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# Chapter 15

# CLOSURE OF CONSTRAINTS AND THE INDIVIDUATION OF CAUSAL SYSTEMS IN BIOLOGY

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# CLOSURE OF CONSTRAINTS AND THE INDIVIDUATION OF CAUSAL SYSTEMS IN BIOLOGY

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#### Key messages:

- In biological research, it is important to individuate living systems (both synchronically and diachronically), clearly establishing their boundaries as causal systems.
- The individuality of living beings as causal systems can be established from the perspective of the theory of biological autonomy, as a promising way of functionally ascertaining the boundaries and unity of living systems based on a causal regime proposed to be distinctively biological, namely, closure of constraints.
- Closure of constraints is a kind of causal circularity through which components of a living system that act as constraints causally bring about one another and constitute the very system and its boundaries.
- Living systems exhibit two distinct albeit interdependent causal regimes: an open regime of thermodynamic processes and reactions, and an organizationally closed regime of dependence between system's components that act as constraints.
- Constraints are local and contingent causes that reduce the degrees of freedom of the dynamics or processes on which they act but remain conserved at the time scale relevant to describe their causal action with respect to that process or dynamics.

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#### 15.1 Introduction

In order to carry out many scientific practices, for instance, doing measurements, building explanations, planning interventions, it is necessary to individuate which causal systems will be measured, explained or intervened upon (Montévil, 2019; Montévil & Mossio, 2020). As Kaiser and Krickel (2023) mention, despite the fact that the expression "causal system" is not often used in organismal biology, it is still the case that organisms – as well as other biological individuals - should be also conceived as causal systems. After all, causal relations are essential to their individuation. Or, to put it differently, organisms are no exception to the claim that, as Beisbart (2023) discusses, systems - as "worldly" entities that are objects of scientific research - are often individuated on the basis of causal knowledge. As individuating something entails demarcating it from its environment, these practices establish boundaries that are crossed by processes that connect what is inside and what is outside a causal system. This is especially consequential in the case of organisms. As open dissipative systems, organisms can only self-maintain by decreasing the entropy within themselves while increasing the entropy at the environment such that there is a net entropy increase in the organism-environment system. Therefore, the boundaries of an organism play a fundamental role in its self-maintenance as a causal system. Moreover, in order to understand what kind of causal system an organism is, we need to decompose it into parts (which typically play a causal role within it, which allow for functional ascription given a certain theory of function) and, also, specify the kind of unity that holds its parts together (Kaiser & Trappes, 2021).

For these reasons, it is important to individuate living systems (both synchronically and diachronically), and to clearly establish what are their boundaries as causal systems, such that we can specify which causal processes are internal to them, and which ones are external influences that nonetheless cross these boundaries, interacting with internal processes. But this may be a challenging task: systems can be conceived as parts of the physical world that occupy some domain of space, with an adjoining environment, but, as the world is complex, we often face difficulties in telling exactly which items belong to or are external to a system and which specific region of space is occupied by it.

In this chapter, we consider the problem of how to ascertain the individuality of living beings as causal systems from the perspective of the theory of biological autonomy (e.g., Moreno & Mossio, 2015). Problems of individuation permeate the biological sciences and must be faced by their practitioners (Haber & Odenbaugh, 2009). But these are concepts about which there is no broad agreement in biology. Rather, it seems that the more we enquire into them the more we realize how complicated it is to ascertain what is a biological individual and how are their boundaries and occupied region in space to be established. The theory of biological autonomy can bring a contribution to such an enquiry by grounding the individuality of living systems on the notion of closure of constraints. This provides, as we intend to show, a promising way of functionally ascertaining the boundaries and the unity of living systems, based on a causal regime proposed to be distinctively biological.

## 15.2 The theory of biological autonomy and the individuation and identity of living systems

The theory of biological autonomy provides a very general and coherent conceptual scheme to think of individuality in living systems. Following Montévil and Mossio (2020), we understand conceptions of organisms' identity in terms of a spectrum from more stringent to more inclusive interpretations. At one end of the spectrum, we find notions of identity that point to the unicity

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of living beings, *i.e.*, the fact that they possess a unique set of properties that make them different from any other organism or, generally speaking, object. At the other end of the spectrum, the identity of living beings refers to their individuation, *i.e.*, the fact that they possess a number of properties that, under a given account, may allow us to ascertain their boundaries and discriminate them from the surroundings. When identity is conceived as unicity, each identity class is supposed to contain only one organism, while when conceived as individuation, a class should contain the largest number of (if not all) organisms. Moreover, as Montévil and Mossio argue, the more inclusive classes are presupposed by the more restrictive ones, *i.e.*, the unicity of a given organism presupposes that it also meets the more general requirements for individuation. In this chapter, we will focus on the problem of individuation, both synchronically and diachronically.

