) = \langle i_1,..., i_n \rangle$, where the number n varies according to the parental individuals); and

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[25]A structure y is a *substructure* of another structure x (in symbols: $y \sqsubseteq x$) when the domains of y are subsets of the domains of x and, therefore, the relationships (or functions) of y are restrictions of the relationships (or functions) of x. A structure y is a *partial substructure* of x (also symbolized by $y \sqsubseteq x$) when, besides being a substructure of x, there is at least one domain or relationship (or function) in x that has no counterpart in y. The important thing is that the *partial* substructure y contains less components—domains or relationships (or functions)—than the structure x. Thus, structures x and y are of different logical types. If y is a *substructure* (either partial or not) of x, it is also said, inversely, that x is an *extension* of y.

[26]Phenomena are represented by means of (structures of the type of) partial potential models, while data are usually represented by finite substructures of (structures of the type of) partial potential models. Due to space limitations, we are unable to go into this topic in more detail. For further discussions on this issue, see Suppes (1962), Bogen and Woodward (1988), Woodward (1989; 1998), Ibarra and Mormann (1989), Mayo (1996), van Fraassen (2008), Massimi (2011), Lorenzano (2012).

[27]Classical Genetics is concerned with populations, inasmuch as reliable frequencies of traits in the progeny are not obtained through consideration of a single mate. Generally, the progeny of individual parents will not even exhaust all possible phenotypes. The real carriers of phenotype are individuals, but a population can be defined in terms of individuals in an explicit way as a subset of the power set of individuals in which their members are linked by kinship relations. A population so conceived is called a "family". In that sense, individual is the real primitive concept, and population and family are defined ones.

- the function of *distribution* of *characteristics (phenotype)* that assigns relative frequencies of occurrence of *characteristics (phenotype) in the progeny* to *characteristics (phenotype)* of pairs of parental individuals ($DIST(\pi_1, \pi_2) = \langle r_1\pi_1,..., r_k\pi_k \rangle$, where $\langle \pi_1,..., \pi_k \rangle$ denotes the sequence of the phenotypes of the progeny, $\langle r_1,..., r_k \rangle$ denotes a distribution written in an explicit manner as a k-tuple of numbers, $r_i \geq 0$, $\sum_{1 \leq i \leq k} = 1$, where each real positive number r_i is the weight or probability of the phenotype number i that occurs in the corresponding sequence of the phenotypes of the progeny).

Structures of type y are used to represent in a model-theoretic, structuralist way those empirical (biological) phenomena that **CG** intends to account for—i.e. empirical (biological) systems, where individuals that make up families possess certain *characteristics* that *mate* and produce *progeny*, which also possess certain *characteristics* whose distributions are expressed in numerical ratios, proportions or relative frequencies—, which also constitute what allows us to test Classical Genetics, that is, its "(empirical) basis of testing".

Let's consider the case of *Peas Seed Color* in more detail, though. The system under consideration is constituted by a set I of individuals (plants or animals in general, peas in this case, parental or offspring). They form the objects involved in this intended application: $I = \{i_1,..., i_n\}$. The considered characteristics only refer to the color of the seed albumen. Thus, P (in general) or π (in this particular case) = $\{c_1, c_2\}$, where c_1 symbolizes the yellow color and c_2 the green color. These are the only characteristics possessed by the individuals of interest in this case: $APP(i_i) = c_1$, $APP(i_i) = c_2$. If we represent the crossing among the parental individuals that give rise to the first filial generation (or F_1) by MAT, we have: $MAT(i_1, i_2) = \langle i_1,..., i_n \rangle$; the same applies to the second filial generation (or F_2): $MAT(i_1, i_2) = \langle i_1,..., i_n \rangle$. If we represent the distribution of parental characteristics in the offspring by $DIST$, we have: $DIST(c_1, c_2) = 1c_1$ in F_1, and: $DIST(c_1, c_1) = \langle 0,7505c_1, 0,2495c_2 \rangle$ in F_2. We can now represent the *model of data* for the case of a monohybrid cross—for the color of the seed albumen—in peas by $\langle I, (C_i)_{i \leq k} \rangle, APP, MAT, DIST \rangle$, that expresses what we want to explain, i.e., the relative frequency $0,7505c_1, 0,2495c_2$ of yellow and green seed coats, respectively, or (approximately) ¾ of offspring have yellow seed coat and ¼ have green seed coat or a proportion 3:1, as follows: $\langle \{i_1,..., i_n\}, \{c_1, c_2\}, \{\langle i_1, c_1 \rangle, \langle i_2, c_1 \rangle\}, \{\langle i_1, i_2, i_1,..., i_n \rangle\}, \{\langle c_1, c_1, 0,7505c_1, 0,2495c_2 \rangle\} \rangle$, in F_2. Let's then call such a structure "the *data model* for **CG** of *Peas Seed Color*", or $DM_{\mathbf{CG}}(PSC)$ for short.

And if we now want to represent in structuralist format the different ways in which the given examples of cases of characteristics distributions are accounted for by introducing appropriate types and numbers of factors or genes(the genotype), the way in which they are distributed or combined in the progeny (as expected or theoretical probabilities), and the specific relationship in which they are with the characteristics of the individuals, we should consider these first as "potential models" of **CG** that, by adding the specific match/fit of genotype-distributions with phenotype-distributions, result then in "(actual) models" of **CG** and lastly in successful applications. That is, they should be conceived as structures of type x of potential models: $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}), COMB \rangle$ that are extensions of the structures of type y, which contain, besides specific instances of the concepts occurring in these structures, also specific instances of the following concepts:

- Firstly, the set of *genotypes* ($G = \{\gamma_1,..., \gamma_s\}$), where each genotype $\gamma \in G$ has the form of a finite list of *pairs of allelic factors* $\langle \langle f_{i1}, f_{i2} \rangle,..., \langle f_{s1}, f_{s2} \rangle \rangle$, where for every $I \leq s$ and any two

factors f_{i1} and f_{i2} that belong to the same set F_i means that f_1 and f_2 are alleles or allelic factors. $(F_i)_{i \leq s}$ symbolizes the whole set of *types of factors*. As can be easily seen, the actual primitive concept is this set of *types of factors*, while the set of genotypes is a defined one).

- Also, the function of *determining* that maps genotypes into phenotypes such that pairs of allelic factors yields a unique π_i (or c_i), but taking into account that in general some phenotypes may be produced by different genotypes (for each genotype, we have equations of the form $DET_i(\gamma_i) = \pi_i$ (or c_i); and the whole function DET is defined as the tuple of all DET_i in the following way: $DET(\gamma) = \langle DET_1(\gamma),..., DET_k(\gamma) \rangle$, where the last expression under consideration yields some phenotype $\langle \pi_1,..., \pi_k \rangle$ (or $\langle c_1,..., c_k \rangle$).

- Lastly, the function of combination or *distribution* of factors (genotype) that assigns probability distributions of factors (genotypes)in the progeny to factors (genotypes)of parental individuals ($COMB(\langle \gamma_1, \gamma_2 \rangle) = \langle \alpha_1\gamma_1,..., \alpha_s\gamma_s \rangle$, where $\langle \gamma_1,..., \gamma_s \rangle$ denotes the sequence of the genotypes of the progeny, $\langle \alpha_1,..., \alpha_s \rangle$ denotes a probability distribution written in an explicit manner as a s-tuple of numbers, $\alpha_i \geq 0$, $\sum_{1 \leq i \leq s} = 1$, where each real positive number α_i is the weight or probability of the genotype number i that occurs in the corresponding sequence of the genotypes of the progeny).

Returning to the case of *Peas Seed Color*, the following is hypothesized:

(i) First, there is only one pair of factors or genes involved (that we can symbolize by $\langle f_1, f_2 \rangle$).

(ii) Next, the factors or genes combination is equally probable, the parental factors or genes are distributed in the offspring with the same probability; such a function can be in general represented in the following manner: $COMB(\langle a_1, b_1 \rangle, \langle c_1, d_1 \rangle) = (\frac{1}{4} a_1 c_1 + \frac{1}{4} a_1 d_1 + \frac{1}{4} b_1 c_1 + \frac{1}{4} b_1 d_1)$, where a_1, b_1, c_1, d_1 symbolize any factor or gene, and, in a specific manner, for the crossing carried out (F_2): $COMB(\langle f_1, f_2 \rangle, \langle f_1, f_2 \rangle) = (\frac{1}{4} f_1 f_1 + \frac{1}{4} f_1 f_2 + \frac{1}{4} f_2 f_1 + \frac{1}{4} f_2 f_2)$.

(iii) Finally, one of the factors (f_1), which is "responsible" for the yellow color of the seed albumen, is *dominant* over the other (f_2), *recessive*, which is "responsible" for the green color of the seed albumen; the determining function can be represented as follows:

$$a) DET_i(f_2, f_2) = c_2$$

$$b) DET_i \left. \begin{matrix} DET_i(f_1, f_1) \\ (f_2, f_1) \\ DET_i(f_1, f_2) \end{matrix} \right\} = c_1$$

If we put all the information of (i), (ii) and (iii) a), b), i.e. the specifications for the **CG**-theoretical concepts, together with the specifications for the **CG**-non-theoretical concepts contained in the structure of type y from above ($\langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST \rangle$), we obtain the following structure of type $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}, COMB \rangle$: $\langle \{i_1,..., i_n\}, \{c_1, c_2\}, \{\{f_1, f_2\}, \langle f_1, f_2 \rangle\}, \{\langle i_1, c_1 \rangle, \langle i_2, c_1 \rangle\}, \{\langle i_1, i_2, i_1,..., i_n \rangle\}, \{\langle c_1, c_1, 0.75c_1, 0.25c_2 \rangle\}, \{\langle f_1, f_1, c_1 \rangle, \langle f_2, f_1, c_1 \rangle, \langle f_1, f_2, c_1 \rangle, \langle f_2, f_2, c_2 \rangle\}, (\frac{1}{4} f_1 f_1 + \frac{1}{4} f_1 f_2 + \frac{1}{4} f_2 f_1 + \frac{1}{4} f_2 f_2) \rangle$. Let's then call it "the *potential model* for *Peas Seed Color* of **CG**", or $PM_{CG}(PSC)$ for short.

When the different specific potential models of **CG** postulate, in addition, a "match" or "fit" between the distribution of characteristics (phenotype-distribution) and the distribution of factors/genes (genotype-distribution) in the progeny, we obtain the "(actual) models" of **CG**—what is the model-theoretic way of saying the "special laws" of **CG**. And if the "match" or "fit" can be established, they result in successful applications (as they actually do in the treatment of the examples presented in Section 2.1).

For the case of *Peas Seed Color*, if it is required that the structure of type x satisfies, *in addition*, the specific form adopted for the treatment of this case of condition (iv) of the Fundamental Law/Guiding Principle of Classical Genetics (**CGGP**), i.e. the match (or fit) of factors distribution $((\frac{1}{4} f_1 f_1 + \frac{1}{4} f_1 f_2 + \frac{1}{4} f_2 f_1 + \frac{1}{4} f_2 f_2))$ with characteristics distribution $(\langle c_1, c_1, 0.75 c_1, 0.25 c_2 \rangle)$, we obtain what we call "the (*actual*)*model* for *Peas Seed Color* of **CG**", or $M_{\mathbf{CG}}(PSC)$ for short.

