Natural Kinds as Homeorhetic Dynamic Systems

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Abstract: Philosophers have become increasingly aware of the difficulties that plague accounts of kinds with objectively determined boundaries, and generally recognise that scientific taxonomies are shaped by human pragmatic interests and non-epistemic values. Against this trend, we propose an account of kinds conceived as dynamic entities, characterised by qualitatively distinct and robust trajectories originating from bifurcation events in the development of complex systems. We argue that the Homeorhetic Dynamic Kinds account (HDK) can be applied to systems investigated in a variety of disciplinary contexts, ranging from biology, medicine, and the social sciences. Shifting the focus from a synchronic (*homeostatic*) to a dynamic and processual (*homeorhetic*) perspective, we show that HDK allows a better characterisation of discontinuities among kinds. We then outline its implications for pluralism, particularly how HDK can help us to understand how scientific categories are shaped both by ontological aspects of developmental trajectories and by pragmatic, value-laden considerations.

Keywords: Natural Kinds; Homeostatic Property Clusters; Historical Kinds; Homeorhesis; Epigenetic Landscape

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[1] This is a *pre-acceptance version* of the manuscript, which was submitted for consideration for publication.

1. Introduction: Kinds, Discontinuities and Boundaries

Since its revival in the Nineteen-Seventies, philosophical research on natural kinds has been dominated by two traditions (Bird & Tobin 2022; Crane 2021). According to *essentialism*, natural kinds are identified by a small set of necessary and sufficient properties. Such properties define boundaries that distinguish sharply between the members of different kinds. In this view, a given entity (an organism, say) belongs to a single kind (e.g., a species) in virtue of a set of characteristics (its genetic endowment, for example) which determine unambiguously its nature. Despite its intuitive appeal, essentialism has been largely abandoned by philosophers of science. Its main weakness is that various paradigmatic kinds of scientific significance – species, pathologies, and even chemical substances – seem to lack essential properties of the required sort (Dupré 1993; Kendler et al. 2011; Mayr 1963; Weisberg 2005). Many philosophers have thus shifted towards accounts that dispense with necessary and sufficient conditions of membership. The most prominent one is the view of kinds as *property clusters*, originally proposed by Richard Boyd (1991, 2000) and further developed by several other theorists (e.g., Griffiths 1999; Millikan 1999, 2017; Khalidi 2013, 2018; Slater 2015).

Although it is generally considered superior to essentialism, the cluster view has raised a number of worries, particularly about the identification of boundaries that reflect sharp discontinuities in nature. The 'naturalness' of kinds is usually associated with their objective existence and independence from human interests (Bird & Tobin 2022). But if clusters lack necessary and sufficient conditions of membership, their boundaries are indeterminate: which entities belong to a given kind must be decided by theorists, rather than by the way the world is. Some philosophers consequently see a tension between the criterion of independence from human interests and the fuzziness of kinds – a tension that, they argue, should be resolved by dropping the concept of natural kind (e.g., Brigandt 2022; Chakravartty 2023; Ludwig 2018). Others instead argue that the tension is only apparent, and that the lack of sharp boundaries does not threaten the reality of kinds (e.g., Boyd 2000; Khalidi 2013; Magnus 2012; Slater 2015).

In this paper we shall not directly take sides on this controversial issue. The claim that kind members are often continuously distributed in the space of properties – the *continuity thesis*, as we shall call it – is vindicated by real and important cases, which we do not intend to challenge here.[2] We also agree that some scientific categories are drawn in ways that seem

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[2] The continuity thesis in fact informs a variety of different approaches towards natural kinds, including eliminativism (Brigandt 2022; Chakravartty 2023; Ludwig 2018), constructionism (Boyd 2000; Haslanger 1995), and

ontologically arbitrary. We would like to argue, however, that in other numerous and equally interesting cases natural discontinuities do exist and can be observed at specific stages in the development of systems. Such cases, if we are right, justify a realist attitude toward certain kinds that constitute the target of human epistemic and non-epistemic interests, in a way that will be explained later.

To appraise the scope and significance of the continuity thesis we shall advocate a shift from a static (or *synchronic*) to a dynamic (or *diachronic*) perspective; that is, from a focus on the properties that are shared by the members of a kind to their common fate or trajectory through time. To highlight this shift, we label our proposal the *Homeorhetic Dynamic account of Kinds* (or HDK, from the Greek word 'homeorhesis', meaning 'similar flow'). The key insight of HDK is that, in order to identify discontinuities among kinds, we must take a time-sensitive perspective: distinct kinds correspond to different trajectories that individual entities take throughout their developmental/evolutionary history. We shall argue that this account encompasses, but does not exclude, traditional cluster theories of natural kinds. We shall also demonstrate that it departs significantly from those accounts that seek to supplement property clusters with historical essences. Most such accounts, in fact, conceive of kindhood in terms of common ancestry and property-sharing, rather than process identity. According to HDK, in contrast, kindhood is determined by continuity *within* and discontinuity *across* processes, which is compatible with the idea that the members of a kind may possess different properties at a given point in time.

The paper is organised as follows. §2 illustrates some concrete examples of the continuity problem, or why some scientific categories do not seem to reflect objective boundaries. Using examples from social science and biomedicine, in §3 we show that some boundaries can be identified by a dynamic perspective. The main features of the HDK account are outlined in §4, while its implications are discussed in §5. In particular, we point out that HDK provides a more precise account of the involvement of human interests in scientific classifications: although kindhood criteria for HDKs are largely based on ontological discontinuities in systems' dynamics, not all discontinuities are relevant or interesting for scientific research and its practical applications.

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pluralism (Dupré 1993; Khalidi 2024a; Magnus 2012). See O'Connor (2019) for representations of property clusters in multidimensional spaces.

2. The Continuity Problem in Science

Philosophical theories traditionally conceive of kinds as sort of 'macro-entities' whose parts – individual entities – are identified by similarity among some of their properties. Such theories typically emphasise the stability of properties and their correlations, which provide an ontological basis for successful induction (Boyd 1991, 1999; Kornblith 1993). Boyd's Homeostatic Property Cluster (HPC) theory is a classic example: it is a *static* view, where kinds are pictured as sets of entities or systems that gravitate towards a stable state. And crucially, since statistical correlations are sufficient for inductive inference (Slater 2015), no sharp discontinuity is required for property clusters to do the epistemic work expected from kinds.

Many cases from science bring support to this view. There is no doubt, for example, that health and disease are extremely important concepts in psychiatry and medicine. It is also clear, however, that distinctions between pathological and healthy states (or individuals) are often murky, and that diagnoses are typically influenced by pragmatic considerations.

Take mental disorders: the psychiatric community has recently redefined numerous conditions to emphasise their continuity with healthy states (Banicki 2020; Keil & Stoecker 2017; Phillips 2020). Traits that are considered typical of autism, psychosis, and mood disorders, to name a few, can be observed in the general population in mild forms, suggesting that categorical distinctions based on diagnostic thresholds are somewhat conventional or normative (Amoretti et al. 2021; Happé & Frith 2020; Haslam 2014; Hyman 2021; Johns & van Os 2001; Sucksmith et al. 2011). The fifth edition of the Diagnostic and Statistical Manual of Mental Disorders (DSM-5, APA 2013) reflected this trend by reclassifying autism sub-categories, for instance, within a wider group of conditions (Autistic Spectrum Disorder) that differ *quantitatively*, rather than categorically, from each other (Serpico & Petrolini 2023).