Let us present some basic notions in the theory of biological autonomy in order to explain how it deals with the individuality of living systems. Autonomy and self-determination are taken in this theory as constitutive dimensions of living systems. In recent theories dealing with biological autonomy, these ideas are expressed through the concept of closure, which refers to how components and operations of a system depend on each other to their own production and maintenance, while also collectively determining the very conditions for the existence of the system itself (Varela, 1979). Surely, this dependence is causal in nature: closure is a particular kind of causal circularity through which components of a living system causally bring about one another and constitute the very system that we individuate, ascertaining their boundaries and the region in space it occupies. But not any causal circularity will do. Living systems show a particular kind of causal circularity we can find in physicochemical systems.

To understand the organizational closure of living systems, we need to differentiate between what is simply closure of thermodynamic processes, which can be found in physicochemical systems, and what is a distinctively biological closure (Moreno & Mossio, 2015; Mossio & Bich, 2017). To do so, we should consider two distinct albeit interdependent causal regimes operating in living systems: an *open* regime of thermodynamic processes and reactions, and an organizationally *closed* regime of dependence between system's components that act as *constraints* (Montévil & Mossio, 2015; Moreno & Mossio, 2015). We need to explain, then, what are constraints and how constraints realize closure, *i.e.*, the particular kind of causal circularity underlying the organization of living systems, according to the theory of biological autonomy. Let us begin by explaining what are constraints.

Constraints are local and contingent causes that reduce the degrees of freedom of the dynamics or processes on which they act (Pattee, 1972) but remain conserved at the time scale relevant to describe their causal action with respect to that process or dynamics. Mossio et al. (2013) provide a more formal definition of constraint in the following terms:

Given a particular process P, a configuration (or material structure, or entity) C acts as a constraint if:

- i In the time scale characteristic of *P*, *C* is not locally affected by *P* in the properties relevant to its causal power. [Conservation]
- ii At the same time scale, *C* exerts a causal power over *P*, *i.e.*, there is some observable difference between *P* without and under the influence of *C*. [Causal power]

Enzymes offer obvious examples of constraints. On the one hand, an enzyme is not altered in properties relevant to its catalytic effect at the time scale of its action on a metabolic reaction (*i.e.*, it is conserved), despite being altered in such properties in time scales smaller or greater than the specific time scale of catalysis. On the other, at this time scale, there is an

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observable difference between a reaction under catalysis or not by an enzyme, and, accordingly, an enzyme exerts a causal power over the reactions under its influence. It is not only at the molecular level, however, that one finds examples of constraints. Considering higher levels of biological systems, we find plenty of constraints, such as, say, an organism's vasculature, which exerts a causal power over blood distribution in the body, reducing the degrees of freedom of blood flow, while it is conserved in the properties relevant to its causal action at the time scale in which this causal power is exerted (in the human body, about 5.6 litres of blood circulates through the body three times every minute).

The explanation of the organizational closure of living systems in the theory of biological autonomy is grounded on an understanding of how these systems are constituted and operate as causal systems. Let us expand, then, our explanation to properly characterize how constraints realize closure, as a causal circular regime. The first step is to define dependence between constraints, which is in itself a causal relation. A relation of dependence between two constraints occurs when the replacement or repair of a constraint (also) depends on the action of another constraint. The former constraint is called in the theory a *dependent* one, while the latter is dubbed an *enabling* one. A minimal causal dependence between constraints involves one dependent and one enabling constraint (Figure 15.1). For instance, while an enzyme acts as a constraint in the time scale of its catalytic action, at longer time scales it is degraded and replaced through processes involving the action of other constraints, say, ribosomes or mRNAs. The enzyme is a dependent constraint while ribosomes and mRNAs are enabling constraints, in this example.

Dependence between constraints leads to organizational closure when, instead of a linear chain of causal dependence relations between constraints, one finds a chain that folds up and establishes mutual dependence (Figure 15.2). In formal terms, a set of constraints C realizes closure if, for each constraint  $C_i$  belonging to C: (i)  $C_i$  depends directly on at least one other constraint of C (*i.e.*,  $C_i$  is dependent); and (ii) there is at least one other constraint  $C_j$  belonging to C which depends on  $C_i$  ( $C_i$  is enabling). Therefore, as a specific mode of dependence in a set of constraints, closure of constraints is a particular type of causal cycle, in which each constraint is involved in at least two different dependence relations, one in which it is enabling and another in which it is dependent. Closure of constraints includes, in sum, all constraints that are both enabling and dependent, showing, thus, mutual dependence (Montévil & Mossio, 2015; Moreno & Mossio, 2015).