In a similar way, as in the case of the different laws, one can ask now what all these data models, all these models and all these successful applications have in common. And the answer to these questions is straightforward, using the notions of class of partial models, of potential models, and of models introduced in the previous section.

What all these data models have in common is that they are specifications of partial potential models of **CG** (i.e. **CG**-non-theoretical concepts); what all these theoretical models have in common is that they are specifications first of potential models of **CG** (i.e. **CG**-non-theoretical concepts as well as **CG**-theoretical concepts), and then, by postulating the match or fit between distributions of genotypes and phenotypes, of (actual) models of **CG**; what all these successful applications have in common is that they are specifications of (actual) models of **CG** in which the match/fit between distributions of genotypes and phenotypes is established.

We will next identify such classes of types of models in **CG**, starting with the class of potential models, continuing with the class of models, and concluding with the class of partial potential models.

The class of *potential models of classical genetics* ($\mathbf{M_p}(\mathbf{CG})$) is constituted by the total class of structures that satisfy the "frame conditions" (the so-called "*improper* axioms") that just settle the formal properties of **CG**'s concepts, but not necessarily the 'substantial laws' of **CG** as well, and for which it makes sense to wonder if they are actual models of **CG**.

We can put together all **CG**'s basic concepts in one structure x, which thus contains the "conceptual framework" of **CG**: $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}, COMB \rangle$, and then formulate the "frame conditions" for **CG**'s basic concepts as follows (by means of the introduction or definition of the set-theoretical predicate "being a potential model of *classical genetics*"):

Definition 1

$\mathbf{M_p}(\mathbf{CG})$: $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}, COMB \rangle$ is a *potential model of classical genetics* ($x \in \mathbf{M_p}(\mathbf{CG})$) if and only if

(1) I is a non-empty, finite set ("individuals": variable i)

(2) $(C_i)_{i \leq k}$ is a non-empty, finite set ("types of characteristics": variable c_i)

(3) $(F_i)_{i \leq s}$ is a non-empty, finite set ("types of (allelic) factors": variable f_i)

(4) $APP: I \rightarrow Po((C_i)_{i \leq k})$ ("appearance": $APP(i) = $)

(5) $MAT: I \times I \rightarrow Po(I)$ is a partial function ("mator": $MAT(i, i') = \langle i_1, ..., i_n \rangle$)

(6) $DIST: Po((C_i)_{i\leq k}) \times Po((C_i)_{i\leq k}) \to D(Po((C_i)_{i\leq k}))$ is a partial function ("distributor": $DIST(\pi, \pi') = \langle r_1\pi_1,..., r_k\pi_k\rangle$)

(7) $(DET_i)_{i\leq k}: Po((F_i)_{i\leq k}) \to Po((C_i)_{i\leq k})$ is surjective ("determiner": $DET_i(\gamma_i) = \pi_i$)

(8) $COMB: Po((F_i)_{i\leq k}) \times Po((F_i)_{i\leq k}) \to D(Po((F_i)_{i\leq k}))$ ("combinator": $COMB(\gamma, \gamma') = \langle \alpha_1\gamma_1,..., \alpha_s\gamma_s\rangle$)

The objects that occur in the predicate *may be interpreted as follows*:

(1) I represents the set of *individuals* (parents and progeny), which constitute populations linked by kinship relations called "families" (see note 3).

(2) $(C_i)_{i\leq k}$ represents the set of *types of characteristics* that constitute the different *phenotypes* $(\pi_1,...,\pi_k)$; each phenotype $\pi \in P$ has the form $\langle c_1,..., c_k\rangle$, where $c_1 \in C_1,..., c_k \in C_k$.

(3) $(F_i)_{i\leq s}$ represents the set of *types of (allelic) factors* that constitute the different *genotypes* $(\gamma_1,...,\gamma_s)$; for every $I \leq s$ and any two factors f_1 and f_2, that f_1 and f_2 belong to the same set F_i means f_1 and f_2 are alleles; each genotype $\gamma \in G$ has the form of a finite list of *pairs of allelic factors* $\langle\langle f_{i1}, f_{i2}\rangle,..., \langle f_{s1}, f_{s2}\rangle\rangle$, where $i \leq s$ and f_{s1} and f_{s2} are members of F_i.
The functions that occur in the predicate *are interpreted as follows*:

(4) APP represents the *appearance* of the individuals—being parental or progeny—, given by *a function that assigns their characteristics to individuals*, symbolized by equations of the form $APP(i_1, i_2) = \langle i_1,..., i_n\rangle$, where the number n varies according to the parental individuals.

$$APP(i_1) = \pi_1, \langle c_1,..., c_k\rangle$$
$$APP(i_2) = \pi_2, \langle c_1,..., c_k\rangle$$
$$APP(i_n) = \pi_j, \langle c_1,..., c_k\rangle \text{ (where } i \leq n, j \leq k).$$

(5) MAT represents the *mating* of the individuals, given by a partial function which represents the transition from the parents to their progeny, symbolized by equations of the form $MAT(i_1, i_2) = \langle i_1,..., i_n\rangle$, where the number n varies according to the parental individuals.

(6) $DIST$ represents the *transition from parental phenotypes to distribution of phenotypes in the progeny* given by relative frequencies (actually, $DIST$ is not a real primitive concept, then it can be defined through MAT and APP; beginning with two parental individuals i_1, i_2, we see the value of $MAT(i_1, i_2)$, i.e., the set of progeny $\{i_1,..., i_n\}$; we determine the value of $APP(i_n)$ for $i \leq n$, i.e, phenotypes that occur in the progeny; we count the total number n of progeny as well as the number m_i of progeny that exhibits a given phenotype and calculate the relative frequency $r_i = m_i/n$ of that phenotype; the list of all relative frequencies obtained for the different progenies is thus the desired distribution of phenotypes in the progeny of i_1 and i_2, that is, the value of $DIST(i_1, i_2)$;[28] the notation $DIST(\pi_1, \pi_2) = \langle r_1\pi_1,..., r_k\pi_k\rangle$, where all r_i are real positive numbers, such that $\sum_{1\leq i \leq k} r_i = 1$, represents a distribution of phenotypes in explicit form.

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[28]For a phenotype $\pi \in P$ and a set of individuals $X \subseteq I$, the *relative frequency of π in X, $RF(\pi/X)$* is defined in the following manner:
If X is a set of proper individuals, then
$RF(\pi/X) =$ (the number of $i \in X$, such that $APP(i) = \pi$) over

(7) $(DET_i)_{i \leq k}$ represents the *determination* of phenotypes by genotypes given by a function that assigns phenotypes to genotypes (for each genotype, we have equations of the form $DET_i(\gamma_i)$ = π_j, and, for all genotypes γ, one equation of the form $DET(\langle \gamma_1,...,\gamma_s \rangle) = \langle DET_1(\gamma),...,DET_k(\gamma) \rangle$, where the last expression under consideration yields some phenotype $\langle \pi_1,...,\pi_k \rangle$ (where $I \leq s, j \leq k$)).

(8) *COMB* represents the *transition from parental genotypes to genotypes in the progeny*, assigning to parental genotypes a combination (distributions) of genotypes in the progeny (we have equations of the form $COMB(\langle \alpha_1\gamma_{11},..., \alpha_s\gamma_{1s} \rangle, \langle \alpha_1\gamma_{21},..., \alpha_s\gamma_{2s} \rangle) = \langle \alpha_1\gamma_{11},..., \alpha_j\gamma_{ij},..., \alpha_s\gamma_{ns} \rangle$ (where all α_i are positive real numbers, such that $\sum_{1 \leq i \leq s} \alpha_i = 1$)).

We can now define the class of (actual) *models of classical genetics* (**M(CG)**), which is the total class of structures of type x: $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}, COMB \rangle$ that satisfy the "frame conditions", and, in addition, the "substantial laws" of **CG** (the so-called "*proper axioms*") as follows:

Definition 2

M(CG): If $x = \langle I, (C_i)_{i \leq k}, (F_i)_{i \leq k}, APP, MAT, DIST, (DET_i)_{i \leq k}, COMB \rangle$, then x is a *model of classical genetics* ($x \in$ **M(CG)**) if and only if

(1) For any I and P: for any $i, i' \in I$ such that MAT is defined for $\langle i, i' \rangle$ and for any $\pi \in P$, there exist s genotypes $G, \gamma_1,..., \gamma_s$, a function $COMB$, and k functions $DET, DET_1,..., DET_k$, such that:

$$COMB(\gamma, \gamma') = DIST(DET_i(\gamma_i), DET_i(\gamma_i'))$$

The condition of definition, or axiom, (1) formulates in a more formal way the fundamental law/guiding principle of classical genetics (**CGGP**) of Section 2.1, which establishes that a "match" or "fit" takes place between the observed distributions of characteristics (phenotype-distributions) and the distributions of factors/genes (genotype-distributions). Every structure of type x that satisfies it is an (actual) model of **CG**.

In order to achieve a thorough understanding of this law, let us consider two parental individuals with phenotypes π, π', genotypes γ, γ' and the corresponding distributions over phenotypes and genotypes in their progeny: $d_{ph} = \langle r_1\pi_1,..., r_k\pi_k \rangle$, $d_{ge} = \langle \alpha_1\gamma_1,..., \alpha_s\gamma_s \rangle$. Consider first the simple case in which DET is one-one. In this case each phenotype π_j comes from exactly one of the genotypes $\gamma_1,..., \gamma_s$. So $k = s$ and we may assume that each π_j is produced by γ_j. The natural notion of fit between the two distributions $\langle r_1\pi_1,..., r_k\pi_k \rangle, \langle \alpha_1\gamma_1,..., \alpha_s\gamma_s \rangle$ is this. We say that d_{ph} and d_{ge} ideally fit with each other if and only if, for all $j \leq s$: $r_j = \alpha_s$.

However, given that, as already mentioned, some phenotypes may be produced by different genotypes, the situation, in general, is not as simple as that. In these cases, we have to compare the probabilities of all these genotypes with the relative frequency of the phenotype they all produce. Formally, let us introduce, for given parental genotypes γ, γ', and given index $j \leq k$ the set $M(\gamma,$

(the number of elements of X).

For a phenotype $\pi \in P$ and a set of populations $X \subseteq \text{Po}(I)$, the *relative frequency of π in X*, $FR(\pi/X)$ is defined in the following manner:

$FR(\pi/X) = $ (the number of elements in the sets $i \in X$, for which $APP(i) = \pi$) over

(the number of elements of elements of X).