Such examples are not limited to psychiatry. When traits are operationalised dimensionally, and categories are defined in terms of multiple variables or properties that vary on a quantitative scale, individual scores are typically distributed along a continuum in a multi-dimensional space. Figure 1a, for example, plots the body mass index (BMI) values of a human population. BMI represents the ratio between individuals' height and weight, which are both distributed continuously along a given range (Figure 1b). Because empirical data are arranged in a cloud-like fashion in this property space, it is not surprising that BMI values form a continuum.

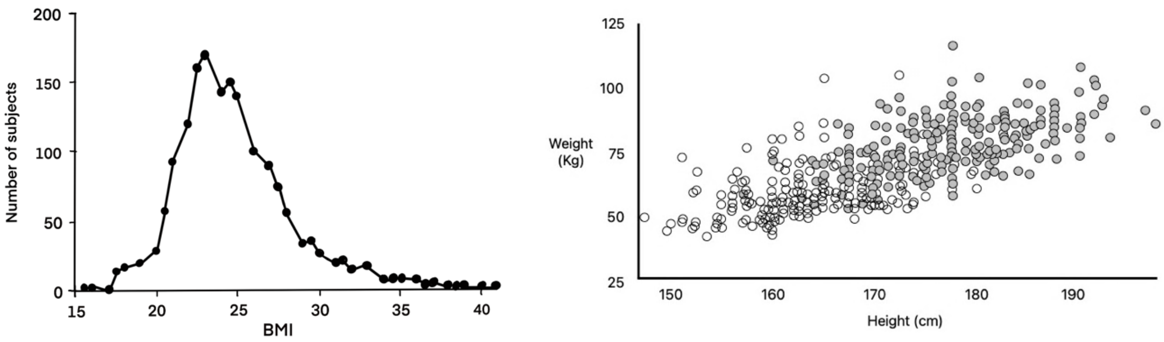

Figure 1: (a) Distribution of BMI values in a human population (adapted from Nuttall 2015); (b) Distribution of height and weight, divided by gender (adapted from Heinz et al. 2003).

One possible reaction is to exclude such cases from the realm of (genuine) natural kinds, noticing for example that they are not identified by a single homeostatic mechanism. But this would risk excluding too much: practitioners often must – and do – distinguish between pathological and healthy BMI values. To account for such cases, some philosophers acknowledge that scientific categories can be epistemically solid or reliable (and thus, fall within the scope of natural kind theory) regardless of whether they are sustained by a single causal mechanism. According to ‘liberalised’ cluster theories, the properties of many kinds in the special sciences are held together by multiple mechanisms or are merely correlated (Boyd 1999; Khalidi 2013; Onishi & Serpico 2022; Slater 2015). Classificatory decisions, as a consequence, ought to be dictated to some extent by pragmatic, value-laden considerations.

This is a plausible approach, which we do not intend to question here. But we would like to suggest that the practice of distinguishing between health and sickness can sometimes be given a more solid justification. Taking a developmental perspective for example allows one to see that individuals at the extremes of the curve (low and high BMI) fall under qualitatively distinct categories. The metabolic states of severely obese or undernourished people are characterised by a remarkable robustness, which constrains future development due to the long-lasting impact of factors like chronic stress and inflammation, adverse experiences, and consumption of ultra-processed food, especially in childhood (Furman et al. 2019; Serpico & Borghini 2021; Vineis et al. 2023). Some individuals with intermediate BMI values, on this view, may be diachronically converging towards one of the extreme (pathological) regions of the distribution: what appears as a continuous cluster at a particular point in time, in other words, is better described as a mixed bunch of stages in a set of potentially heterogeneous trajectories (other examples can be found in the distribution of IQ values, see De Boeck et al. 2005; Michell 2012; Serpico 2018).

Another way to put it is that continuity may be a 'synchronic artefact' – an illusory effect created by the adoption of a limited temporal perspective. Such artefacts are ubiquitous in science. Social scientists, to take another example, are aware that the choice of temporal scale is crucial for the identification of empirical patterns of theoretical interest. Figure 2 plots the relationship between economic growth and public debt in several countries over a period of sixty years. Each point is a temporal 'snapshot', representing the GDP growth and debt/GDP ratio of a given country in a given year. The regression curve reveals the existence of an inverse statistical relation between these two variables: fast-growing countries tend to have low debt-GDP ratios, whereas severely indebted countries tend to grow sluggishly.

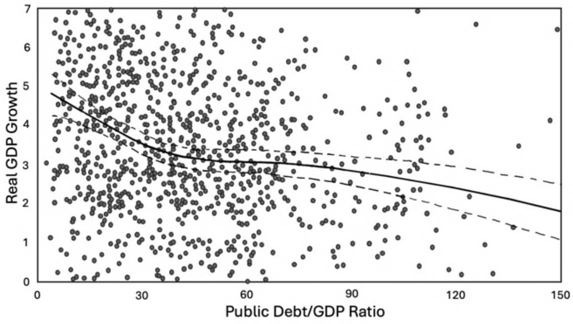

Figure 2: Real GDP growth vs. public debt/GDP, country-years, 1946-2009 (adapted from Herndon et al 2013).

Is it possible to classify countries into clearcut categories according to these characteristics? In practical terms, it would be very helpful to draw a boundary between countries that are doomed to stagnation and countries that are not. Such a distinction could inform the policies of governments and intergovernmental institutions, such as the International Monetary Fund, concerning money-lending or the restructuring of public debts, for example. But the distinction between 'pathological' and 'healthy' levels of debt, unfortunately, seems irreducibly fuzzy.[3]

The data plotted in Figure 2 span a period of half a century or so. This may seem appropriate, given the outlook of policy-making. But there is no guarantee that such a temporal scale is appropriate to analyse the dynamics of large, complex, and relatively inertial systems like nations. Several historians instead focus on *secular* cycles in population and economic growth,

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[3] The consensus among experts is that attempts to identify a quantitative threshold separating growing from stagnating economies have failed so far. See, for example, the controversy over Reinhart & Rogoff's (2010) 'ninety percent' threshold, in particular Herndon et al. (2013), Égert (2015), and Heimberger (2023).

with average amplitudes of two to three hundred years (Braudel 1988; Cameron 1989; Goldstone 1988; Fisher 1996; Turchin & Nefedov 2009). The idea is that working with a larger temporal scale should reveal trajectories and discontinuities that would not emerge from a short-term analysis of statistical correlations. If nations are slowly evolving dynamic systems, short-term correlations between their occurrent properties might provide flimsy and unreliable information about their boundaries.

These suggestions are worth exploring in more detail. As we shall see in the course of this paper, many kinds are best characterised as dynamic processes with common trajectories, rather than as sui-generis macro-entities. A diachronic perspective can make discontinuities appear in place of what would otherwise look like synchronically continuous distributions of properties. Borrowing a terminology from developmental and systems biology, we shall call these natural kinds *Homeorhetic Dynamic Kinds* (HDKs).

3. Case Studies

To articulate the HDK account, in this section we analyse cases where discontinuity emerges from a seemingly continuous order, and where historical canalisation effects seem particularly strong. These cases highlight different aspects of our account, which will be developed in §4. In later sections we will compare the HDK account with existing theories – in particular with theories that appeal to homeostatic mechanisms and historical essences.