Closure of constraints is, in these terms, a general invariant in biological organization, *i.e.*, in any architecture of relations that is specific of living beings, there must be closure in at least a subset of the constraints as a requisite for the system being able to self-maintain and show autonomy. Surely, this invariance of closure does not mean that biological systems will not



Figure 15.1 Minimal causal dependence between constraints.  $C_1$  acts as a constraint over the process  $A_1 \rightarrow B_1$  at time scale  $\tau_1$ , being conserved at this time scale. In another time scale,  $\tau_2$ ,  $C_1$  is produced under the influence of another constraint,  $C_2$ .  $C_1$  is evidently not conserved at  $\tau_2$ , while  $C_2$  is conserved at that time scale. In the vocabulary of the theory of biological autonomy,  $C_1$  is called a "dependent" constraint and  $C_2$ , an enabling constraint. Elaborated by Maël Montévil.

Source: Reproduced under permission from Montévil and Mossio (2015).



*Figure 15.2* Closure of constraints.  $C_1-C_5$  satisfy the definition of constraint at  $\tau$ .  $C_1-C_4$  are dependent constraints.  $C_2-C_5$  are enabling constraints. Therefore,  $(C_2, C_3, C_4)$  is a subset of constraints that are both enabling and dependent. This subset realizes closure of constraints.  $C_1$  is a constraint that is dependent but not enabling (within the system at stake).  $C_5$  is a constraint that is enabling but not dependent (within the system at stake).  $C_1$  and  $C_5$  connect this system with other systems. Elaborated by Maël Montévil.

Source: Reproduced under permission from Montévil and Mossio (2015).

show variability, or that variability is not a central aspect for understanding biological systems, but only that each variation shown by living systems should be conceived as variation of an organization. Once variations in the organization of biological individuals in a population are available, a selection of those containing constraints that contribute to a more efficient maintenance of that organization can take place (Bich & Bechtel, 2022a).

According to the theory of biological autonomy, a living system can be individuated based on its closure of constraints. As Moreno and Mossio (2015: 23, emphasis in the original) argue, "constraints subject to closure *constitute* the biological organisation and, accordingly, make an essential contribution to determining the identity of the system. Biological individuality [...] has much to do with organisational closure, to the extent that one may conjecture that closure in fact defines biological individuality".

An important aspect to notice is that this is a *functional* mode of individuating a living system, grounded on ascertaining where its organizational closure lies, not where one finds its physical boundaries. The boundaries of a living system – as a causal system – are found here in the set of enabling and dependent constraints that *functionally* constitute its organization.

#### 15.3 Biological autonomy and the identity and individuality of living systems

Biological individuality is both a fundamental philosophical problem (with a long history) and an important issue for biological research. Moreover, this issue gets metaphysically laden when we think of concepts of biological individuality in relation to questions about whether there might be a single way to "carve nature at its joints" and, if not, how should we deal with pluralism about biological individuals (see, e.g., Nyhart & Lidgard, 2017). Individuality is a complex and contested topic both in biology and philosophy of biology and is of central interest to other issues, ranging from the levels of selection to major transitions in evolution to the nature of coloniality and multicellularity to immunological recognition and tolerance. It is also a relevant topic for causal understanding in the biological realm, since without a way of individuating biological systems, one cannot assess how they stand in causal relations to one another. It is no surprise, then, that there is much interest in individuality in both biological

and philosophical research (e.g., Wilson, 1999; Wilson, 2004; Clarke, 2010; Bouchard & Huneman, 2013; Godfrey-Smith, 2013; Lidgard & Nyhart, 2017; Love & Brigandt, 2017; Montévil & Mossio, 2020; Meincke & Dupré, 2021).

A single, unified concept of biological individuality has been difficult to obtain. This does not come as a surprise, given both the diversity of structural and dynamic aspects of living beings, and the fact that this is a concept crossing frontiers between biological disciplines, between biology and other sciences, and between sciences and other domains of thinking, while also extending over a wide range of our experiences. Biological individuality is also related to questions of identity, the idea that each being is in a sense unique, different from any other living being, and applies both synchronically and diachronically, as biological individuals are not supposed to exist in a single time-slice but rather extend across time, maintaining themselves despite continuous change. Moreover, biological individuals establish boundaries to causal processes, which can be either entirely internal to them or cross their limits, establishing connections to other systems constituting their environment. This connects issues concerning individuality in the biological realm with problems related to the boundaries of causal systems in living phenomena.