γ', j) of all probabilities α_i occurring in d_{ge} such that the corresponding genotype γ_i produces phenotype r_j (compare Figure 3). Moreover, let us write $m_j = \sum \alpha_i$, $i \in M(\gamma, \gamma', j)$, for the sum of all those probabilities α_i whose corresponding genotype γ_i give rise to the same π_j with relative frequency r_j.

$$M(\gamma, \gamma', j) = \{2, l, q\}$$

$$COMB(\gamma, \gamma') = d_{ge} = \alpha_1\gamma_1,\ \alpha_2\gamma_2,...,\ \alpha_l\gamma_l,...,\ \alpha_q\gamma_q,...,\ \alpha_s\gamma_s$$

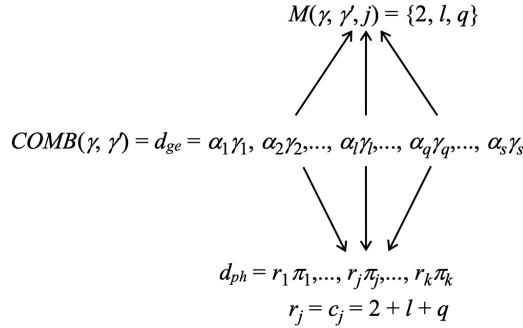$$d_{ph} = r_1\pi_1,...,\ r_j\pi_j,...,\ r_k\pi_k$$
$$r_j = c_j = 2 + l + q$$

Figure 3

In order to fit d_{ph} and d_{ge} we then have to compare each relative frequency π_j with the sum m_j. We say that, in the general case, d_{ph} and d_{ge} ideally fit if and only if, for all $j \le k$: $r_j = m_j$.

Two distributions of genotypes $\langle\alpha_1\gamma_1,..., \alpha_s\gamma_s\rangle$ and of phenotypes $\langle r_1\pi_1,..., r_k\pi_k\rangle$ *ideally fit together* if and only if:

i) $k \le s$,[29]

ii) each phenotype π_j arises from one genotype γ_i or more different genotypes γ_i by means of DET_i,

iii) the probability coefficients of the items related in ii) ideally fit with each other.

Taking into account these clarifications about the notion of fit, we can reformulate the general equation $COMB(\gamma, \gamma') = DIST(DET(\gamma), DET(\gamma'))$ of the fundamental law/guiding principle of classical genetics (**CGGP**) in the following ways, either as

$$\sum_{\alpha \in M(\gamma, \gamma', j)} \alpha = r_j$$

or, considering also the definition of *DIST* through *MAT* and *APP*, as

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[29]Through this characterization of genotypes (in which it is not required that $s = k$, that is, admitting that various pairs of allelic factors may determine one and the same character) it is possible to include in the model both the *interaction of factors* and the so-called *hypothesis of multiple factors*. Note also that the present formalism captures the phenomenon of *multiple allelism*. This phenomenon is given by the fact that different individuals in a species may have different genotype components from the same factor set F_i. We allow for arbitrary, finite factor sets F_i. So, within a species there may be hundred or even thousands of different allelic pairs that are formed from one factor set.

$$\sum_{\alpha \in M(\gamma, \gamma', j)} \alpha = \frac{\| PROGENY\_j \|}{\| PROGENY\_1 \| + \ldots + \| PROGENY\_k \|}.$$

The class of *partial potential models* of **CG** characterizes the point of departure for Classical Genetics. It is constituted by that which is intended to systematize, explain and predict. In order to characterize this class, it is necessary to distinguish between theoretical and non-theoretical concepts within **CG**, i.e. between specific concepts of *classical genetics* (or **CG**-theoretical) and non-specific concepts of *classical genetics* (or **CG**-non-theoretical).

A detailed discussion of the application of the **T**-theoreticity criterion to every **CG**'s term (or concept) is beyond the aim of this paper. But we did it elsewhere (Lorenzano 2002), and reached the result that the set of *factors* or *genes* $(F_i)_{i \le k}$ that may possess different alternative forms, even though they are paired in the individual, called "alleles", the *function* $(DET_i)_{i \le k}$ *that assigns characteristics to pairs of factors* or *genes*, and the *function COMB that represents the transition from parental factors* or *genes to factors* or *genes in the progeny* are **CG**-theoretical while the rest of the concepts are **CG**-non-theoretical.

We are now able to characterize the class of partial potential models of **CG** through the set-theoretical predicate "being a partial potential model of *classical genetics*" as follows:

Definition 3

$\mathbf{M_{pp}(CG)}$: $y = \langle I, (C_i)_{i \le k}, APP, MAT, DIST \rangle$ *is a partial potential model of classical genetics* ($y \in \mathbf{M_{pp}(CG)}$) if and only if exists an x such that

(1) $x = \langle I, (C_i)_{i \le k}, (F_i)_{i \le k}, APP, MAT, DIST, (DET_i)_{i \le k}, COMB \rangle$ is a $\mathbf{M_p(CG)}$

(2) $y = \langle I, (C_i)_{i \le k}, APP, MAT, DIST \rangle$.

4. The Concept of Theory from the Point of View of Metatheoretical Structuralism

4.1. Introduction

The term "theory", in English, appears in late 16th century denoting a mental scheme of something to be done, comes from the Latin word "theoria", which, in turn, comes from the ancient Greek word "θεωρία" (theōría), meaning "to see", "to look", "to observe" and then "knowledge". According to some, the Greek word derives from "Θεωρεῖν" (theorein) which comes from "θεωρός", "one who sees a spectacle", such as festivals of the gods or religious processions, oracles or theatrical scenes; while already in antiquity, some derived the etymology from the first part of the compound "θεωρός" from the word for god ("θεός") (König 1998). Later, the term "theory" is not only used for the observation or contemplation of certain sacred or festive events, but also for the "purely intellectual" consideration of abstract ideas, facts or states of affairs that are not accessible to sensory perception. Hence, since then, it has been customary to contrast "theory" with "experience"—from the Latin "experientĭa"—or with "empirical"—from the Greek "ἐμπειρικός" ("empeirikós"). In turn, in colloquial language, the term "theory" is used either as a vague supposition or pure speculation (without much hold) or as something that has not yet been "tested"

(or contrasted); in the latter case, "theory" is used in the sense of "hypothesis" and the expression "hypothetically" is replaced by the phrase "in theory". Sometimes, the term "theory" is used in a (rather pejorative) sense as "mere theory" as opposed to "practice"—from the Greek "πρᾶξις" ("praxis")—or to "*actually functional* practice" (Thiel 1996).[30]

A primary use of the term "theory" is to refer to that (usually very complex) entity that organizes the phenomena of a subject area and describes the basic properties and relationships of the objects belonging to that area, postulating general laws (or principles) for them and making it possible to give explanations and to provide predictions about the occurrence of certain phenomena within that area.

In modern science, the term "theory" refers to scientific theories, and this is the meaning that interests us here.

However, with the constitution and development of different scientific disciplines and sub-disciplines, the existence of theories with different levels of abstraction and pursuing different objectives can be recognized. Moreover, unlike what happens in philosophy of science, in what we would call the "meta-scientific-language-in-use-of-scientists" (and even "of-those-who-write-textbooks" or "of-those-who-dedicate-themselves-to-the-public-communication-of-science") a terminologically precise distinction is rarely made between hypotheses, laws (of different types and levels) and theories.

In the same way as in the case of the concept of law above there has long been discussed the problem of establishing the nature, structure and function of a scientific theory. After decades of discussion, different conceptions coexist, often at odds, of what a theory is, whether there is a theory structure that is shared by all scientific disciplines, and how a theory works.

As was already said, three main philosophical conceptions about scientific theories have been developed during the 20th and the 21st century so far: the "classical (or received)" view, the "historical (or historicist)" view and the "semantic (or model-theoretic)" view.

In all three of these metatheoretical conceptions, we can distinguish three general aspects in the explication of the concept of theory: one referring to the (more) "theoretical" (or "formal")

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[30]This sense is discussed, and rejected, by Kant in his "On the saying: This may be correct in theory, but it does not apply to practice" of 1793, in the following terms in the field that interests us:

> [...] it was not the fault of theory if it was of little use in practice, but rather of there having been *not enough* theory, which the man in question should have learned from experience and which is true theory even if he is not in a position to state it himself and, as a teacher [...]. (Kant 1793, pp. 202-203)

> Thus no one can pretend to be practically proficient in a science and yet scorn theory without declaring that he is an ignoramus in his field, inasmuch as he believes that by groping about in experiments and experiences, without putting together certain principles (which really constitute what is called theory) and without having thought out some whole relevant to his business (which, if one proceeds methodically in it, is called a system). (Kant 1793, p. 203)

> Now if an empirical engineer tried to disparage general mechanics, or an artilleryman the mathematical doctrine of ballistics, by saying that whereas the theory of it is nicely thought out it is not valid in practice since, when it comes to application, experience yields quite different results than theory, one would merely laugh at him (for, if the theory of friction were added to the first and the theory of the resistance of air to the second, hence if only still more theory were added, these would accord very well with experience). (Kant 1793, p. 204)

part, another to the (more) "empirical" ("applicative" or "testing") part, and the last referring to the relationship between both parts, between the "theoretical" and the "empirical", between the "theory" and the "experience". And one of the main differences between the classical, the historical and the semantic views lies in the central basic ideas they have about the general way of conceiving each of these aspects. On the other hand, it should be said that, despite the use of the singular definite article to refer to the three previous philosophical conceptions, each of them groups a number of versions, variants or approaches, which while sharing certain basic general ideas on these three aspects, differ from each other in the particular way they understand or elaborate these basic ideas.

Regarding the *classical view* it could be said that, although all classical philosophers of science considered theories to be sets of statements organized deductively or axiomatically, not all agreed on the specific way in which this should be understood and clarified (e.g. Popper 1935; Carnap 1956; Hempel 1958). For instance, in the most well-known and developed of Carnap's versions, the "theoretical" or "formal" part is constituted by the formal axiomatic system or "calculus" (symbolized by "T")—which only contain descriptive theoretical terms—; the (more) "empirical" or "testing" part is given by pure observational statements—which only contain descriptive observational terms—; and the relationship between "theory" and "experience" is established through linguistic means, the so-called correspondence rules (symbolized by "C")—which connect theoretical terms with observational terms.

The main representative of the classical conception of scientific theories in biology during the first half of the twentieth century was Joseph Henry Woodger, who aimed to apply and develop the philosophy of the science of logical positivism for the specific field of biology (Woodger 1937; 1939; 1952; 1959; 1965; for his axiomatization of classical genetics, see esp. Woodger 1959). A continuation of Woodger's work in the field of genetics can be found in H. Kyburg (1968), A. Lindenmayer and N. Simon (1980) and M. Rizzotti and A. Zanardo (1986a; 1986b).

In relation now to the general adequacy of the classical view for the analysis of biological theories, we could say that, though scientists like Conrad Hal Waddington (1968-1972) promoted and employed such a view, opinion about the applicability of the classical view to biology was divided among the philosophers. Thus, Morton Beckner (1959) did not accept the classical view, but assumed that its application to biology was, at best, limited and, with its treatment of biological theories as families of models, anticipated to some extent the analysis of such theories later carried out within the framework of the semantic conception. Thomas Goudge (1961; 1967), for his part, was quite explicit in pointing out that, regardless of the applicability that this conception might have in physics, it would not capture important features of biological theories and explanations. On the other hand, Mary Williams (1970), Michael Ruse (1973) and Alexander Rosenberg (1985) were philosophers who during the seventies and eighties sustained the applicability of the classical view of theories to biology. In particular, it has been argued (Thompson 1989) that the two most explicit and detailed attempts to provide an analysis of evolutionary theory within the classical conception are Michael Ruse's (1973) outline of the axiomatic structure of population genetics—which, he claims, constitutes the core of evolutionary theory—and Mary Williams' (1970) axiomatization of the theory of natural selection—which, we would say, contains a few peculiarities regarding the standard presentations and applications of the classical conception of theories. Here we should also mention the analysis of evolutionary theory carried out by Mario Bunge and Gregorio Klimovsky in terms of the classical conception, understanding theories as hypothetico-deductive

systems consisting of a set of starting hypotheses, fundamentals, or principles, and all their logical consequences (which include derived hypotheses and observational consequences) (Klimovsky 1994), or as sets of propositions closed under deduction (Bunge and Mahner 1997). Other philosophers, on the other hand, argued in favor of the relevance of this conception for biological theorization, although with varying degrees of caveats and subtleties (e.g., Hull 1974).