3.1 The rise and fall of nations

As a first example, we shall focus on a classic issue in demography, geography, economics, and political science. Major thinkers like Adam Smith, Robert Malthus, and Alexis de Tocqueville devoted hundreds of pages to explain the success of expanding nations in the age of empires. But explaining the fate of nations – their prosperity, decline, and eventual demise – is still urgent today, as the increasing volume of research demonstrates (e.g., Turchin 2007; Diamond 2011; Acemoglu & Robinson 2013). Following an established practice, we shall denote the basic unit of analysis in this area of research using the term ‘polity’ (e.g., Ferguson et al. 2000; Hix 2007). A polity is a socio-political organisation that coordinates the behaviour of numerous social groups, consisting of thousands, sometimes even millions of individuals. Such organisations tend to share a handful of characteristics: polities control territories and mobilise resources for collective projects (building infrastructures, waging war); they usually identify membership by means of cultural markers (language, religion, real or fictional history, geographic proximity); and enjoy a significant level of collective solidarity.

Understanding why some polities are more successful than others raises a typical instance of the continuity problem. Some states are very small (Lichtenstein) and others very large (China), with almost every intermediate size in between. Their growth rates – measured in terms of population, or per capita income – are also continuously distributed: there do not seem to be obvious 'gaps' or 'boundaries' that would justify a non-arbitrary classification into separate kinds. Things, however, look different from a dynamic perspective: over time, the growth and fall of nations seem to follow distinctive patterns or trajectories (Kuznets 1971; Modelski 1978; Olson 2022).

In the course of several centuries, polities alternate periods of stability with periods of fast growth or decline, but do not all evolve in the same way. Some states become empires, while others remain relatively small for a long time. Both small and large polities endure periods of crises which may eventually lead to their collapse and disappearance. Scientists interested in the *longue durée* of history have formulated various hypotheses concerning the way in which polities are 'canalised' into these trajectories (Braudel 1988; Goldstone 1988; Cameron 1989; Fisher 1996; Turchin 2007; Turchin & Nefedov 2009). Such theories try to identify the factors that make growth possible, but also the structural constraints that impose limits on the expansion of polities, and that govern cyclical processes of adjustment.

To give an idea, we shall focus here on the demographic-structural theory proposed by Jack Goldstone (1988, 1991) and developed in mathematical form by Peter Turchin (2003). The theory is meant to apply primarily to agrarian states, which constitute the most common economic and political organisations during the bulk of recorded human history (from the invention of writing until the industrial revolution). According to the Goldstone-Turchin theory, the key engine of growth during the early phases of polity expansion is demographic growth itself: increases in the size of population make increasing quantities of surplus available.[4] Part of the surplus is appropriated by governments and elites (land owners), who take it from peasants and invest it partially in public projects (roads, deforestation, irrigation systems) and technological innovation, fuelling further growth (Boserup 1966). Another consequence of increased surplus, however, is the expansion of governments and elites. State expenditures increase to support large armies and bureaucracies, while the elites engage in conspicuous consumption (Bagwell & Bernheim 1996). As a consequence, over time there is a tendency for the growth of surplus to diminish at the margin.

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[4] Surplus is defined as the difference between the resources that are produced by a population and those needed for its subsistence.

This dynamic trajectory is represented schematically in Figure 3 (adapted from Turchin 2003): the solid curves (*N*) track changes in the size of a polity's population, while the segmented curve (*S*) represents the typical trend of state expenditure. The horizontal lines (K_0, K_1, K_2) represent different 'carrying capacities' of a human ecosystem (Cohen 1995) – the 'ceilings' that constrain population growth, depending on exogenous factors such as geography (the amount of land that can be exploited for agriculture), as well as endogenous factors such as population size and state investments.

Notice that the solid curve (demography) increases steeply in the early stages of state development but begins to slow down before it reaches 'carrying capacity' k_1 (where it would exploit its maximum productivity level). This phase of diminishing surplus, according to the Goldstone-Turchin model, generates *tipping points* in the trajectories of polities. The historical record suggests that different channels of development open up at this stage: some polities undergo a period of severe crisis leading to disaggregation and eventually the collapse of the state (N_0). The population then reaches an equilibrium only at k_0, the carrying capacity of a stateless society. Other polities experience instead a period of internal strife, characterised by in-fighting among elites that try to maintain high levels of extraction from a declining population (N_1). This trajectory may persist for a long time and eventually trigger a new period of growth and a new cycle. The third possible solution is territorial expansion, which raises carrying capacity (from k_1 to k_2 in the picture), and creates the conditions for a longer period of growth (N_2). 'Imperial states' are thus able to delay stagflation, but their expansion typically faces limits which sooner or later will result in another crisis.

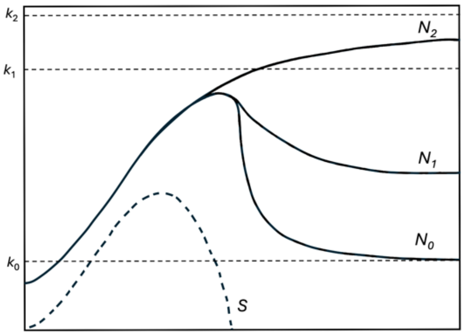

Figure 3: Three trajectories (N_0, N_1, N_2) in the growth of the population of an agrarian society, following a tipping point. The S curve represents the typical trend of government and elite expenditure under fixed resources (adapted from Turchin 2003).

The fate of a polity or nation, according to this perspective, is not determined merely by its occurrent properties, but also by its stage of development in a dynamic process. Polities that may look similar from a synchronic point of view are often *canalised* towards radically different outcomes. Another important point, for our concerns, is that cycles extend over entire centuries, and include both long stretches of relative stability and periods of sudden change. The specific mechanisms that sustain stability can be captured by equilibrium models, which are used to make a number of locally successful inductive inferences. Population growth, for example, can be curbed during long stretches of time by homeostatic mechanisms such as internal warfare, crime, famines, epidemics and migration. But by focusing on local equilibria one risks missing the point that homeostasis is a *stage* within a broader trajectory. The temporal scale of the analysis is crucial: different systems evolve in different ways because they are canalised onto different pathways at critical thresholds (tipping points). The notion of homeorhetic kind, as we shall argue, is able to capture this ontology better than alternative accounts.

3.2 Cancer and cell types

The explanatory power of a dynamic approach is not limited to the ontology of social science. Cancer research must routinely deal with various facets of the continuity problem: How can we draw clear-cut distinctions between tumoral and non-tumoral cells? What are the boundaries between health and cancer, or, in other words, where does cancer begin? The very notion of tumour seems fuzzy: cancer cells exhibit significant plasticity, allowing them to undergo complex phenotypic transitions and contributing to intra-tumour heterogeneity (Batlle & Clevers 2017; Pérez-Gonzàlez et al. 2023; Ponomarev et al. 2022). Due to this plasticity, the fate of some cells appears indeterminate, indicating the existence of ‘grey areas’ between cancer and non-cancer. In this section we would like to argue that the appearance of continuity partly depends on taking a *synchronic* perspective. A temporally sensitive perspective allows us to see cancer as a robust and *qualitatively distinct kind of process*. Cancer, in other words, is best conceived as a HDK.

In principle, it seems possible to conceptualise cancer as a property cluster, as a process, or as a mixture of both. Khalidi (2013: 181-188), for instance, proposes to see cancer as a *kind of process* reducible to *cancer cell entities*, where the latter constitute the foundations of the medical condition. In this view, the various “hallmarks” of cancer form a cluster where one key property (a genetic mutation) determines auxiliary properties such as proliferative signalling, replicative immortality, metastasis, etc.[5] The genetic mutation thus represents a *necessary* feature of cancer (the homeostatic mechanism, say), while the other characteristics are merely *sufficient*.

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[5] Other hallmarks of cancer include evading growth suppressors, resisting cell death, inducing angiogenesis, activating invasion (see Hanahan & Weinberg 2011).