One of the most important developments in debates about biological individuals has been the distinction between two possible kinds: evolutionary and physiological individuals. Since Hull (1980), it has become clear that evolutionary biology can provide a theory-based concept of individuality. Godfrey-Smith (2009, 2013) articulated this concept based on an understanding of Darwinian individuals belonging to Darwinian populations, which are formed by "things" fulfilling the following conditions: (i) they exhibit variations in their traits; (ii) these traits are heritable through reproductive events; and (iii) some of these traits confer reproductive and/or survival advantages to the Darwinian individuals. As Godfrey-Smith discusses, some organisms conceived from a physiological point of view are not Darwinian individuals, because they do not satisfy these three conditions.

Other theory-based views of individuals are grounded on physiology, including developmental views (e.g., Nuño de la Rosa, 2010), immunology-centered (Pradeu, 2010), and autonomybased views (e.g., Moreno & Mossio, 2015). Physiological individuals share some characteristics that allow us to treat them as such: (i) they have a metabolism, carrying out anabolic and catabolic chemical reactions that guarantee the maintenance of their internal structures and functioning; (ii) they have structural properties, related to the heterogeneity of their parts, which interact through a variety of internal mechanisms; and (iii) they have functional or dispositional properties, such as reproduction, self-repair, growth and development capabilities, which underlie their capacity to maintain themselves and the lineages in which they may be included.

In a related but also importantly different manner, Montévil and Mossio (2020) distinguish between a historical conception of organisms (which are prototypical cases of biological individuals) that characterizes their identity by considering their genealogical connection with a common ancestor, and a relational conception, which interprets their identity by referring to a set of distinctive relations between properties and traits they possess, as well as between the organism and its environment. While in the historical conception, what matters are genealogical relations between organisms, from the relational perspective what matters are the form of the relation, the kind of structure that connects two or more objects, and, accordingly, the observable organization and functioning of the living system. Relational identity requires, thus, a stability of the relations among relevant properties in order to ascertain synchronic and diachronic identity to a set of organisms.

Individuation of living systems based on closure of constraints concern physiological individuals and, considering the distinction introduced by Montévil and Mossio, is based on one of the relational approaches used in biology, namely, the organizational approach. To individuate

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physiological individuals based on such a relational approach is connected to an underlying discussion on whether there is a set of distinctive properties and a general principle of organization of living systems that make them different from merely physicochemical systems. By biological "organization", one specifically means the mutual dependence among the living system's parts that account for its persistent existence, and, thus, for the persistent existence of the parts themselves. Relational approaches that exhibit commonalities and differences have been proposed in the history of biology by scientists like Nicolas Rashevsky (1954), Humberto Maturana and Francisco Varela (Varela et al., 1974), Robert Rosen (1991), and Stuart Kauffman (1993).

The theory of biological autonomy, developed in a series of works and presented in Moreno and Mossio (2015), provides one such relational approach. According to the theory of biological autonomy, a particular kind of organization, involving closure of constraints, is a unique and striking feature of living systems, as discussed above. According to this theory, physiological individuals, in addition to their organization, also have a certain degree of autonomy and perform activities that are important for the control of that organization itself, while also depending on other systems that can be regarded as an environmental context in which the individual is embedded. Thus, we can say that these individuals exhibit a relative individual autonomy with a specific degree of control over the parts constituting them. According to this theory, there is a mutual relation between organization, autonomy and functionality that explains how biological systems work, from a relational perspective. There is also a normative dimension in how this theory conceives of a living system and its boundaries, as a living being needs to carry out a diversity of activities, involving both its internal medium and boundaries, in order to maintain its internal organization. These activities are carried out by means of a division of labour among the constituent parts that contribute to the organization and properties of the living system. It is important to emphasize, also, that the maintenance of the internal organization and autonomy of a living system depends on the exchange of matter and energy with the surrounding environment, such that a living system is thermodynamically open, while being organizationally closed (Piaget, 1967). As Moreno and Mossio (2015, p. xxiii) write, "individual organisms are systems capable of [...] constituting an identity that distinguishes them from their environment (at the same time as they continue interacting with it as open, far-from-equilibrium systems)".