As of the 1950s, the classical view on the scientific theories has been very much criticized. There were mainly two kinds of criticisms: a) criticisms of certain aspects of the classical view (e.g. the distinction between theoretical and observational terms), and b) a global criticism which attacks mainly the bases of this conception, proposing an alternative view on science.

Notwithstanding, it is possible to claim that the classical view of theories has been the most adopted in scientific disciplines in the last part of the twentieth century and is still presupposed nowadays in many of them.

The second kind of criticisms to the classical view of theories came mainly from historicist philosophers of science, such as Toulmin, Hanson, Feyerabend, Lakatos, Kuhn, Laudan and Shapere. And as a result of this, a new conception about the nature and the synchronic structure of scientific theories (without this being implied in a strict sense and without it being systematically developed) underlies the majority of diachronic studies and analyses, which is supposed to be closer to scientific practice, as history presents it to us. This new notion is developed in different ways by the so-called *new philosophers* of science. Central to the *historicist view* was the idea that scientific theories—which the historicist philosophers refer to with different terms—are not sentences or sentence sequences, and in a proper sense they cannot be described as true or false (although true or false empirical claims are certainly made with them), but they are highly complex and ductile entities, susceptible of evolving in time without losing their identity.

It may be said that, in the best known and most widespread version of the historical conception, namely, that provided by Kuhn (1970), the (more) "theoretical" or "formal" part of the theories (paradigms/disciplinary matrices) is constituted by the (verbal and) symbolic generalizations, while the (more) "empirical" or "applicative" part is given by the exemplars (or "examples of their function in use"). On the other hand, the link between both parts is established by what Kuhn calls "special (or appropriate) versions" and "particular (or detailed) symbolic forms (or versions or expressions)", which acquire the symbolic generalizations in order to be applied to particular problems (situations, phenomena). And although Kuhn does not elaborate in detail what the relationship between symbolic generalizations and their particular forms is, as stated before, he makes it very clear that this is not one of logical deduction.

As for the application of Kuhnian views to the field of biology, we already find mentions of Darwin in Kuhn ([1962] 1970), in his argument against the understanding of the history of science in terms of teleological development towards truth (Kuhn [1962] 1970, p. 172) and as an example of one of the "great revolutions" (Kuhn [1962] 1970, p. 180), and to the *Origin of Species* (Darwin 1959) as one of "the classic books in which these accepted examples first appeared" (Kuhn [1962] 1970, p. 20). However, we do not see in it a systematic use and application of the notions of paradigm/disciplinary matrix in the analysis of particular cases pertaining to the field of biology,[31] but a discussion of whether or not a scientific revolution took place—although it is clear that the very notion of scientific revolution presupposes the notion of paradigm/disciplinary matrix, since

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[31]Something similar can be said about Laudan's consideration of "Darwinism" as a research tradition.

"here we regard as scientific revolutions those episodes of non-cumulative development in which *an old paradigm is replaced in whole or in part by a new one* incompatible with it" (Kuhn [1962] 1970, p. 92; emphasis ours). And the same can be said about other historians and philosophers of science in general or of biology in particular,[32] who, even when they mention other cases such as Gregor Mendel and genetics (Cohen 1985), concentrate mainly on the discussion of, in the words of Mayr (1972), "the nature of the Darwinian revolution". (On the controversies surrounding Darwinian ideas and revolution, see, among other works, Ghiselin (1969; 2005), Hull (1973; 1985), Greene (1971), Mayr (1972; 1977; 1988; 1990), Ruse (1979; 1982; 2009), Oldroyd (1980), Wuketits (1987), Bowler (1988), Burian (1989), Levine (1992), Stefoff (1996), Proctor (1998), Junker and Hossfeld (2001), Herbert (2005), Hodge (2005), Smocovitis (2005). Even before Kuhn's proposals, there are already authors who refer to the "Darwinian revolution" (Judd 1912; Himmelfarb 1959). Sometimes (Maienschein, Rainger and Benson 1981; 1991), even accepting the revolutionary character of Darwin's work, it is questioned whether it implied a "radical", "total" or "absolute" rupture, since both discontinuities and continuities can be pointed out—which is perfectly compatible with Kuhn's thinking—, as well as the difficulty to say, in terms of "paradigms"/"disciplinary matrices", what this change consisted of—which shows, in our opinion, that no satisfactory notion of "theory"/"paradigm"/"disciplinary matrix", with clear criteria of identity, is presupposed).

On the other hand, we should note that the notion of paradigm that eventually historians and philosophers of biology have found most fruitful in carrying out their analyses, to which we have already referred, is that of "exemplar", either arguing that the theories of the biological (and/or biomedical) sciences possess a particular structure distinct from that of physical theories (Schaffner 1980; 1986; Darden 1991) or considering that this is not the case, if they are analyzed within the framework of some version of the semantic conception of theories (Schaffner 1993; Lorenzano 2007a; 2008a; 2012).

Moreover, even if it has not been a particularly privileged field, biology has not been completely alien to the use of Lakatos' concept of research program in its analyses. Thus, for example, it is used by Michod (1981) to analyze the history of population genetics, by Meijer (1983), Van Balen (1986; 1987), Martins (2002) and Lorenzano (2006a; 2013a) to analyze the history of the so-called "classical", "formal" or "Mendelian" genetics, by Denegri (2008) to analyze parasitology, and by Piavani (2012) to analyze the shift from the modern synthesis to the extended evolutionary synthesis.

Shapere's concept of field has also been applied to biology. In particular, the concept of field, and its derivatives of intra-field theory and inter-field theories, have been used mainly by Darden to analyze some biological theories, their development over time, as well as their interrelationships. We would like to mention especially the analysis of the theory of the gene as an intrafield theory, that of the chromosomal theory as an interfield theory (Darden and Maull 1977), and that of the changes that occurred in "Mendelian Genetics" between 1900 and 1926 as changes in the field of heredity (Darden 1974; 1991).

The new notion of theory proposed by the historicist philosophers is, however, so extremely

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[32]A notable exception, although in the field of biochemistry and in a "structuralized" version—that is, passed through the sieve of the structuralist conception of theories, to which we will refer later—, is Lorenzano, C. (1994).

imprecise at times that it ends up blurring almost completely what seem to be correct intuitions. The main motivation positivists or logical empiricists had for developing a formal philosophy of science was precisely to avoid a vague and imprecise metascientific discourse. And much of the controversy that arose after the appearance of the new philosophers was generated by the imprecision and ambiguity of some of its main notions.

The majority of the philosophers of science who were sensitive to the historicist perspective concluded that the complexity and richness of the elements involved in science, escaped any attempt at formalization. It was considered that not only were the formalizations like those made within the classical view of theories totally inadequate to express these entities in all their complexity, but it did not seem reasonable to expect that any other procedure of formal analysis should grasp the minimum elements of this new characterization. This is the antiformalist moral that spread in many metascientific environments after the *historicist revolt*.

However, some of the more recent currents in philosophy of science show that vagueness and ambiguity are not necessary components of the philosophical reflection about science and that at least part of the new elements mentioned by the new philosophers are susceptible to formal reconstruction and reasonable formal analysis. Thus, during the 1970s trust in the viability of the formal or semiformal analyses of science is recovered, at least in some of its areas, particularly in that which refers to the nature of theories.

An example of this is Philip Kitcher's concept of *practice* (1983; 1984), which bears important analogies to Kuhn's *paradigm* and also to other metascientific units such as Shapere's *field* and Laudan's *research tradition*. According to Kitcher, a crucial part in scientists' practice are the patterns of reasoning, explanatory schemata, argumentative patterns or argumentative schemata, which he uses in his analyses of several biological theories, such as Darwin's natural selection and common descent theories (Kitcher 1989; 1993), theoretical or mathematical population genetics, i.e. Fisher's, Haldane's and Wright's genetic trajectories (Kitcher 1993), neo-Darwinian selectionism (Kitcher 1993), different theories from the classical period of genetics (Kitcher 1989; 1993) and molecular genetics (Kitcher 1993), besides in his account of the relationships between classical and molecular genetics (Kitcher 1984).

But most important is the new way of understanding the nature of theories that is now known as *semantic* or model-theoretic *view*, which resumes and continues to develop the work carried out in the first half of the twentieth century by Hermann Weyl (1927; 1928), John von Neumann (1932), and Garrett Birkhoff (Birkhoff and von Neumann 1936), and after the Second World War by Evert Willem Beth (1948a; 1948b; 1949; 1960) and Patrick Suppes (1957; 1962; 1969; 1970; 2002; McKinsey, Sugar and Suppes 1953). This new conception of scientific theories, which, with its different approaches, variants or versions, constitutes an authentic family, becomes established towards the end of the seventies and during the eighties as an alternative to the classical and historicist views.

Among the members of this family, we find the *set-theoretical* approach of Patrick Suppes, whose first version was developed/supplemented by his disciple Ernest W. Adams (1959), and by Suppes himself; the *structuralist* view of theories (also called *metatheoretical structuralism* or *Sneedian structuralism*) of Joseph D. Sneed and his first followers, Wolfgang Stegmüller and his disciples C. Ulises Moulines and Wolfgang Balzer (Sneed 1971; Stegmüller 1973; 1979; 1986; Balzer, Moulines and Sneed 1987; 2000; Balzer and Moulines 1996); the *partial structures* approach of Newton C. A. da Costa, Steven French, James Ladyman and Otávio Bueno (da Costa and

French 1990; 2003; Bueno 1997; French and Ladyman1999); the *state-space* approach of Bas van Fraassen (1970; 1972; 1974; 1976; 1980; 1987; 1989; 2008); the *phase-space* approach of Frederick Suppe (1967; 1972; 1989); the *model-based* proposal of Ronald N. Giere (1979; 1983; 1985; 1988; 1994); the approach proposed by Roberto Torretti (1990); and several "European" versions, such as that of Maria Luisa Dalla Chiara and Giuliano Toraldo di Francia (Dalla Chiara and Toraldo di Francia 1973) in Italy, Marian Przełecki (1969) and Ryszard Wójcicki (1974) in Poland, and Günther Ludwig (1970; 1978) and Erhard Scheibe (1997; 1999; 2001) in Germany.

All members of this family share the "formalistic spirit" of the received view though not the letter: the *classical virtue of conceptual clarity and precision* is a regulative principle for them; nevertheless, they consider that the best way of approaching this ideal is *to make use of all the logico-mathematical instruments which may contribute to* the attainment of this aim. But they adopting a pragmatic stance on this issue, e.g. the version of the semantic conception that will present later, Metatheoretical Structuralism, normally prefers the use of set theory, but other formal tools, such as first-order and higher-order logic, model theory, category theory, and topology, as well as informal ways of analysis, are also used.