Classical taxonomic projects, similarly, tended to focus on the cell-of-origin and organic material of different cancers, or relied on the view that different cancers are driven by different genetic mutations (Creighton 2023; Ding et al. 2018; Salem et al. 2015), as in a HPC-like interpretation of cancer. In recent years, however, research has shifted towards more dynamic and processual approaches, departing from the view that the original genetic mutation could provide the basis for the identity of cancer cells. Both new and old approaches, to be sure, recognise that cancers are historical entities, whose characteristics are inherited at later stages (e.g., mutations found in the original tumour are also found in remote metastatic cells; see Plutynski 2021). But a stronger emphasis on the processual character of cancer follows from two main considerations.

First, deep sequencing and ‘omics’ technologies, focusing on multi-level properties (e.g., gene-expression profiles, transcriptome, proteome), have revealed inconsistencies in the paradigm of driver mutation: tumours’ tissues are far less homogeneous than expected, presenting multiple molecular subtypes both between different regions of a tumour in the same individual and between instances of the same cancer across individuals (Brock & Huang 2017; Creighton 2023; Roberts et al. 2018). Tumour heterogeneity characterises phenotypic features, too – including metabolism, motility, and metastatic potential – and complexity is exacerbated by entities and processes that interact at different spatial-temporal scales (Burrell et al. 2013; Geyer et al. 2010; Martelotto et al. 2014; Plutynski 2021). Although driver mutations may be causally necessary for pathogenesis, to be sure, many mutations may actually be *the result*, rather than the cause, of carcinogenesis (Baker 2015; Bertolaso & Dupré 2018), suggesting a complex relation between lower-level (e.g., genetic) and higher-level (phenotypic) properties of cancer cells.

Second, it is now widely acknowledged that cancer cells have features that are associated with de-differentiation processes, or a kind of “regression” to stem-like developmental states (Friedmann-Morvinski & Verma 2014; Yamada et al. 2014). For example, cancer stem cells (CSCs) across various tumours can undergo phenotypic transitions in response to environmental stimuli and stochastic processes (Batlle & Clevers 2017; Pérez-Gonzàlez et al. 2023; Ponomarev et al. 2022). The upshot is that, in order to understand cancer progression and enhance intervention, we need to focus not just on the conditions that make cancer *emerge*, but also on those that make it persist over time.

Embracing this dynamic perspective, recent taxonomic projects (e.g., *iClusters,* see Boniolo & Campaner 2019) reflect a shift towards a more dynamic view of cancer categories, where the latter are open to revision in light of the clinical development of patients and the evolving information on their conditions. Similarly, many researchers have started to look at systemic, phenotypic characteristics to understand how cancer emerges from typical cellular development. This phenotype-based approach often leverages models and methods from Dynamical Systems Theory (DyST) and Waddington's epigenetic landscape metaphor (Davila-Velderrain et al. 2015; Ferrell 2012; Huang 2012; Huang & Kauffman 2013; Mojtahedi et al. 2016; Moris et al. 2016). As we shall explain, these approaches provide a conceptual architecture that is consistent with the HDK conception of kinds.

Processual approaches understand cells as dynamic systems, the state of which can be described, at a certain time, by a set of time-dependent variables (different proteins, transcription factors, and Gene Regulatory Networks, GRNs): "imagine an abstract space termed the state space of the system, [where] the state space comprises all the theoretically possible states a cell can exhibit; each point in this abstract space represents one particular expression profile. [...] Furthermore, it is assumed that the cell state at a certain time and the cell state at a later time are connected by a state trajectory in a causal way" (Davila-Velderrain et al. 2015: 2-3). Phenotypic transitions are here conceived as perturbations in the system that generate *tipping points*, *switch points*, or *critical-state transitions* in the developmental trajectory. Such perturbations, which can be caused by environmental factors (e.g., nutrients, signals, and oxygenation), alterations in GRNs, and systemic conditions such as chronic inflammation or toxic stress, can destabilise the system and force a population of cells into a new pathway (metaphorically, a different valley in the epigenetic landscape).

This approach makes sense of cancer's *plasticity* and *robustness*. Cells are plastic and flexible systems (relevant perturbations can generate new trajectories) but, under certain circumstances, cell development can become *canalised* into specific trajectories. One way to represent this feature is to understand cancer as an *attractor state,* namely, a subregion of phenotype states towards which the trajectories tend to converge due to their higher stability. The robustness of cancer is thus explained by the tendency of a system to return to a given state despite minor oscillations and perturbations.[6] The combination of plasticity and canalisation

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[6] In most cases analysed in DyST models, phenotypic transitions are *qualitative*, although other transitions appear to be *gradual* (Jaeger & Monk 2014). The latter case applies, for instance, to transitions in highly plastic cancer cells, such as metastasis-initiating cells (MICs), which display different degrees of stemness (Pérez-Gonzàlez et al. 2023). In contrast, early and late epithelial-to-mesenchymal transitions (EMTs) are relatively stable in comparison to other intermediate states (Bierie et al. 2017; Kroger et al. 2019). In such cases, the endpoints of trajectories remain qualitatively distinct from each other in many respects, thus influencing the future potential of a

effects has important implications for treatment and recovery. The plasticity of cancer cells allows them to differentiate into diverse cell types within a tumour, adapt to various microenvironments, and evade therapeutic interventions. Conversely, the robustness of cancer suggests that the phenotypic traits of cancer cells become fixed due to the accumulation of genetic mutations and epigenetic changes that stabilise their malignant behaviour: once a perturbation generates a bifurcation and a population of cells take a tumoral trajectory, the original perturbation may cease to be what sustains the trajectory. That is, cancer's robustness becomes dependent on other phenotypic features that constrain future development (Brock & Huang 2017), and an individual's disease trajectory can be predicted through landscape models (Foo et al. 2022, p. 9). Overall, the extreme adaptability and plasticity of cancer cells generate a strong tendency for cancer conditions to persist over time.

To summarise, recent developments in cancer research allow us to see cancer cells as *discrete*, *qualitatively* different states that a cellular system can take. Such states originate from ongoing dynamic and plastic processes that are well captured by the notion of *homeorhesis*: cells are *not* stable configurations of properties, but rather robust flows that dynamically pursue stability through continuous adaptation to perturbations – a condition that, however, might never be achieved (Dupré 2021; Fabris 2018; Waddington 1968). What we might perceive, at a given point in time, as a stable cluster of properties is in reality just a snapshot in the continuously evolving trajectory of the complex systems we call cells.

4. Homeorhetic Dynamic Kinds

Thinking about complex systems in diachronic terms provides the basis for a new type of realism about kinds. Although the HDK theory makes substantive use of the vocabulary of systems biology, its key elements can capture clear-cut distinctions between kinds at various levels of analysis, including those of psychology and social science. In this section, we outline the main ontological and epistemological elements of HDKs.

We take *systems* as the main units of analysis of our model, representing individual entities that, collectively, constitute a HDK. Individual entities (the members of dynamic kinds) are integrated, complex wholes characterised by multileveled, interconnected properties. The notion of system provides a general ontological category that allows us to encompass various

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system. For similar considerations in other medical areas, see Olthof et al. (2023), Serpico & Petrolini (2023), and Trefois et al. (2015).

phenomena and levels of complexity in the same explanatory framework. Systems are characterised by several features, among which *flexibility* and *robustness* are particularly important for the HDK account. The developmental trajectories of systems are *flexible:* indeed, systems have a tendency to continuously adapt to their environments, but significant changes can occur when they are destabilised by major perturbations and critical-stage transitions. These special circumstances can generate bifurcations in their developmental trajectories. Once canalised into specific trajectories, however, systems become somewhat *robust* to minor interferences. The notion of *attractor* represents these relatively stable developmental outcomes: attractors are resilient configurations of systems that tend to persist over time. Because they can resist minor perturbations, the development of systems tends to follow a given trajectory until major perturbations occur.