A few years later, Montévil and Mossio (2020) introduced the idea that the historical/genealogical and relational conceptions of the identity of organisms are not opposed but rather complementary, such that an adequate conception of organisms' identity would require a hybrid conception integrating both perspectives. In their view, only by doing so we will be able to accommodate at least part of the contingency and unpredictable variation that organisms show across evolutionary time. In this hybrid conception, historical and relational (and more specifically, organizational) aspects of organisms' identity would sustain and justify each other.

## 15.4 A first implication of the theory: Boundaries of biological systems and varying degrees of individuality

For instance, how can we establish that an item (either biotic or abiotic, say, bacteria in our bodies or fire in an ecosystem) is inside or outside the boundaries of a biological individual? This is consequential, for sure, to any effort to ascertain what are the boundaries of different biological systems, from cells to organisms to ecosystems. In order to self-maintain, biological systems need to interact with a host of other systems and the constraints operating in them. If we consider that constraints that are exclusively enabling or dependent put into interaction different systems individuated by closure of constraints, we can account for both the thermodynamic openness and the organizational closure of these systems in terms that allow for establishing

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what is internal to any of them and what is external and connect them. Let us consider a case discussed by El-Hani et al. (2024), concerning the conditions that should be fulfilled for an abiotic item such as fire to be treated as a functional component within an ecosystem.

According to the organizational account of ecological functions (Nunes-Neto et al., 2014; El-Hani & Nunes-Neto, 2020; El-Hani et al., 2024), an abiotic item can only be a functional component of an ecosystem if it is subject to closure within that system and is, thus, under its control. Here, we contend that this claim can be generalized to the conditions to be fulfilled for a biotic or an abiotic item to be regarded as internal to any living system, at different levels of organization. It is important to remember here that the mode of individuating a living system according to the theory of biological autonomy is functional in nature, ascertaining the boundaries of a living system – as a causal system – based on the set of enabling and dependent constraints constituting its organization. Therefore, the criterion to be fulfilled for establishing if any item (biotic or abiotic) is internal to the boundaries of a living system is clear: to be included in the system, a biotic or abiotic item should be internal to its closed organization, being both a dependent and an enabling constraint.

Consider the case of fire in ecological systems (as weakly individual biological systems; see, e.g., Huneman, 2014b). Fire will be an internal component if and when integrated into the dynamics of an ecosystem as both an enabling (e.g., of regrowth processes) and a dependent constraint (on fireadapted plant species) (e.g., Mutch, 1970; Schwilk & Ackerly, 2001; McLauchlan et al., 2020). For instance, in savannah ecosystems, fire-adapted plant species exhibit traits that promote flammability and, thus, influence fire frequency (e.g., Mutch, 1970; Schwilk & Ackerly, 2001), while fire is in such ecosystems not merely destructive but rather enabling, leading to regrowth processes that are crucial to the system's dynamics. In these cases, vegetation is a driver of fire regimes, and one can even talk about coevolution of fire and biota (McLauchlan et al., 2020). In turn, if fire is not under the control of constraints internal to an ecological system, it cannot be regarded as an internal component of that system, even if it may be eventually enabling some processes within it. In this case, fire will be just an external constraint, despite its significance to the system's dynamics. The fact that fire is not internal to this system does not deny its relevance to its dynamics, as external constraints are relevant to system's dynamics no matter if they are not part of its closed organization. As Moreno and Mossio (2015: 23, emphasis in the original) write, "... closure is a context-dependent determination, to the extent that it is always realised with respect to a set of specific boundary conditions, which include several external (and independent) constraints acting on the system." Closure does not include all constraints that are relevant to a system's dynamics, but only those constraints fulfilling the definition proposed by the theory, namely, constraints that are both enabling and dependent.

The same goes for a bacterium as a biotic item. A bacterium will be internal to a biological individual if it is both dependent on physiological processes involving at least one constraint operating within it and enabling of physiological processes involved in the causal production of at least one such constraint. If it is an exclusively enabling or exclusively dependent constraint, a bacterium will be external to the biological individual, even if found within its physical boundaries. In the terms of the theory of biological autonomy, this latter fact does not matter, as individuation is done on functional grounds.

We expect it is clear at this point that the theory of biological autonomy offers conceptual resources to deal with the nature of biological individuals, in particular, physiological individuals. Based on this theory we can ascertain the boundaries of systems from our knowledge of interactions, by considering what kind of interactions among systems' components provides a basis for individuating them. In these terms, individuality is explicated in terms of causation, what raises the interesting point that, on this account, individuals needed for causal claims to be constructed are themselves defined causally.