On the other hand, some of them—particularly the structuralist view and the partial structure approach—are conscious of the numerous philosophically essential aspects of science which resist to be dealt with in a purely formal way, be it either because we do not have at our disposal the suitable tools for the task (at least not at the present time), or because we encounter elements which are *irreductively pragmatic and historically relative*, like the ones which have been mentioned in the historicist view.

The basic central idea, shared by the different "members", approaches, variants or versions of this family, is that concepts related to models are more useful for the philosophical analysis of scientific theories, of their nature and functioning, than those related to statements, i.e. that the nature, function and structure of theories are better understood when their characterization, analysis or metatheoretical reconstruction is centered on the models they determine, not on a particular set of axioms or linguistic resources by means of which they do so, even when the determination of the models is made by means of a series of principles or laws, which define a class of models (a class sometimes called "set", "collection", "population" or "family").

Within the multiplicity of kinds of scientific models, the semantic conception is centered on the so-called "theoretical models". As previously stated (Section 3.2), a (theoretical) *model*, in its minimal informal meaning, is a system or structure which intends to *represent*, in a more or less approximative way, a "portion of reality", made up by entities of various kinds, which *makes* true a series of claims, in the sense that in this system "what the claims say occurs", or more precisely, the claims are *true* in this system.

Since the notion of model is fundamentally a semantic notion (something is a model of a claim or sentence if the claim is *true* for it), and its most frequent analysis is made by model theory, this new approach which emphasizes the importance of models in the analysis of science is called a *semantic* or *model-theoretic conception*. In contrast, the received view of theories is called *syntactic* because it characterizes theories as sets of sentences or statements and it places general emphasis on the linguistic-syntactic aspects.

It is worth noting that the semantic option neither supposes nor intends to disregard state-ments (sentences or propositions) or, in general, certain resources or devices or even linguistic formulations. It does not mean that resources or devices of any kind, including linguistic ones, are

superfluous for the meta-theoretical characterization of theories. Of course, we need some resource, device or language in order to determine or define a class of models. Nobody intends to deny this. Insofar as the models are determined in an explicit and precise manner in the meta-theoretical analysis, they are usually determined by giving a series of axioms, principles or laws, i.e. through statements. But even when the determination of the models is usually made through a series of axioms, the identity of the theory does not depend on specific resources or specific linguistic formulations. The different resources, devices or linguistic formulations are essential in the (trivial) sense of being the necessary means for the determination of the models, but in a really important sense, they are not, since nothing in the identity of a theory depends on whether the resource, device or linguistic formulation is one or another. It is a misrepresentation to say that, according to the semantic conception, a theory *is* a class of models, in the sense of being *identified with* a class of models or being *identical to* a class of models.[33] The semantic conception claims, rather, that a theory can be characterized in the first place for defining/determining the class, set, population, collection or family of its models, i.e. that a theory is *identified through* its models, *not with* them: to present/identify a theory means mostly presenting/identifying the characteristic models as a family, because it is an essential component of a theory, but not the only one.[34]

Considering now the most general aspects in the explication of the concept of theory, in relation to the semantic conception, the following could be stated. The (more) "theoretical" (or "formal") part of a theory would be constituted (at least) by the class (set, collection, population, family) of models—in general not determined by using first-order logic, but by means of other formal tools, such as higher-order logic, type theory, set theory (either elementary or naïve set theory or axiomatic set theory like Zermelo-Fraenkel or von Neumann-Bernays-Gödel axiom systems), structure species or category theory, or even by using semi-formal or informal tools, and identified (just to mention the most well-known versions of "the" semantic view) by *defining* or introducing *a set-theoretical predicate*, for Suppes, da Costa *et al*. and also normally for the Sneedian structuralism; by *characterizing state* or *phase spaces* governed by certain laws, for van Fraassen and Suppe; or directly *by postulates*, *laws*, *and equations* that appear on scientific texts, for Giere—and given some understanding of models—in the sense of *formal semantics* or *model theory*, for Suppes, da Costa *et al*. and usually for Sneedian structuralism; or as *trajectories* or *points* in *state* or *phase spaces*, for van Fraassen and Suppe; or as model in any *informal* acceptable *sense* of the term, for Giere.

The (more) "empirical" ("applicative" or "testing") part would be constituted by the "phe-nomena" conceived in one of the following ways: as *models of data* for Suppes, or *intended interpretations* or *intended models* in the modification introduced by Adams in the Suppesian approach; as *intended applications* formally represented as "partial potential models" in Sneedian structuralism; as *partial structures* in the *partial structures* approach; as *empirical substructures*

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[33]Admittedly, some "sloppy" presentations or assertions by members of the semantic family can lead to this misunderstanding of the general characterization of that family. Several authors make an understandable criticism of this identification of a theory *with* the class of its models (see, e.g., Portides 2017). In any case, such a critique would not apply to Metatheoretical Structuralism, which does not carry out such an identification.

[34]Although due to space limitations we cannot deal in depth with the problem, see footnote 22 for indications on the possible compatibility, pointed out as problematic (Thompson-Jones 2006), between the two notions of model as a *truth-making structure* and as a *mathematical model* (and even other notions of model) and an account of scientific representation.

that only contain observable entities in van Fraassen's approach; as *physical systems* that function as *nonproblematic 'hard-data'* for the theory in Suppe's approach; or as *real systems* in Giere's approach.

And bearing in mind that, with the exception of Giere's case, the other versions conceive the "theoretical" and the "empirical" parts as systems or structures of a certain type, the relation between the two would be of a sort of morphism, generally weaker than isomorphism, such as homomorphism, or of isomorphism but between the systems or structures representing the "phenomena" and a part of the systems or structures representing the models (be it a partial structure or substructure or even a partial substructure of them), a relation which is usually called "embedding".

As for the qualification of "at least" concerning that the (more) "theoretical" (or "formal") part of a theory would be constituted by the class of models is due to the following. Sneedian structuralism offers a more detailed analysis of the fine structure of the theories than all other versions of the semanticist family, allowing the identification of a greater number of components of such part of them. Therefore, unlike the other versions of the semantic family, it is not enough to have the class of models in order to have the whole (more) "theoretical" (or "formal") part of a theory.

The semantic view has had an impact in diverse areas of biology, and some of its versions have been applied to them. For example, Suppe (1974) tries to shed light on some philosophical problems related to speciation and taxonomy through the use of his own version of the semantic conception. In addition, attempts have also been made to apply in a systematic way van Fraassen's state-space approach to the analysis of the structure of the theory of evolution, and thus eventually of population genetics (Beatty 1980; 1981; Lloyd 1984; 1986; Thompson 1983; 1986). This, in turn, has motivated the position taken by authors such as Sloep and van der Steen (1987a; 1987b) and Ereshefsky (1991) and the response and/or further developments of Beatty (1987), Lloyd (1987; 1988) and Thompson (1987; 1989; 2007). This variant of semantic conception has also been applied to the analysis of theories of sex and gender (Crasnow 2001) and of ecology (Castle 2001).

Ronald Giere himself, in his introductory book to the philosophy of science (Giere 1979), provides an informal analysis of classical genetics, in the form of a definition of a kind of system—a Mendelian breeding system—and of some of the theoretical hypotheses employing this theory.

We also find the works of Magalhães and Krause (2000, 2006), which make use of the axiomatization *à la* Suppes in an attempt to identify the class of models of the theory of evolution by natural selection and of population genetics.

However, it is the Metatheoretical Structuralism that has produced the greatest number of analyses of particular theories belonging to the biological sciences[35]—even though this fact has

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[35]Just to mention a few, in the field of evolutionary biology, we can see the analyses of the structure of the theory of evolution by natural selection made by Ginnobili (2010; 2012; 2016; 2018), Ginnobili and Blanco (2019), Díez and Lorenzano (2013; 2015), as well as of the theory of common descent made by Blanco (2012) and of population dynamics by Díaz and Lorenzano (2017) and Lorenzano and Díaz (2020); in the field of inheritance and genetic theories (classical, molecular and population genetics), the works of Balzer and Dawe (1986a; 1986b; 1990), Balzer and Lorenzano (2000), Casanueva (1997; 2002; 2003), Casanueva and Méndez (2005), Dawe (1982), Lorenzano (1995; 2000; 2002; 2014) and Méndez (2006); cellular and tissue theories have been the object of structuralist analysis by Asúa and Klimovsky (1987; 1990), as has the theory of excitable

gone largely unnoticed by the international audience, perhaps because most of their works have been published in Spanish or German and not in the contemporary *lingua franca*, English.[36]

Finally, to conclude this overview, we can say that in classical genetics in particular, the analyses have made their historical journey in parallel with the philosophy of science. We have already mentioned authors who have analyzed it within the framework of the received view (such as Woodger, Kyburg, Lindenmayer and Simon, and Rizzotti and Zanardo); others who have done this using some version of the historicist conception (like Van Balen, Martins and Lorenzano) or other "post-classical view" (like Darden and Kitcher); and also those who have done it applying the semantic conception of theories (such as Giere, Dawe, Balzer, Lorenzano, Casanueva and Méndez).[37]

4.2. The Structuralist Concept(s) of Theory

The point of departure of the structuralist explication of the concept of a theory is the recognition that the term "scientific theory" is ambiguous, or better: polysemic, in its pre-systematic use. Sometimes it means just one law (like when one speaks indistinctly of the *law* of gravitation or of the *theory* of gravitation). This sense is not explicated by the structuralist concept of a theory, but by the structuralist concept of a law. Sometimes, the use of the term "scientific theory" corresponds to what is explicated by the structuralist notion of *theory-element*. In this sense, a theory-element is the smallest portion of science that seems to possess all the characteristics usually associated to theories. However, even this smallest sense of theory *cannot be identified with a clas*s (or set or population or collection or family) *of models, although it can be identified mainly through them. Despite the fact that* such a class is the most basic component for the identity of a theory, it is not the only one. A *theory-element*—i.e. the simplest kind of set-theoretical structure that can be identified with, or can be used as a rational reconstruction of, or can be regarded as a formal explication of, a theory (in an informal, intuitive sense)—can be identified, as a first approximation, with an ordered pair consisting of the "(formal) *core*", symbolized by $\mathbf{K}$, and the theory's "domain of intended applications", symbolized by $\mathbf{I}$: $\mathbf{T} = \langle \mathbf{K}, \mathbf{I} \rangle$.

The *core* $\mathbf{K}$ constitutes the formal identity of any empirical theory with a certain degree of complexity, which is composed by the ordered classes of *potential models*, *actual models*, *partial potential models*, *constraints* and *links,* i.e. $\mathbf{K} = \langle \mathbf{M_p}, \mathbf{M}, \mathbf{M_{pp}}, \mathbf{C}, \mathbf{L} \rangle$.

In the previous section we already introduced the classes of *potential models*, (*actual) models*, and *partial potential models.*

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membranes by Müller and Pilatus (1982), of neuroendocrinology by Bernabé (2019), and of cladistics by Roffé (2020). For further references, see Diederich, Ibarra and Mormann (1989; 1994), Abreu, Lorenzano and Moulines (2013) and Lorenzano (2023).