These dynamics are well captured by Waddington's popular epigenetic landscape model (Figure 4), which depicts the development of a system as a ball rolling down a series of valleys (called *chreods*). Each valley represents a set of developmental features that shape and canalise development over time, determining the system's future options. Using this conceptual architecture, the HDK framework can address various important epistemological and ontological questions: When does a new kind emerge (*emergence*)? How are kinds maintained over time (*robustness*)? Where does a kind begin and another one end, and how can we determine whether an entity belongs to a given kind (*kindhood criteria*)?

Starting with *emergence*, a HDK begins at a bifurcation in a developmental or evolutionary trajectory of a set of systems – when the latter, that is, take a new path. Importantly, bifurcations are often caused both by internal and by external factors. Cancer, for instance, begins when a cell (or a population of cells) moves out of a previous attractor due to changes in the expression of multiple genes triggered by endocrine factors and/or environmental exposures. In political history, the origins of empires coincide with the adoption of geographical expansion as a solution to demographic pressure and stagflation. Territorial expansion may be triggered by external pressure (war) but also require the existence of internal facilitating conditions, such as high solidarity and large investments in public projects (Collins 1978; Turchin 2003). Likewise, the process of speciation – where a new species originates from a previously existing one – involves the combination of genetic and ecological events that trigger changes in the developmental mechanisms of a sub-population of organisms. In short, the emergence of a new HDK coincides with a tipping point from which a new developmental or evolutionary trajectory is generated.

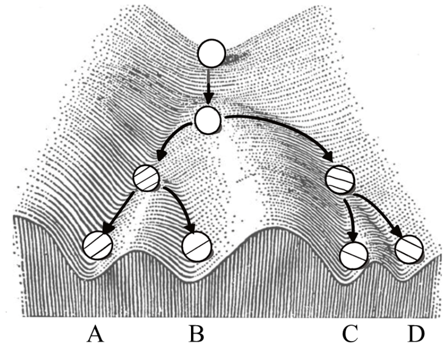

Figure 4: A representation of the epigenetic landscape. Different points in time (t_1, t_2, t_3) represent switch points or bifurcations in developmental trajectories. Letters (A, B, C, D) represent robust configurations towards which the system tends to gravitate (attractors) (adapted from Waddington 1957).

Such trajectories, once triggered, are characterised by a high degree of *robustness*. Robustness should not be interpreted as the absence of change, or the tendency of a system to preserve its current properties (as already mentioned, systems are flexible to an important extent). Under a dynamic perspective, both stasis and change can be encompassed within the same explanatory framework: the notion of attractor explains why a system *tends* to develop towards certain stable configurations and why it will probably persist in a robust state unless significant perturbations intervene. An important epistemic implication of the HDK account is that dynamic robustness can be difficult to observe from the synchronic perspective of property cluster theories. Canalisation effects, in fact, are entirely compatible with significant heterogeneity among the members of a HDK: the properties of individual systems may be very different at the beginning and at the end of a trajectory, for example; yet, different systems may belong to the same kind in virtue of their common dynamic fate and to the attracting and stabilising forces that maintain their development onto a given pathway.

Kindhood criteria, according to the HDK theory, are strictly related with diachronic development and with the impossibility for a single system to go through more than one trajectory at a time. Channelling effects make it hard for a system (e.g., a cell population, a social group) to reverse its development or, in other words, to travel its trajectory backwards (metaphorically, to pass into another valley of the epigenetic landscape). The developmental potential of many complex systems narrows down during their lifetime: after a given switch point, some trajectories become unlikely or unavailable. Some models of cancer, for example, emphasise that individual trajectories are difficult to reverse, although cancer cells have a high degree of plasticity (see above). And the same is true of other types of systems: internal strife between political factions, for example, usually prevents the adoption of expansionist strategies and steers polities towards trajectories of slow decline or stagnation, although these processes are not necessarily unidirectional.

It is worth stressing that the HDK account does not imply that all processes are irreversible or equally constrained: entities at different spatiotemporal scales exhibit different degrees of flexibility and robustness. For instance, processes at higher levels of complexity (and evolving at slower time rates) usually display more robustness and stability, compared to processes at lower levels (that evolve at faster time rates) (DiFrisco 2017; Green et al. 2017; Dupré & Nicholson 2018; Wimsatt 2021). Here, we do not take a position on the degree of robustness of processes at various spatiotemporal scales, which is obviously an empirical matter.[7] But the HDK perspective suggests that recovery from disease, in many cases, should be conceptualised not so much as the *inversion* of a developmental trajectory (say, from a diseased condition to a previous healthy configuration), but as the creation of a bifurcation, at a later time, that will have a new, distinct path ahead. This new configuration may share various characteristics – but still not be identical – with the healthy state of an individual who never became ill (Olthof et al. 2023; Serpico & Petrolini 2023).

For example, if kind *A* tends to evolve towards attractor *a*, but a major event at t_1 creates a bifurcation towards *b* (and the emergence of a new kind *B*), the entities in *B* cannot return to kind *A*. But an available developmental pathway from *B* to *a* may well exist. This would require *B* to give rise to a new kind *C* in future developmental transitions (t_2), and at various stages *C* may happen to have similar properties to kind *A* (Figure 5).

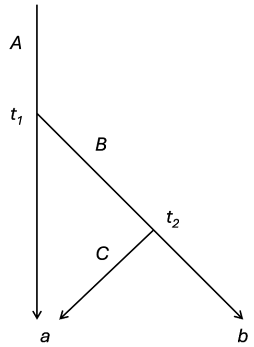

Figure 5: Although different trajectories (*A*, *C*) can lead to similar outcomes or attractors (*a*), according to a diachronic perspective the developmental process of a system tends to become canalised over time.

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[7] Strict irreversibility is a feature of the *models* – like landscape models – that we use to conceptualise the development of systems. Such models are helpful to highlight the challenges faced by scientists, doctors, and policymakers when they try to modify the trajectory of a system. Whether such models should be read literally or loosely – to allow for limited or partial reversibility – is ultimately an empirical matter, too. A strict interpretation would be consistent with physical principles concerning the time arrow and the irreversibility of macroscopic events (Lebowitz 1993; Levesque & Sourlas 2024).

With the main elements of the framework in place, we can now see how the HDK account tackles the continuity problem. Recall that, in traditional cluster accounts, ontological continuity emerges from the fact that some individual entities do not clearly belong to one kind or another. There are some grey areas, in synchronic states space, where entities can be assigned to two or more kinds depending on pragmatic considerations (see §1). From the perspective of HDKs, some grey areas might be an artefact of our limited temporal outlook: if we look at them from a sufficiently wide temporal perspective, intermediate states appear transitory, because there are other, more stable configurations towards which the system tends to gravitate (namely, attractors). So, the boundaries between kinds can be *ontologically discontinuous* even though, epistemically, such discontinuities may be hard to detect. The transitions from a robust configuration (a given HDK) to another involve discrete changes that can be identified with the stabilising forces that render trajectories robust after tipping points. In this sense, each HDK is qualitatively different from other potential configurations: what matters for the boundaries between two kinds is not whether their members display different properties, but whether they are canalised into distinct paths. Another way to draw this contrast is to see continuity as holding *within* the same homeorhetic process – and thus *vertically*, in the same trajectory in the epigenetic landscape – but not *between* distinct processes or *horizontally*, so to say.