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What we need, then, is to derive a scheme to pick up individuals in a set of many interactions based on models of interactions that rely upon criteria provided by the theory of biological autonomy. The fundamental basis to pick up biological individuals in terms of this theory lies precisely in the closure of constraints, which defines biological individuality (even though further specifications will be needed to diachronically deal with identity, as we will see below). Constraints subject to closure constitute biological organization and allow us to pick up biological individuals by establishing which constraints acting over the thermodynamic processes and reactions in a given set of interactions are both enabling and dependent. This set of enabling and dependent constraints constitutes the organization and, accordingly, the individuality of a living system, while constraints that are either dependent but not enabling or enabling but not dependent connect this system with other systems.<sup>1</sup> In these terms, the claim that a system shows organizational closure does not conflate the self-specification of its functional boundaries with a requisite of functional self-sufficiency (Bich, 2019). One of the theoretical consequences is that we may be able to define a degree of openness for biological individuals ascertained based on closure of constraints through a ratio between the number of constraints affecting their dynamics that are both enabling and dependent, and the number of constraints that connect them to other systems (being exclusively enabling or exclusively dependent). Surely, this is a theoretical idea demanding further development.

A view that has gained wide currency lately is that biological individuality comes in degrees (e.g., Clarke, 2010; Strassmann & Queller, 2010; Godfrey-Smith, 2013; Huneman, 2014a,b; Sterner, 2015; Wilson & Barker, 2021). To ascribe individuality we can use several criteria spelled out in different concepts of individuality - and, thus, between a set of books in a library shelf, which is evidently not an individual but just a set of multiple things, and a paradigmatic individual like ourselves, there are many intermediaries that are individuals to a larger degree than the former (displaying more features regarded as characteristic of individuality, according to some underlying concept) but are also individuals to a lesser degree than the latter. The individuation of living systems based on closure of constraints makes it possible to attribute different degrees of individuality to them, in inverse relation to their degrees of openness. For example, from cells to organisms to ecosystems, we can think of biological individuals in different degrees. By considering how the functional components of a biological organization are wired together to collectively achieve self-maintenance, we can also propose criteria to characterize the degree of functional integration of different systems and, accordingly, the degree of internal cohesion of a system, i.e., the different ways and extents in which constraints are mutually dependent and realize closure (Bich, 2019; Bich & Bechtel, 2022b).

By being able to account for biological individuals showing different degrees of functional integration and internal cohesion, the theory can be applied to individuate even challenging cases like ecological systems, avoiding to take their openness as an insurmountable barrier for individuation (El-Hani et al., 2024). These systems and other weakly individual systems can be ascertained based on the set of enabling and dependent constraints constituting their organization, while connected to other systems through exclusively enabling or dependent constraints, as explained above. In these terms, we can characterize ecosystems as biological individuals with no commitment to the idea that they are superorganisms. After all, there are important differences that hinder the application of the concept of organism to ecosystems, as their relative lack of internal cohesion and functional integration in comparison to at least paradigmatic organisms. By taking closure of constraints as a basis to ascertain biological individuals, we can uncover a shared characteristic between ecosystems and organisms despite their being rather different kinds of individuals. In short, closure of constraints provides a more general criterion to biological individuality, which can lead to the identification of distinct individuals in the biological domain, some of which are organisms, some of which are not so.

### 15.5 A second implication of the theory: Biological individuality based on closure of constraints and a processual view of life

Let us turn now to a second point. A theory-based approach to biological individuality grounded on closure of constraints, as a distinctively biological causal regime, entails a processual view of living systems, as it assumes an inseparability between what living systems are - their "being", individuality, identity - and what they do - their "doing", as reflected in their metabolism, without which they cannot be, as they are not able to self-maintain (Jonas, 1966/2001; Moreno & Mossio, 2015). To assume a processual view on living systems (see, e.g., Nicholson & Dupré, 2018) does not entail that we can simply avoid the whole issue with individuality, since it is still the case that to understand living phenomena, including causal understanding, we will need to somehow individuate biological individuals standing in relation to one another, even if they are conceived as just bunches of coexisting processes in time and space for a given (and variable) period. We can indeed explain what are individuals in terms that do not enter into tension with a processual view. As Dewey (1938: 135) writes, "To remain and endure is a mode of action". Biological individuals can be conceived as coexisting processes that remain temporarily and spatially interconnected and cohesive (to different degrees), such that we can identify them as enduring as systems for a given temporal span, while they are constantly traversed by processes that cross the boundaries between their inner medium and their external environments, up to a point in which they reach the limit of their self-maintenance as living systems. Biological individuals, while enduring, undergo modification. Accordingly, "continuity is not bare repetition of identities" (Dewey, 1938: 245), such that to diachronically ascribe individuality we need to reidentify the same biological individuals in different time-slices.