[36]For a concise presentation and evaluation of the reconstructions of theories in biology carried out using both the classical view and the different semantic variants, see, in German, Krohs (2004; 2005). For a discussion of theories in biology from other perspectives, but which we believe are to some extent compatible with Metatheoretical Structuralism and the analysis carried out here, see *Biological Theory* (2013), Vol. 7 (June 2013, issue 4).

[37]For an exposition and evaluation of the reconstructions of Woodger (1959), Lindenmayer and Simon (1980) and Balzer and Dawe (1990), see Lorenzano (1995). For a critical commentary on the reconstruction of Rizzotti & Zanardo (1986), see Balzer and Lorenzano (2000). And for one of Kitcher's analysis (1989; 1993), see Blanco, Ginnobili and Lorenzano (2019).

While the innertheoretical relationships between the different models of a theory are represented by the so-called *constraints* **C**, the intertheoretical relationships are represented by the so-called (*intertheoretical*) *links* **L**. They characterize the theory's "essential" relationships to other theories by connecting the **T**-non-theoretical terms with the theories they come from.

Any empirical theory is related to "reality" or "outside world", i.e. to some specific phenomena or empirical systems submitted to some specific conditions, to which it is intended to be applied and for which it has been devised. These empirical systems also belong to a theory's identity because otherwise we would not know what the theory is about, for the class of models contains "all" models, intended as well as non-intended. They constitute what is called the theory's *domain of intended applications* **I**. The domain of *intended applications* of a theory, even when it is a kind of entity strongly depending on pragmatic and historical factors that, by their very nature, are not formalizable, is conceptually determined through concepts already available, i.e. through **T**-non-theoretical concepts; thus, each intended application may be conceived as an empirical (i.e. **T**-non-theoretical) system represented by means of a structure of the type of the partial potential models M_{pp}. All we can formally say about **I** is, thus, that it is a subset of the class of partial potential models M_{pp}.

Theories are not statements, but are *used* to make statements or claims, which then have to be tested. The (empirical) statements (or claims) made by means of scientific theories are, intuitively speaking, of the following kind: that a given domain of intended applications may actually be (exactly or approximately) *subsumed* (or *embedded*) under the theory's principles (laws, constraints, and links), or to put it more precisely, under appropriate structures that satisfy theory's principles (laws, constraints, and links).[38] Normally, in any "really existing" theory, the "exact version" of the so-called *central empirical claim* of the theory—that the whole domain of intended applications may actually be (exactly) subsumed (or embedded) under (appropriate structures that satisfy) the theory's principles—will be strictly false. What usually happens is that either there is a subclass of intended applications for which the empirical claim is true, or that the central empirical claim is, strictly speaking, false but *approximately true*.[39]

Some "real-life" examples of scientific theories can actually be reconstructed as *one* theory-

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[38]It is worth noting that the subsumption or embedding relation, unlike that of isomorphism or similarity, is asymmetric.

[39]For a structuralist approach to features of approximation and a precise formal explication of the notion of the approximative empirical claim, see Balzer, Moulines and Sneed (1987, Chapter VII). On the other hand, Metatheoretical Structuralism acknowledges that, besides approximation, abstraction (also called "Aristotelian idealization") and idealization (also called "Galilean idealization") play an important role at different levels of scientific practice, and, of course, in model(s) construction, i.e. in the construction of potential models, (actual) models and partial potential models. At this point, and considering, among others, the historical and pragmatic aspects of intended applications, it should be clear that, if the problem of the scientific representation of phenomena by means of models were to be posed, for Metatheoretical Structuralism, this kind of representation could not be exclusively explicated by mapping of structures (as thought as constitutive of the semantic view by some authors; see, again, Portides (2017)). Moreover, if we accept in our analysis the standard notion of mathematical structure as set-theoretical structure, together with Etchemendy's representational perspective on model theory, on the one hand, and also accept the structuralist distinction between types of models, in addition to the pragmatic and intentional aspects of representation, we can refer, not only to the "representation of phenomena by means of models", but also to the "representation of theoretical systems by (theoretical) models" and to the "representation of 'empirical' systems by partial potential models". But, insofar as the subsumption or embedding relation is a relation between structures (between theoretical models and those

element, but usually single theories in the intuitive sense have to be conceived as aggregates of several (sometimes a great number of) theory-elements. These aggregates are called *theory-nets*. This reflects the fact that most scientific theories have laws of very different degrees of generality within the same conceptual setting. Usually there is a single fundamental law or guiding principle "on the top" of the hierarchy and a vast array of more special laws—which apply to specific situations—with different degrees of specialization.

Each special law determines a new theory-element. What holds together the whole array of laws in the hierarchy is, first, the common conceptual framework (represented in a model-theoretic way by the class of potential models), second, the common **T**-theoretical and **T**-non-theoretical distinction, and third, the fact that they are all specializations of the same fundamental law.

The theory-element containing the fundamental law(s)/guiding principle(s) is called the "*basic theory-element*" of the theory, i.e. of the theory-net. The other theory-elements of the theory-net are specializations or "*specialized theory-elements*".

When the highest degree of concretization or specificity has been reached, i.e. when all functional dependencies (concepts) are completely concretized or specified, "*terminal* special laws", which determine the most specific class of (theoretical) models, are obtained. The empirical claims associated to the corresponding "*terminal* specialized theory-elements" can be seen as particular, testable and, eventually, refutable hypotheses, which enables the application of the theory to particular empirical systems.[40] In the simplest model-theoretic way of representing these particular empirical claims, they state following: "*data model* d of **T** can actually be (exactly or approximately) extended to, or subsumed or embedded in, the "*theoretical model*" m of **T**.

The resulting structure of a theory may be represented as a net, where the nodes are given by the different theory-elements, and the links represent different relations of specialization[41] (see Figure 4).

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used to characterize or represent "empirical" systems, namely, partial potential models), such a formal relation should be considered a necessary condition for representation of phenomena, but by no means also sufficient. (For an updated discussion of the problem of representation by models or model-representation, see Frigg and Nguyen (2017; 2020) and Frigg (2023)). Having said this, it should be pointed out that not every representation is considered to be a *scientific* representation and not every scientific representation is considered to be a *model-representation* (and the representational function is not the only epistemic value of (any type of) model (see Knuuttila 2005; 2011)).

[40] This is the model-theoretic, semantic, in particular structuralist version of what has been said in Section 2.2 about the testability and eventually refutability of particular hypotheses/terminal special laws. While in the classical approach of testing the particular hypotheses/terminal special laws are the entities to be tested, in the structuralist approach the "empirical claims" associated to *terminal* special laws are the entities that carry the weight of testing and to which it is able to direct "the arrow of *modus tollens*" (Lakatos 1970, p. 102).

[41] From a formal point of view, a *theory-net* **N** is a sup-semilattice $\langle \overline{\mathbf{T}}, \sigma \rangle$, with theory-elements as elements of the set $\overline{\mathbf{T}}$ and the specialization relation σ as the relation between the elements of the set $\overline{\mathbf{T}}$ dominated by a supremum $\mathbf{T}_0$ called *basic theory-element* of theory-net **N** (García de la Sierra 2019).
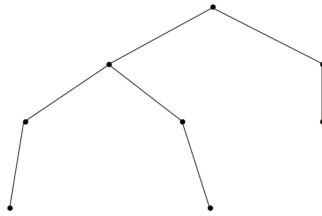
Figure 4

A theory-net **N** is the standard structuralist conception of a theory from a static or *synchronic* point of view. In this sense, a theory is *a complex*, *strongly hierarchical* and *multi-level* entity.

But a theory can also be conceived as a kind of entity that develops over time. A theory in the *diachronic* sense is not just a theory-net, which exists in the same form through history, but a *changing* theory-net, which grows and/or shrinks over time. Such an entity is called a *theory-evolution* **E**. It is basically a sequence of theory-nets satisfying two conditions: at the level of cores, it is required for every new theory-net in the sequence that all its theory-elements are specializations of some theory-elements of the previous theory-net; at the level of intended applications, it is required that the domains of the new theory-net have at least some partial overlapping with the domains of the previous theory-net.

Finally, it can be said that the structuralist view has been proposed to represent not just *intra*theoretical changes that occur in science (by means of the concept of a *theory-evolution*), but also different types of *intertheoretical changes*, such as *crystallization*, *embedding*, and *replacement with (partial) incommensurability*. It is worth noting that the process of crystallization of a theory would allow the treatment of the role of models (in the sense of laws or theory-elements) in the genesis of new empirical theories (in the sense of theory-nets and, later, of theory-evolutions) within the structuralist framework.[42]

4.3. The Theory-Net of Classical Genetics

According to our proposal, and as any other robust unified theory such as classical mechanics or thermodynamics, **CG** can also be better analyzed as a theory-net.

4.3.1. The basic theory-element of classical genetics

The "*basic* theory-element" of **CG** consists of its "(formal) *core*", symbolized by **K(CG)**, and its "domain of intended applications", symbolized by **I(CG)**.

The basic core of classical genetics

The basic *core* of classical genetics **K(CG)**, which constitutes its formal identity, is composed by the ordered classes of *potential models*, *actual models*, *partial potential models*, *constraints* and *links*.

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[42]We believe that, on careful consideration, Metatheoretical Structuralism is unaffected by the worries or criticisms expressed by Love (2010; 2013) about the semantic view, including the criticisms he considers "damning" (like those stated by Halverson 2012; for a response to Halverson from the semantic approach, see van Frassen 2019).

In the previous section we already defined the classes of *potential models* $\mathbf{M_p(CG)}$, (*actual*) *models* $\mathbf{M(CG)}$, and *partial potential models* $\mathbf{M_{pp}(CG)}$.

In a truly complete reconstruction of **CG** we should include the constraints and the links this theory has to other (underlying) theories. However, due to space limitations, we won't discuss them or make them explicit. So, the *basic core of classical genetics* (**K(CG)**) will be characterized as follows:

Definition 4
$\mathbf{K(CG)}: = \langle \mathbf{M_p(CG)}, \mathbf{M(CG)}, \mathbf{M_{pp}(CG)} \rangle$.

The intended applications and the basic theory-element of classical genetics

The *domain of intended applications* constitutes the class of those empirical systems to which one wishes to apply the fundamental law/guiding principle of the theory. They cannot be characterized by purely formal means. All we *can* say from a formal point of view is that an intended application is a partial potential model, which means that $\mathbf{I(CG)} \subseteq \mathbf{M_{pp}(CG)}$. Members of $\mathbf{I(CG)}$—to which one wishes to apply the fundamental law/guiding principle of **CG**—are biological systems, characterized in **CG**-non-theoretical terms—i.e. systems represented by structures/data models of type y ($\langle I, (C_i)_{i \leq k}, APP, MAT, DIST \rangle$), where the transmission of several traits or characteristics (phenotype) of certain individuals, that make up a family, is followed from generation to generation, such as the case of peas, genus *Pisum*, investigated by Mendel, of fowls, investigated by Bateson and collaborators, and of the fruit-fly, *Drosophila melanogaster*, investigated by Morgan and disciples.