Before we move on, one may wonder whether the HDK account can provide guidelines for the identification of tipping points from which new kinds emerge. As we mentioned, in many cases it is practically impossible to identify *exactly* when a bifurcation occurs. This is partly due to our limited (and relatively static) viewpoint and, therefore, is essentially an empirical, *a posteriori* matter. But scientists constantly make hypotheses about the systemic changes that make individuals fall into one trajectory or another. Their explanatory models often assume that a tipping point has occurred, without telling exactly when.

Cell biologists, for example, use the expression "cell-fate decision" to refer to the combination of environmental perturbations and switches in GNRs that lead a cell population to 'choose' between alternative phenotypic profiles. In the case of species, we can assume that a speciation process has taken place, at a certain point in time, due to a combination of factors that lead to the recruitment of unexpressed genetic variability for new phenotypic resources.[8] In social science, researchers routinely fail to predict major institutional transitions and revolutions, especially in undemocratic regimes, because the tectonic shifts in public mood that push political systems close to their tipping points are largely unobservable (Kuran 1998). But

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[8] For similar considerations on the retrospective nature of historical explanations, see Ereshefsky & Turner 2020.

while posterior explanations may be missing some of the details, in many analyses of complex systems our limited knowledge of the exact location of a tipping point does not raise any ontological puzzle. Consider climatic events like tornados: although we have no epistemic access to the exact point in time when a system has shifted towards the generation of a tornado, we know that such a moment must have existed for the event to occur. Similarly, the HDK account can merely assume that, in the generation of a new kind, it is *necessary* for a bifurcation to have occurred.

The HDK framework thus rationalises the scientific practice of reconstructing the identity of a kind from its 'downstream' states, which are usually observable after the bifurcation event. If the bifurcation occurs at t_0, indeed, we may not be able to tell until the two kinds are different enough from each other to catch our eye (say, at t_2). At time t_1, near the bifurcation, two trajectories could be ontologically independent, and their entities belong to two different HDKs. Nonetheless, they can be rather similar in terms of their property profiles, making it epistemically difficult to determine that they do not belong to the same kind.

4.1 Homeorhetic, Homeostatic, and Historical Kinds

The HDK account is compatible with several existing theories in science and philosophy. Our proposal, therefore, does not intend to replace, but rather to complement existing accounts, highlighting aspects of scientific ontology that are overlooked in the existing literature. For reasons of space, it would be impossible to provide a comprehensive list of comparisons in this paper.[9] There are, however, two classical accounts that occupy centre stage in contemporary debates about kinds that ought to be directly compared with ours: the Homeostatic Property Cluster (HPC) and the Historical Kinds (HK) approach. Discussing them in more detail will allow us to highlight the novelty of the HDK account and to explain how it contributes to progress in the debate on natural kinds.

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[9] HDK is, for example, compatible with the Stable Property Clusters theory (Slater 2015) and with network models in psychiatry (Borsboom 2017; Robinaugh et al. 2020). HDK also shares several features with process biology, particularly the idea that entities at higher levels (e.g., cells) owe their stability to a continuous flow of processes at lower, molecular levels (Dupré & Nicholson 2018). Although we cannot engage in a full comparison here, we would like to notice that HDK and process biology address the continuity/discontinuity problem differently: HDK distinguishes continuity *within* a process (captured by the process philosophy motto 'everything flows', which HDK endorses) from discontinuities *between the trajectories* that systems can take throughout their lifetimes. Discrete states can often be identified at *this* level, providing an ontological basis for the individuation of kind boundaries.

4.1.1 Homeorhetic Dynamic Kinds versus Homeostatic Property Clusters

We begin by clarifying the distinction between *homeostasis* and *homeorhesis*. Each concept can be used to capture a specific kind of robustness. Homeostasis in particular is connected with stability, staticity, and the pursuit of equilibrium – a condition that open complex systems never achieve. This focus on the static properties of systems is narrow and potentially misleading from the perspective of HDK: homeostasis represents a 'snapshot', at a given point in time, of a system that is in constant homeorhetic flow.

The explanatory potential of HPCs is linked to their ability to provide a basis for successful induction (Boyd 1991, 1999; Kornblith 1993). More precisely, the inferential power of homeostasis relies primarily on a relation of co-occurrence between the properties of a system. A set of properties – say, $\{P_1, P_2, P_3\}$ – connected by a homeostatic mechanism tend to be correlated, and deviations from this 'normal' state tend to be only temporary. The fact that system *S* has properties P_1, P_2, at time *t* for example, supports the inductive inference that property P_3 is also (probably) instantiated. It also supports the inference that, should P_3 not occur, it will probably be re-instantiated again at a later time t+1 – *as long as no major perturbations occur*.

The latter caveat is important for the distinction between HPC and HDK accounts. From our perspective, HPC taxonomies enable scientists to capture sufficiently stabilised patterns of properties *at a specific timescale*. But, crucially, *both* homeostasis and homeorhesis provide good grounds for prediction, in different contexts and with different scopes. HPC theories capture the ontological basis of inductive inferences at relatively shorter temporal scales. They are, in other words, able to explain inductive success during the periods of relative stasis that occur between bifurcations in the history of a system. Such periods may be extremely brief or relatively long, depending on the kind of system and the level of analysis (depending, for instance, on whether we focus on macro- or micro-properties). But in general, they will constitute only *slices* of a longer homeorhetic process. The illusions we have called 'synchronic artefacts' are a consequence of this methodological outlook. If we focus on a time slice, we might not see that a tipping point has sorted individuals into two or more (qualitatively distinct) kinds. *Property clusters are stabilised processes*, in a nutshell, configurations of properties that appear stable *relative to a given time frame*.

Emphasis on homeostasis may be a consequence of the extensive use of equilibrium analysis in those disciplines – such as physics, biology, and the social sciences – that rely on mathematical models (Sober 1983; Pettit 1996; Kuorikoski 2007). Equilibrium models are extremely useful to map the forces that preserve the stability of systems for extended periods of time, but tend to relegate their diachronic development to the background. Figure 6 provides a simplified landscape model of cancer, representing canalisation processes oriented towards two opposite attractors and the transition of a cell phenotype from one state to another, associated with distinct and robust gene-expression profiles. In cases of this sort, the transition is drastic and qualitative due to the relative instability of intermediate states.

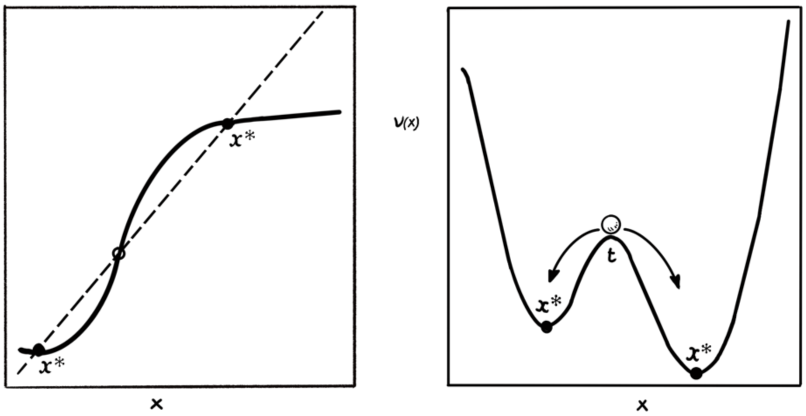

Figure 6: Different aspects of the same phenomenon can be represented using equilibrium (left) and landscape models (right). The dotted line (left) represents a linear protein degradation rate; the solid curve represents a non-linear synthesis rate for a circuit's gene. The intersections are points where the rates are balanced, and the system is in a steady state. The white circle is an unstable state and the black circles (x^*) denote attractors. The ball (right panel) represents two possible fates of a cell, moving from higher to lower regions in the state space after reaching a critical-stage transition (*t*) in its developmental history. The arrows represent two trajectories available at this stage, each leading to an attractor (x^*) with strong homeostatic properties (adapted from Davila-Velderrain et al. 2015).