We can consider, then, a difficulty related to ascertaining biological individuals based on closure of constraints, which results from their dynamics across time. Biological systems are in constant flow, they are always crossed by various fluxes, their parts are constantly replaced by other parts that are in some sense (functionally) equivalents, among other dynamical aspects. How can we accommodate these dynamics while individuating and identifying living systems based on closure of constraints?

We need to deal, in short, with a fundamental issue related to identity, namely, that it can be ascertained both in a single time-slice (synchronically) and across time, in successive time-slices (diachronically) (Boniolo & Testa, 2012; Huneman, 2014a). No matter how one conceives of identity, along the spectrum from more stringent to more inclusive interpretations discussed by Montévil and Mossio (2020), one can investigate both whether, say, a given organism meets the criteria of membership to a reference class here and now, and whether it keeps complying with them over time. The more stringent the definition of identity, the more restrictive the reference class, and the less it tolerates changes across time.

Then, a first point to consider is that an account of biological individuals based on closure of constraints is rather inclusive, and, thus, while it may seem synchronic in nature, it is not so, and, accordingly, does not leave aside living systems' diachronic changes. To put it shortly, the theory of biological autonomy has resources to deal with diachronic individuality. Firstly, the relations between constraints subject to closure involve time, as explicitly shown in the different time scales in which the very constraints are defined. An important aspect of the theory of biological autonomy is that it explicitly includes in its theoretical treatment that not all entities (or configurations) involved in closure, i.e., constraints, as well as their causal interactions among themselves and with processes, relate to the same time scales. This is relevant because this temporal aspect of living organization is not often sufficiently recognized. The relevant opposition between diachronic and synchronic in this case is not, therefore, between instantaneous and temporally extended (Huneman, 2014a), since the very idea of closure of constraints concerns a set of entities (or configurations) that extends in time. While some interactions involving constraints and processes are rapid, taking place over short time intervals, others are slow and extend through longer time intervals.

Secondly, if we consider that in the biological domain an important aspect of individuality is the persistence through time of identical or at least similar features in biological individuals, we may argue that closure of constraints persists while systems maintain themselves, despite changing across time, exactly because enabling and dependent constraints constituting it are replaced by other constraints through the system's dynamics, and these constraints carry out equivalent functions in relation to the self-maintenance of the systems. A system's closure of constraints can be thus maintained despite continuous turnover of components. Thus, if we wish to capture the persistence of biological individuals through successive time-slices, we can stipulate that, for such persistence, it may be the case that (a) a topology of relations between enabling and dependent constraints is the same or sufficiently similar (as established, say, by an analysis of the network of relations among constraints in the system; for instance, enabling and dependent constraints can change while some network metrics remain the same, e.g., modularity); and/or (b) an equivalent set of functional roles (as established by functional analysis of processes contributing to the system's self-maintenance) is preserved in those successive time-slices.<sup>2</sup> In this manner, we can say that by satisfying (a) and/or (b) we can reidentify the same biological individual in the different time-slices, being able, thus, to deal with the question of diachronic individuality (Huneman, 2014a). Ultimately, this will mean that there is an overlap between the systems identified across the successive time-slices, since constraints, relations and/or functions can be reidentified across these time-slices as included in the systems of interest, entailing a continuity of the systems across time as they keep changing their components, topology of relations and/or functions. By identifying such overlaps between individuals as delimited by closure of constraints across successive time-slices, we will be in fact establishing the persistence of individuality in terms of the robustness of diachronic individuals, defined according to the theory of biological autonomy in terms of the maintenance of a topology of relations among constraints and/or of functional roles played by constraints.

It appears as an important question for theoretical and empirical research, then, to establish what type of robustness can be realized by distinct biological individuals that can be picked up by using the theory of biological autonomy to identify specific patterns of causal interaction among constraints leading to closure in living systems. This will amount, ultimately, to two lines of enquiry: (i) what are the basic properties of a diachronic dynamics of individuality? (ii) which distinct kinds of individuality can we find among living systems and how can we rank their capacities to be dynamically stable and persist? These questions are being currently investigated in our team.