Now the *basic theory-element of classical genetics* (**T(CG)**) can be characterized as follows:

Definition 5
$\mathbf{T(CG)}: = \langle \mathbf{K(CG)}, \mathbf{I(CG)} \rangle$.

The empirical claim of classical genetics

Classical genetics (**CG**) assumes that certain empirical systems such as those characterized above, characterized in **CG**-non-theoretical terms, satisfy the conditions imposed by **CG** in the following sense: those are the data of the experience that should be obtained, if reality behaves as **CG** says. This pretension is asserted by the empirical claim of classical genetics, which may be formulated in the following way:

(I) Any given intended system can be, when adding a set of **CG**-theoretical components $(F_i)_{i \leq s}$, $(DET_i)_{i \leq s}$, and *COMB* to the **CG**-non-theoretical part of the corresponding theory-core ($\langle I, (C_i)_{i \leq k}, APP, MAT, DIST \rangle$), (exactly or approximately) extended to, or subsumed or embedded in, a **CG** (actual) model.

This claim may be trivial if the conditions imposed by the core on the **CG**-theoretical components are weak. But this should not be a reason for rejecting the core as trivial. This core serves as a basic core for *all* the intended applications of classical genetics. Interesting, non-trivial claims may be obtained by incorporating additional restrictions through the so-called "specializations".

4.3.2. Specializations of classical genetics

There are different possible ways of specializing classical genetics. As already advanced in Section 2.3, specializations consist of specifications of

(i) types and numbers of (pairs of) factors or genes ($(F_i)_{i \leq s}$—the genotype $\gamma \in G$—(either one or more),

(ii) the way in which they are distributed in the progeny (*COMB*) (as expected or theoretical probabilities, with combinations of factors or genes with the same probability or not), and of

(iii) the specific relationship ($DET_i)_{i \leq s}$, in which they are with the characteristics of the individuals—their phenotype $\pi \in P$—(with complete or incomplete dominance, codominance or epistasis).

The diverse possibilities of specialization can be partially or totally realized, in an isolated or joint way. One specialization of **CG** in which the three types of specification have been fully realized is denominated *terminal specialization*.These are what we have in specific **CG** applications. As in other robust unified theories, **CG** particular applications to particular empirical systems include specific versions/applications of this "law". Thus, we had a specific version/application of this "law", i.e. a special law, for each type of paradigmatic example presented before.

The Theory-Net of Classical Genetics (**N(CG)**) looks as follows—with the "*basic* theory-element" of **CG** at the top and in which are only depicted "*specialized* theory-elements" of **CG** corresponding to the examples given in Section 2.3:
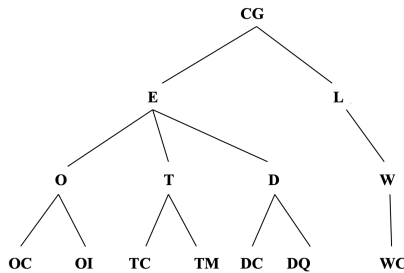

Figure 5

On a first level of specialization of **CG** theory-net we have either that all combinations of factors have equal probabilities (**E**) or that not all the combinations of factors are equally probable, i.e. that "linkage" takes place (**L**). On the other hand, we can further specialize **E**. Thus, on a second level of specialization of **CG** theory-net, it can be considered either that just one pair of factors are involved in the determination of the characteristics, and that there are four different possible combinations of factors (**O**), or that two pairs of factors are involved in the determination of the characteristics, and that there are sixteen different possible combinations of factors (**T**), or that three pairs of factors are involved in the determination of characteristics, and that there are sixty-four different possible combinations of factors (**D**). On a third level of specialization of **CG** theory-net we reach the level of terminal specializations. If **O** is further specialized, we can have either a case of complete dominance (**OC**) (see case 1 from Section 2.3 of the color of pea seed albumen), or a case of incomplete dominance (**OI**) (see case 2 from Section 2.3 of the

color of four o'clock flowers). If **T** is further specialized, we can have either a case of complete dominance (**TC**) (see case 3 from Section 2.3 of the color of pea seed albumen together with the form of pea seeds), or a case of multifactorial inheritance (**TM**) (see case 6 from Section 2.1 of the form of fowls comb). If **D** is further specialized, we can have either a case of complete dominance (**DC**) (see case 4 from Section 2.3 of the color of pea seed albumen together with the form of pea seeds and the color of pea flowers), or a case of quantitative characteristics (**DQ**) (see case 5 from Section 2.3 of the length of corn ear). Finally, we also can specialize **L** further. Thus, on a second level of specialization of **CG** theory-net, it can be considered that just one pair of factors is involved in the determination of the characteristics, and that there are four different possible combinations of factors (**W**). As before, on the third level of specialization of **CG** theory-net we reach the level of terminal specializations. If **W** is further specialized, we can have either a case of complete dominance (**WC**) (see case 7 from Section 2.3 of the color of pea flowers together with the length of pea pollen grain).

5. Making Them Explicit: Laws and the Connection of Models to Theories. Discussion on the Basis of Previous Analyses

We would like to discuss now the issues of: a) the existence of laws in biological sciences, b) the place of models in theories of biology, and c) the unifying power of biological theories, in the light of the analyses carried out.

5.1. On Claim a) that there are "Laws" in Biological Sciences

It is worth mentioning that in the literature it has been recognized that there exist certain areas of science where fundamental laws/guiding principles—though maybe with another terminology, such as "basic principles" or "fundamental equations"—occur explicitly formulated in linguistic terms, and sometimes even in an axiomatic or quasi-axiomatic way. Newton's Second Law is an example of that, i.e., of a fundamental law/guiding principle explicitly formulated in linguistic terms, even in an axiomatic way since its first public occurrence, in the first edition of *Principia Mathematica Philosophia Naturalis* (Newton 1687)—although it was mistakenly ranked at the same level of the other two "Axioms, or Laws of Motion": the Law of Inertia and the Law of Action and Reaction.

On the other hand, in the literature of philosophy of science it has also been pointed out that there are other areas of science where fundamental laws/guiding principles do not occur explicitly and clearly formulated in linguistic terms. An example of one of these areas is evolutionary biology and the so-called "Principle of Natural Selection". In biology textbooks (beginning with Darwin's *Origin of Species*) we cannot find nor "observe" that principle formulated in all their generality, abstraction and schematization—although there is an agreement about the fact that a fundamental law/guiding principle "is there" and a lot of discussion about the right and convenient way of identifying and formulating it.[43]

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[43]For a discussion and a proposal on this issue from a structuralist point of view, see Ginnobili (2016) and Díez and Lorenzano (2015).

However, philosophers of science have also pointed out to other areas of science where nothing can be found or "observed" at all that possesses the criteria mentioned in Section 2.2 and that would, therefore, be considered a fundamental law/guiding principle in a plausible way. And precisely the field of Classical Genetics is an example of that. If we consider what is sometimes called a "law" in the area of Classical Genetics, namely, the so-called "Mendel's Laws", it is easy to recognize that neither Mendel's First Law (Law of Segregation) nor Mendel's Second Law (Law of Independent Assortment) or the sometimes mentioned Mendel's Third Law (Law of Dominance or Law of Uniformity) are schematic and general enough to connect all or almost all of the terms of Classical Genetics nor to be accepted by the respective community of geneticists as valid for all applications, with modal import, and as providing a conceptual framework adequate to formulate all the special laws of Classical Genetics. These laws therefore cannot be considered fundamental laws of Classical Genetics. That is to say no such law can be "observed" in the literature of genetics (Smart 1959: 1963; Kitcher 1984).

We grant that, sometimes, we cannot "observe" (explicit linguistic formulations of) general laws (or guiding principles) in the standard presentations of the respective theories, i.e. in the different texts (either journal articles, manuals or textbooks) written by scientists or science teachers.

Nevertheless, this article has argued for the existence of a fundamental law/guiding principle of Classical Genetics that even though not stated explicitly in biological literature, underlies implicitly the usual formulations of the theories, systematizing them, making sense of geneticists' practice, and unifying the different and heterogeneous models under just one theory.

In Section 2.3 a fundamental law/guiding principle in this area has been made *explicit*—against what can be called "narrow inductivism" or "restricted empiricism" in metascience.[44] And it is easy to realize that in the formulated fundamental law/guiding principle we can identify all criteria of fundamental laws/guiding principles indicated in Section 2.2. First, **CG** fundamental law/guiding principle can be seen as a *synoptic* law because it establishes a substantial connection between the most important terms of **CG** in a "big" formula. It contains all the important terms that occur in **CG**, both the **CG**-theoretical ones (the set of factors/genes, the function that assigns characteristics to pairs of factors or genes, and the function that represents the transition from

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[44]Nowadays, it can be considered a truism in philosophy of science that empirical science goes beyond "appearances", "phenomena", or "facts", in order to understand them better. Empirical science postulates, in addition, a realm of entities that are not directly empirically accessible, but they are accepted, *at least* inasmuch as the linguistic frameworks or theories in which they essentially occur are accepted as well (Carnap 1950). Thus, for instance, electric fields and wave functions are accepted, at least inasmuch as the theories of electromagnetism and quantum mechanics, respectively, are accepted. And scientists had good reasons to do so. Let's call that view on science "non-narrow inductivism" (inspired by Hempel 1966) or "non-restricted empiricism" (inspired by Carnap 1956). The analyses—or explications—of (metascientific) concepts, such as *law*, *model* or *theory*, can be considered as forming *interpretative eschemes* or *explanatory models*—in the sense of Hintikka (1968) within epistemic logic, and of Stegmüller (1979) and Moulines (1991; 2002) within philosophy of science—, of a philosophical nature, which propose or exhort us to "see the world" of science in a certain way. And a philosopher of science who uses one of these explanatory models overcomes narrow inductivism and restricted empiricism on a metascientific level in a similar way to what has been said and recommended for the case of the scientist. She/he interprets in a non-narrow inductive or non-restricted empiricist way what scientists do: not because we do not (directly) "see" their "fundamental laws/guiding principles", they are not "(in some sense) there" to be seen. As Goodman says, "We see what we did not see before, and see in a new way. We have *learned*" (Goodman 1978, p. 173).