The same formal apparatus is routinely used to model phenomena that may appear remote from the development of cancer, but that in fact display similar dynamics. Changes of political regime, for example, tend to occur at the end of crises during which the decay of coalitions that have ruled for long stretches of time (decades, sometimes centuries) accelerates dramatically. Political scientists emphasise that stability is compatible with widespread dissatisfaction, which however does not lead to concerted efforts to overthrow the government. The main obstacle to regime change is 'pluralistic ignorance' (O'Gorman 1986; Miller & McFarland 1991; Bjerring et al. 2014), in this case, lack of information about dissent and about people's willingness to challenge the system.

The equilibrium model on the left, indeed, can be used to represent the dynamics of belief change in a population of individuals facing a problem of collective political action (Granovetter 1978; Schelling 1978; Kuran 1998; Guala 2016). The proportion of citizens who are *expected* to take action (e.g., challenge the government) is represented on the vertical axis, while the proportion of those who *actually* do it is represented on the horizontal axis. At any point in time the system is in a state that corresponds to a location on the S-shaped curve ('propagation function'). When the curve is *above* the 45-degrees line, more people manifest their dissent than are expected. This triggers belief-revision, leading more people to join the protest, and causing a shift of the system to the right. In contrast, when the curve is below the 45-degree line, fewer people than expected manifest their dissent, inducing withdrawal from collective action (the system shifts to the left).

Propagation processes are oriented towards attraction points, and persist until the system reaches one of the equilibria. The points on the diagonal are such equilibria, where people's behaviour is consistent with their beliefs. Notice that propagation processes make the system *converge* on x^* but *diverge* from t. The former two are homeostatic states, while the latter is a tipping point. Such models have the resources to explain both phases of change and periods of stability in the history of a system. But, because they are easier to detect and often last longer, homeostatic states seem to support a wide range of inferences, while periods of change tend to be relatively abrupt and unpredictable. This probably explains why homeostasis has been long considered a fundamental feature of natural kinds. The dynamic approach, we contend, helps us to put it in perspective and to appreciate that *processes*, rather than property clusters, provide more general foundations for kindhood.

4.1.2 Homeorhetic Dynamic Kinds versus Historical Kinds

The idea that the ontology of natural kinds is better understood from a temporal perspective is not new. It is, in fact, the main pillar upon which the so-called theory of Historical Kinds (HK) has been built (Griffiths 1997, 1999; Millikan 1999, 2017; Bach 2012; Godman 2020; Khalidi 2021, 2024b). There are obvious similarities between historical and homeorhetic kinds: both adopt a diachronic perspective to kindhood. The main difference, however, concerns the role played by history and its explanatory potential. In classic HK theories, history is primarily used *to explain similarities between the properties* of kind members. Griffiths, revealingly, presents his historical-essentialist account of species as a special case of Boyd's HPC: "the principle of heredity acts as a sort of inertial force, maintaining organisms in their existing forms until some adaptive force acts to change that form. This *phylogenetic inertia* is what licences induction and explanation of a wide range of properties – morphological, physiological, and behavioural – using kinds defined purely by common ancestry. If we observe a property in an organism, we are more likely to see it again in related organisms than in unrelated organisms" (1999: 220). The sort of inductive inferences Griffiths has in mind are those that exploit resemblances among individuals. Historical essences thus play the role of homeostatic mechanisms: they keep a species in a relatively homogeneous state. Millikan similarly claims that many HPCs are historical kinds, in the sense that successful induction is grounded in common ancestry: "The members of these kinds are like one another because of certain historical relations they bear to one another (that is the essence)" (1999: 54).

From the perspective of HDK, in contrast, it is mistaken to combine historicity and staticity (that is, to focus on property clusters with historical essences): the tension between stability and change must be solved by thinking about kinds in processual, dynamic terms. Successful induction, in the HDK view, is supported by *canalisation effects*, rather than by correlations between properties. To appreciate the difference, consider that historical continuity may well imply *change* in the set of properties shared by the members of a kind. The members of a HDK, in other words, may be very different from each other, and kind membership may not guarantee inferential powers of the Boyd-Griffith-Millikan sort (see Figure 7). Compare, for example, the properties of a newborn and those of an adult member of a species; or the properties of a patient at the onset of a pathology with those of the same patient when the symptoms are fully displayed.

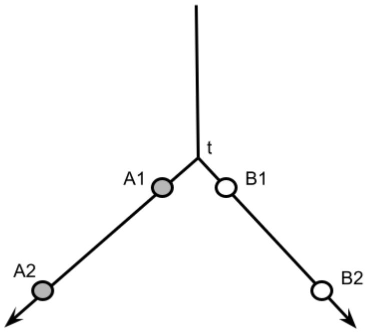

Figure 7: Development of a system undergoing distinct canalization processes at tipping point t. Instances of the system lying at different stages of the same pathway (e.g., A1 and A2) may display very different properties. Being closer to t, A1 might share more properties with B1 than with A2. But the fact that they belong to the same (homeorhetic) kind allows one to infer reliably what will happen down the pathway. A purely synchronic outlook or 'snapshot,' in contrast, might mistakenly bundle A1 and B1 under the same kind.

The fact that a system at time t has properties P_1, P_2, P_3 does not allow us to infer that it will have the same properties at $t + n$. It *does* allow us, however, to infer that the system at $t + n$ will lie within a certain range of possible states. HDKs, therefore, are projectable in Goodman's sense. But property clustering is just a possible *stage* within a process that is characterised primarily by canalisation, i.e., the restriction over time of the space of possibilities.

To take a concrete case, consider a classic problem of biological taxonomy: from the HDK perspective, whales are not fishes for reasons that depart from standard cladistic reasoning. The main point is that, even if whales have evolved fish-like traits, they cannot reverse the developmental-evolutionary tape and partake in the fish HDK. Our account thus differs from the HK approach by putting an emphasis on the (total or partial) *irreversibility of historical* *trajectories*: it is impossible for mammals to revert their trajectory towards fish-hood, and this impossibility provides a principled basis to treat them as members of a separate kind.

Like the HDK account, some versions of HKs emphasise the role of developmental properties in the creation and maintenance of 'phylogenetic inertia' – the tendency of traits to be transmitted across generations and to be displayed by members of the same species (Griffiths 1999: 222-224). HK theorists are sceptical, however, that development can be elevated to the status of 'essence' – an invariant element shared by all members of a kind.[10] The HDK account, in contrast, is not primarily preoccupied with the identification of essential mechanisms or properties. To undermine the continuity thesis, HDK highlights the fact that kind membership is not determined mainly by *past* history, but (more importantly) by *future* landscapes – the range of states that are accessible from a certain point or developmental stage, and which are determined, over time, by the stabilising forces that make a kind robust in spite of minor variations and oscillations (see §4). The homeorhetic theory, in other words, emphasises the *counterfactual relevance of natural kinds* – intended as processes that shape (typically constrain) the range of possibilities that individual entities enjoy at various points during their existence.[11]

In this respect, the HDK account shares important insights with Ereshefsky's (2014) account of biological species (see also Ereshefsky & Turner 2020; Godman 2021). Ereshefsky argues that speciation is a path-dependent process involving both an original branching event and a sequence of later events (e.g., a specific order of genetic mutations, genetic drift, and new phenotypic characteristics acquired through adaptation to new environments), which ultimately make the new group of organisms reproductively isolated from the one from which it branched out. Notably, this account differs from traditional HKs, where being a member of a particular species depends on having a certain ancestor.