However, in order to account for diachronic changes in living systems, properly considering their contingency and variability, the ideas above will not be sufficient. We need to consider a principle of variation, as stated by Montévil and colleagues (2016). This principle builds on evolutionary biology and states that biological objects can vary in a stronger sense than objects described by physical theories. We need to complement, then, a relational ascription of identity, as established by closure of constraints, with a genealogical conception of identity that allows us to consider changes undergone by constraints across evolutionary time, as proposed by Montévil (2019) and Montévil and Mossio (2020) (see Figures 15.3 and 15.4). After all, constraints exist as products of a historical process and, accordingly, we cannot theoretically describe biological individuals sufficiently by considering only invariants such as constraints and invariant-preserving transformations (symmetries) that would give a generic



*Figure 15.3* Integration of genealogical and relational conceptions of identity. The relational conception considered here is based on closure of constraints, as explained in the body of the text (see also Figure 15.2). This conception is, however, insufficient to define living systems as specific objects, which vary along evolutionary time in a contingent manner. This is so because living systems are fundamentally historical, and, as such, the constraints operating in their organization, as closure of constraints, are only valid for some specified interval of evolutionary time, i.e., they can change over time. Elaborated by Maël Montévil.

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meaning to the observed characteristics. In fact, regularities in a living system come from a history and are maintained collectively in a given context. Constraints can change over time as living systems continue to generate a history across physiological, developmental and evolutionary time scales. There is, therefore, an intrinsically diachronic character to living systems that must be accommodated when delimiting the closure of constraints (Montévil, 2019).



*Figure 15.4* A historical perspective on organizational closure of constraints. A new symbol is introduced,  $\chi$ , to represent historical aspects of organism's identity.  $\chi$  relies on a genealogical connection with an ancestor and complements the relational description of identity, based on closure of constraints. It accommodates past variations and contexts that have shaped the present (class of) organism(s) in evolutionary time. In (a), there is a global closure involving  $\chi$ , while (b) includes an additional partial closure of constraint in relational terms. Zigzag arrows: relational constraints; straight arrows: processes; spring arrows: constraining effects that relate to  $\chi$  and are therefore not entirely relational; dashed arrows: hypothetical processes constrained by spring arrows. Constraints are defined in relational terms while  $\chi$  is defined genealogically, by reference to the past. Elaborated by Maël Montévil.

Source: Reproduced under permission from Montévil and Mossio (2020).

#### 15.6 Concluding remarks

The theory of biological autonomy provides a fruitful way to study living systems as individuals at different levels, showing different degrees of individuality, by taking all such systems to show closure of constraint, self-determination, autonomy, among other features. Taking Beisbart's arguments into account (2023), it is worth highlighting that this theory defines living systems as biological individuals by appealing to causal knowledge, as we stressed above, and provides a basis for successful investigation of these systems as units, leading to novel inferences for explaining phenomena related, e.g., to functionality and regulation (Mossio et al., 2009; Saborido et al., 2011; Nunes-Neto et al., 2014; Bich et al., 2016; Bich & Bechtel, 2022a; El-Hani et al., 2024).

Biological individuality is based, in this theory, on closure of constraints, as a distinctively biological causal regime. A biological individual (in a physiological sense) is identified in functional terms, based on organizational closure of constraints, realized by all constraints that are both enabling and dependent within that system, constituting its organization. In this manner, we can identify a biological individual on functional terms, explain its persistence along time (if we include contingent changes in constraints subject to closure) and characterize its dynamics and degree of openness.

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#### Notes

- 1 It is interesting to point out that this theory allows us to ascertain whether a given constraint is internal or external to a biological system or individual in the absence of a full model of a given set of interactions, something that is quite useful for modelling purposes. We just need to establish whether that constraint is both enabling and dependent in a given set of constraints. Notice, also, that we can set the boundary of the systems being modelled using the theory of biological autonomy so as to include smaller or larger regions of space, depending on our research purposes. Suppose we identify the organization of a system  $S_1$  based on closure of constraints and, also, some constraints connecting it to another system  $S_2$ , at a given scale, for a given research goal. If we intend to tackle another research goal, we can expand our model to a larger scale such that both  $S_1$  and  $S_2$  now fall within the same overarching system  $S_3$ , including enabling and dependent constraints that realize closure of constraints encompassing both  $S_1$  and  $S_2$ . Those constraints that were just enabling or dependent when we were modelling only  $S_1$  now can be described as both enabling and dependent if they are produced under the influence of constraints or influence the production of constraints connecting it to other systems in its environment.
- 2 Given the necessary generality of an account of biological individuals based on the theory of biological autonomy, the precise qualification of what would be "sufficiently similar" or "equivalent" will depend on the relevant models derived from the theory to deal with particular domains of phenomena. The notion of closure of constraint is an abstract concept that always needs fleshing out when one intends to model its actual realizations in specific biological systems.

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