parental factors/genes to factors/genes in the progeny) and the **CG**-non-theoretical ones, which are empirically more accessible (the set of individuals, the set of characteristics, the function that assigns their characteristics to individuals, the function of mating that assigns a progeny to parental individuals, and the function that represents the transition from parental characteristics to characteristics in the progeny). Second, **CG** fundamental law/guiding principle has been *implicitly accepted as valid in every intended application of the theory* by the respective community of scientists, i.e. by the community of geneticists who accept or use **CG**. In fact, accepting **CG** implies accepting **CG** fundamental law/guiding principle, while rejecting **CG** fundamental law/guiding principle implies rejecting **CG**. And of course, geneticists may not succeed in applying **CG** to particular empirical systems, and may decide to use another theory, with another fundamental law(s)/guiding principle(s). But to the extent that they work with **CG**, they accept as valid, even though just implicitly, **CG** fundamental law/guiding principle. Third, **CG** fundamental law/guiding principle is *highly schematic* and *general* and it possesses *very little empirical content*; such that is, when considered in isolation, irrefutable or "empirically non-restrict" (Moulines 1984) (i.e. it has a "*quasi-vacuous*" character). This is because to test what **CG** fundamental law/guiding-principle claims—namely, that the coefficients of the empirically determined distribution of characteristics and of the theoretically postulated distribution of factors in the progeny, given the also theoretically postulated relation between factors and characteristics, are equal—, without introducing any kind of further restrictions, amounts to a "pencil and paper" exercise that does not involve any empirical work. Nevertheless, fourth, as we would expect in the case of any fundamental law/guiding principle, despite being irrefutable, it *provides a conceptual framework* in which all special laws can be formulated; that is, special laws with an increasingly high degree of specificity and with an ever more limited domain of application, until we reach "terminal" specializations whose associated empirical claims can be seen as particular, testable and, eventually, refutable hypotheses, which enables the application of **CG** to particular empirical systems (its *systematizing* or *unifying* role). And fifth, **CG** fundamental law/guiding principle expresses a non-accidental regularity that is able to give support to counter-factual statements (if it is taken "together-with-their-specializations" within the corresponding theory-net), even when it is context-sensitive and with a domain of local application, and that, in its minimal sense, what is attributed is the *necessity of the models*, and, in that sense, it should be considered as *necessary in its area of application* (i.e. it possesses *modal import*). This means that, when the theory-net of **CG** contains an application with *s* as the relevant specialization of **CG** fundamental law/guiding principle and *i* as the empirical system/application, then, given the constrictions that the specialization *s* determines at the **CG**-non-theoretical level, a certain data model *should* be obtained for the empirical system *i* to which the theory-net of **CG** is intended to apply, i.e. the empirical system *i* to which the theory-net of **CG** is intended to apply *should* behave in a certain way—represented by the corresponding data model. Recalling that any specialization presupposes all that is "above" it in the corresponding branch of the theory-net of **CG**, notably the fundamental law/guiding principle, the counterfactual "if *s* were the case, then *i* (i.e. its corresponding data model), would be the case" is true according to the theory-net of **CG**.

Regarding the place of the so-called "Mendel's Laws" in the theory-net of **CG**, we can say the following. Mendel's Laws, inasmuch as they impose additional restrictions on the **CG** fundamental law/guiding principle, thereby adding information that is not already contained in its highly schematic formulation and restricting its area of application, can be obtained from the fundamental law through specialization and hence must be considered "special laws" of **CG** though not "terminal

specializations". This is because Mendel's First and Second Lawsare a kind of "(pure) theoretical laws" (specific versions of the theoretical analogue of the transition of phenotypes), which only establishes what happens at the level of the (allelic) factors or genotypes, through function *COMB*, but doesn't say anything about how to connect such a level with that of "the experience", "the empirical", that is, with the characteristics or phenotypes. On the other hand, the sometimes-mentioned Mendel's Third Law must also be considered a "special law" of **CG** though not a "terminal specialization". Mendel's Third Law, understood either as the Law of Dominance or as the Law of Uniformity, consists in a specification of the function *DET* that establishes a relationship of (allelic) factors or genotypes with the characteristics or phenotypes.

5.2. On Claim b) that many of the Heterogeneous and Different "Models" of Biology Can be accommodated under Some "Theory"

Let us suppose that a theory (a theory-net in the structuralist sense) is not clearly visualized and, nevertheless, certain "laws" or "equations" or (theoretical) "models" are clearly identified, but they cannot be taken as fundamental laws/guiding principles or (theoretical) "models" *of a theory*; they are rather considered "autonomous" with respect to "theories" and do not cover the entire supposed domain of application of the corresponding realm.

This situation could arise under the following two circumstances:

The first occurs when these laws, equations or models are *indeed isolated laws* or *equations* or *models*. This circumstance can occur *in a synchronic* or *in a diachronic way*. Both situations are "entirely compatible" with Metatheoretical Structuralism.

In fact, the law of ideal gases and Ohm's law are mentioned in the structuralist literature (Balzer 1996) as examples of isolated laws. Even though they are not part of theory-nets, they are perfectly conceptualizable in structuralist terms, namely, as theories that can actually be reconstructed as *only one theory-element* (see Figure 6).

Figure 6

On the other hand, this "isolation" of the theory-elements, in the structuralist terminology (or "autonomy" of the "models", in the "model views" terminology), not only can be systematically and synchronously established, but also may or may not remain diachronically invariable.

If it were the last thing, it could be a case where "a law is in search of a fundamental law/guiding principle, of which it becomes a special law" or, in other words, where "a (theoretical) model is in search of its theory (i.e. its theory-net) to which it can be incorporated" (see Figure 7).
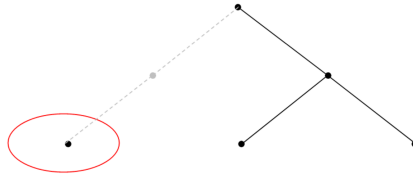
Figure 7

Or it could be a case where "a law, or a (theoretical) model, from which—together with many other things—a theory (i.e. a theory-net) is developed (and, finally, ends up consolidating or crystallizing)" (see Figure 8).
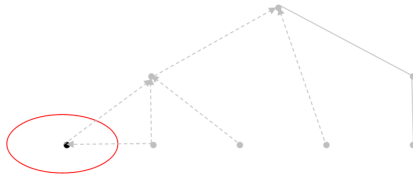

Figure 8

And although this can only be determined retrospectively, all these circumstances, whether it be an isolated law or model, which so remains, or an isolated (or incipient) law or model, which is later incorporated into a theory or from which a theory is developed and ends up crystallizing a theory (theory-net), would be susceptible of being represented by the structuralist metatheory, through their conceptualization as an isolated theory-element (the simplest and smallest notion of theory) or as its incorporation (or reduction, exact or approximate) to a theory-net (as specialization) or as part of a crystallization process, respectively.[45]

Up to this point we have referred to what could take place in general in relation to theoretical models. But, without going deep into the history of Classical Genetics, we could distinguish what happened in relation to the two of the types of models present in a theory according to Metatheoretical Structuralism—models of data and theoretical models. It might be said that the former reached a definitive stabilization, initiated with Mendel's experiments, with respect to phenomena and experimental techniques, at the beginning of the 20th century.[46] But this stabilization and permanence contrasts with the continuous modification of the theoretical models—i.e. their theoretical extension or expansion, and conceptualization and theorization, trying to explain the former, to account for them, in the articulation of all their concepts in regularities of a certain type—in a process of crystallization, which leads to the emergence of the first paradigm/research program/theory in Genetics, Bateson's Mendelism, and its subsequent replacement by Morgan's Classical Genetics (Darden 1977; 1991; Lorenzano 2013).

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[45] For a systematic treatment of this less known metascientific concept, see Moulines (1997, 2011, 2014).

[46] This analysis of (part of the history of) Classical Genetics would be compatible with the so-called "experimental model systems" (Rheinberger 2007).

Another circumstance occurs when the *laws*, or (theoretical) *models*, despite their appearance of "autonomy" from "theories" and from any fundamental law/guiding principle, *are not*, in fact, *autonomous* in a sense that can be made precise as follows. Here we would be faced with cases of laws, or models, which would be special cases of fundamental laws/guiding principles that are not "observed" in their greater generality and schematism, but which, whether or not their existence is accepted in the usual way, "are there", being susceptible of becoming explicit. As it has been argued above, the really different and heterogeneous models (laws) of Classical Genetics can be accommodated under one theory, i.e. one theory-net. Despite the differences and heterogeneity of the models presented in Section 3.1 they can be placed in the theory-net of Classical Genetics.

5.3. On Claim c) about the Unifying Power of Biological Theories

As stated before, what all models of Classical Genetics share is that they appeal to the *same* theory, i.e. theory-net. Such models may differ substantially in their form. In fact, the laws obtained by specialization from the fundamental law/guiding principle do not preserve the logical or mathematical form.

The theory-net of Classical Genetics arises from the specification received of the concepts of (allelic) factors, of *determination* of phenotypes by genotypes and of *transition from parental genotypes to genotypes in the progeny*. In each specific case, specific pairs of (allelic) factors, and specific forms of the functions of *determination* of phenotypes by genotypes and of *transition from parental genotypes to genotypes in the progeny* should be searched for in order to account for the specific *distribution of phenotypes in the progeny*. The different ways in which Classical Genetics can be applied are established by the different special laws of the theory.

The interrelations between different theory-elements allow them to be seen as parts of "something unitary". In other words: the relation of specialization in a theory-net seems to be a guarantee of cohesion, and allows a better understanding of what the valuable unification of bona fide scientific theories consists of.

The unifying power of a theory depends not only on the number of successful applications/models but also (and more prominently) on how heterogeneous such applications/models are. Therefore, the evaluation of the unifying capacity of a theory must take into account the heterogeneity of cases in which it is applied, through the heterogeneity of the different specializations, of the different specifications that the concepts of the theory receive. Classical Genetics applies to a heterogeneity of cases—from the **CG**-"empirical"/non-theoretical level—thanks to the heterogeneous way in which the set of factors or genes $(F_i)_{i\leq k}$, the function $(DET_i)_{i\leq k}$, and the function $COMB$—from the **CG**-theoretical level—are specified. The reason why Classical Genetics is unifying is because it constitutes a collection of theory-elements that deal with different types of cases by subsuming or embedding them in some line of specialization of its theory-net, which is the "multidirectional development" of a common fundamental law/guiding principle.

6. Conclusion

In this article a unifying analysis of the concepts of law, model and theory has been first presented and then applied to Classical Genetics. In this area a fundamental law/guiding principle and special laws as well as its theory-net have been identified and made explicit. Finally, the consequences of the

analysis were drawn in favor of the ideas that there are "laws" in biology (special and fundamental laws/guiding principles where a theory-net has been identified), that many of the heterogeneous and different (theoretical) models of biology can be accommodated under some "theory" (in case a theory-net has been identified), and that theory-nets in biology possess unifying power.

What an approach to the theme of the unifying power of science must achieve is not only to show how more cases of those already known are incorporated, but also the association in the same framework of different parcels of the world. This is, we insist, where the true unifying power of theories resides. With its notion of theory-net Metatheoretical Structuralism is the perspective that most clearly captures both the different successful applications/models of a theory and what they all have in common.

Just as the unifying capacity counts as an epistemic virtue when choosing between conflicting theories, the ability to explicate that merit may well count as a virtuous criterion for the choice of metascientific approaches to such theories at the same time. Something similar can be said about the very unifying power of the metatheoretical view. And Metatheoretical Structuralism has shown its unifying power with the unifying analysis (explication) of the (metascientific) concepts of law, model and theory presented here.

On the other hand, the proposal of Metatheoretical Structuralism in general, and the analysis presented here in particular, should be considered as compatible with and/or complementary to the analyses susceptible of being carried out by the "model views", the "model-based science" and to pluralistic accounts of models, as well as to the "practice-oriented" philosophies of science (especially those which do not deny or even emphasize the practice of theorizing). However, Metatheoretical Structuralism, and the analysis presented here, would not be compatible to any "atheoretical" account according to which "there are no theories at all" (in any precise sense of theory) or "there are only practices".

In any case, our analysis proposes or exhorts us to "see the world" of science in a certain way. We hope to have contributed with the present article to the plausibility of such a way of seeing the world of science and to encourage other philosophers of biology to do the same.

Acknowledgments

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