We take Ereshefsky's theory as a convincing way to see the evolution of HDKs in the species' context, but we would like to extend it by generalising its main elements to types of processes observed in other areas of science, such as medicine and the social sciences. As we explained above, in the HDK account, kindhood criteria are not solely based on the *historical origins* of a bifurcation but, crucially, on the *future trajectories* of a set of entities, which is determined by the initial tipping point *and* by the following canalisation effects, stabilising

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[10] This move, for instance, would violate the Darwinian principle of variation underlying evolution by natural selection.

[11] See Bach (2012) for a HK account of gender that goes in this direction.

forces, and reduced developmental potentials. In other words, HDK is not just meant to describe the *emergence* of a new kind in terms of a single branching event or tipping point, but also to capture what makes a new kind robust and qualitatively different from other kinds. We hope that this conceptual architecture will help scholars to see under a new light not just cases where the formation of kinds is inherently (and intuitively) *historical*, as in the case of species, but also cases where there are no intuitive reasons to adopt a dynamic viewpoint, as in the case of psychiatric disorders and social systems: in many of such cases, only a dynamic perspective can make discontinuities emerge from a seemingly continuous distribution of properties.

5. Conclusions

Natural kind theory is in retreat these days. Philosophers have become increasingly aware of the difficulties that a strong realist account must face, and have shifted towards theories in which not only ontological factors, but also theoretical decisions play a key role in the identification of kinds. According to ‘pragmatic realism’ (Magnus 2012) and ‘promiscuous realism’ (Dupré 1993), for example, scientific inquiries have different aims, which determine which taxonomies are adequate or ‘natural’ for the purpose at hand. Cognitive approaches to the emergence of categorisation emphasise how kind terms track down properties the grouping of which is tied to our interests (Gardenfors 2004; O’Connor 2019). Boyd’s later defences of HPC recognise that kinds are relative to disciplinary matrices, leaving the door open to social constructionism (Boyd 1999, 2000), while Reydon and Ereshefsky (2019) see them as ‘grounded’ representations of reality that are functionally designed to attain a variety of (epistemic, non-epistemic) goals. From here, it is just a small step to recognise that kinds are neither natural nor objective (Chakravartty 2023; Ludwig 2018; Reydon & Ereshefsky 2022).

The HDK account provides an alternative way to characterise the ontological basis of kinds: the existence of robust developmental trajectories, separated from each other by bifurcation events, indicates the existence of objective differences in nature. According to this view, the continuity thesis does not constitute a formidable threat to the identification of kinds: although properties can be distributed continuously at any given point in time, many individual systems tend to partake in distinct categories when considered *diachronically*. HDK thus imposes some limitations on ontological pluralism: although there might be many ways to draw taxonomies, perhaps, there are not *as many* as pluralists believe.[12]

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[12] The implications of the HDK approach, in this respect, are similar to those of Franklin-Hall’s (2015) ‘categorical bottlenecks’ theory. Canalisation effects and robust trajectories would belong, in Franklin-Hall’s terminology, to

This does not imply that ontology alone is sufficient for the identification of a HDK and to determine to which kind individual entities belong. Other considerations count, too. Although HDK classifications are supposed to reflect objective differences, they also need to be relevant for some scientific or pragmatic purpose. This involves: a) the identification of generalisable patterns between developmental trajectories; and b) determining whether the dynamic trajectories of two entities are similar enough, given our epistemic and non-epistemic goals, to categorise them as part of the same HDK. These questions are challenging, as each individual entity has a somewhat unique history determined by contextual factors. But kind reasoning needs to 'abstract away' from some details and focus on the relevant ones. For example: What makes two populations of organisms 'different enough', in terms of their past and future trajectories, to partake in different species? What makes two individuals 'similar enough', in their clinical history, for them to belong to the same HDK? How can we characterise different kinds of social systems to capture similarities and differences in their trajectories?

Pluralism is, to begin with, a necessary consequence of our epistemic limitations. In many disciplinary contexts, incomplete knowledge and conflicting data require us to take a non-committal stance on which taxonomies better fit the causal structure of the world. The historical dynamics of complex systems indicate that, in principle, discontinuities should exist, although we may not always be in the best position to see them clearly (see §4). Even assuming a dynamic perspective, we may have epistemic access only to specific time windows. Whether we focus on some kinds instead of others, therefore, depends on what is empirically accessible to us, and we should better leave the door open to taxonomies that are sufficiently fluid to be revised according to the processes that we observe in the evolution of a system.

Although the HDK account predicts that entities will tend to group around robust dynamic configurations, moreover, our interests determine the choice of variables and the level of granularity to identify similarities for the construction of kinds. For example, two individuals may be similar in terms of their symptoms – leading them to receive the same diagnosis – but may have different future potentials that are relevant to recovery and treatment. As another example, every moment of cellular life involves 'choices' and bifurcations, but only some are investigated in biomedicine – those that are clinically relevant. Similarly, even though societies

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the 'multi-use architectural' features of the world that induce agents with similar interests to adopt classification systems that largely overlap. While Franklin-Hall's proposal is explicitly anti-realist in spirit, however, we see HDK as a contribution to the realist approach to natural kinds.

are in constant flux, only some changes are relevant for citizens, social planners, and policy-makers. HDK classifications reflect (diachronic) differences in the real world, as informed by the interests of human beings.

HDK categorisations can vary depending on what level of complexity one is focusing on, a choice that is largely dependent on one's interests. In the hotly debated case of ethno-racial categories, for example (Malinowska & Serpico 2023; Malinowska & Żuradzki 2022; Winsberg 2022), it is clearly emerging that higher-level phenotypic traits (e.g., skin colour, hair) do not closely match properties at lower levels (e.g., physiology, immunology, genetics).[13] And contrary to what has been argued (e.g., by Tsou 2020), there is no reason to believe that taxonomies at lower levels identify more robust or stable kinds. If the aim is to capture how racialisation processes affect health disparities (Hochman 2019; Malinowska & Żuradzki 2022), then focusing on cultural and physical factors will make perfect sense and will require a relatively short temporal scale of analysis (e.g., hundreds of years or decades). But if the aim is to capture the distribution of genetic variability across human groups, one will need to consider a much longer time span, focusing on the patterns of geographic migration over *hominidae* history.

In short, not all the discrete transitions a system may go through are relevant to us in scientific or practical terms: some (if not most) of them go unnoticed because they are not associated with relevant outcomes in scientific or social terms. At the same time, only some differences matter to understand the developmental history of individuals. Focusing on certain trajectories and properties and not others *is* value-laden in the traditional sense. One may argue, with Khalidi (2024a), that drawing taxonomies is a value-free enterprise, while values intervene only in their practical use. We prefer to consider the HDK account as an intervention-oriented approach: science, in many of the cases analysed above, is a pragmatic enterprise, and knowledge about kinds is relevant to predict and manipulate our environment. Some taxonomies reflect real differences (determined by historical canalisation processes) that happen to be salient and relevant *to us.*

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[13] A potential explanation is that biological systems are non-linear to an important extent, meaning that variation of properties at higher levels may not match variation of properties at lower levels (Green 2018; Wimsatt 2021).

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