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Contribution of phylomemories to the understanding of the dynamics of science

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1. Philosophy of science : processes and patterns?

Starting from a very generic definition of Science as “1) *body of knowledge*, 2) method, and 3) way of knowing” (Abell & Lederman 2007), this paper poses the question of what can be said about the evolution of a *body of knowledge* given some agreement on points 2 and 3. We develop here a methodology that is independent of any particular agreement, although its application requires that there be a strong enough consensus to delineate the materials that correspond to legitimate records of the body of knowledge (e.g. the peer reviewed papers). Although we will refer to the evolution of this body of knowledge as “the evolution of science”, it should be clearly stated, in order to avoid confusion, that this article does not deal either with the evolution of the scientific method or with the evolution of the scientific way of knowing.

Making sense of the way science evolves is a basic concern for philosophy of science. This concern involves two kinds of questions. The first one concerns the patterns of the evolution of science: is it gradual ? Is it continuous ? discontinuous ? how is the growth of knowledge likely to be measured and assessed ? The second one concerns the processes causing those patterns : what are the basic features of science likely to yield such patterns ? For instance, if science proceeds by accumulation of observations, supporting in turn inductive inferences, the growth of knowledge will be cumulative, with possibly some acceleration due to novel experimental or technical accesses to new data. If the evolution of scientific ideas is rather mostly due to refutation of previous hypotheses, as in Popper's fallibilistic account (Popper 1959), then science should rather appear as a discontinuous process.

Addressing the former kind of question implies the examination of long term historical data; the latter kind of question is addressed through the study of the ways science is done, by focusing either on historical case studies or on contemporary science. In each case one examines the way theories are formed, hypotheses are tested, models are elaborated and validated, theories are revised or changed. And in each case, the meaning of all those terms, both for the scientists themselves and for the philosopher who focuses on them, has to be questioned.

Thus, the question of the evolution of science or scientific progress receives two sets of answers, regarding those two issues of the historical patterns and of the processes. These two issues are not decoupled and the views on one issue often rely on a conception of the other issue.

This dependence has traditionally tended to be unidirectional. In most cases, philosophers draw their account of the patterns of scientific progress - its continuous character, discontinuous character, rate of increase etc. - upon a conception of how science works, elaborates and revises theories and hypotheses. For instance, Kuhn's idea of the discontinuity proper to scientific progress is directly related to his account of scientific activity, focused on the two notions of "normal science" (with its usual "riddles") and "scientific revolution" - and in turn, these notions are derived from his examination of the genuine practice of science and the way science is taught.

This shows an interesting contrast with what is often done in some empirical sciences, where approaches related to each way of reasoning coexist. For example, in evolutionary biology, the first approach, from processes to patterns, is well exemplified by the neutral theory in molecular evolution : here, the theoretical modeling of neutral evolution and the constancy of the substitution rate supports some ideas regarding patterns of evolution - starting with the notion of an "evolutionary clock" (Kimura 1983; Ohta 1977). The second approach, from patterns to processes, is often found in paleobiology (Ruse and Sepkoski 2009). For instance, the famous theory of the "punctuated equilibria" elaborated by Gould and Eldredge (1972) intends to challenge traditional Darwinian gradualism. The arguments they suggest in favor of punctuated patterns are what set the agenda for the subsequent research about processes; the question then consists in identifying the processes likely to promote such patterns, namely, the stasis (long periods of almost no evolutionary change) and the punctuation (short periods of important morphological and functional change in clades). Then, various candidate processes have been proposed which are supposed to best account for these patterns. And importantly, those processes are confronted to a neutral model showing which pattern of clades would result from the absence of processes of natural selection (Raup et al. 1977).

In this article, we argue that the time has come for the philosophy of science to develop a two-ways of reasoning through a quali-quantitative methodology that takes advantage of the recent evolution in the media that record the *body of knowledge* of Science. Throughout history, this *body of knowledge* has been distributed over several supports : people's minds, artifacts and textual materials to mention only the main ones. But over the past few decades, text documents have migrated to machine-readable media that harness the power of methods derived from text-mining and complex system modeling. This paves the way to the study of the evolution of the body of knowledge of science through the evolution of its textual digitized traces. The fact that textual records are both the most commonly used and the most enduring medium for recording and transmitting knowledge legitimizes this approach.

Yet the huge amount of digitized data currently available on scientific output over the past decade is a unique opportunity to make this "two ways of reasoning" leap possible, the nature of which should be comparable to the leap made by biology at the end of the 20th century when large amounts of data on living processes became available. We briefly analyze some reasons that have prevented philosophy of science from fully exploring this direction of research to date while showing that fruitful perspectives already exist. We will link our argument to current debates about the role of case studies in philosophy of science, on the one hand, and on the other hand, to conceptual frameworks used in evolutionary biology to make sense of evolution, and more generally in the computer assisted study of complex systems dynamics.

In the following section, we will introduce the notions of phenomenological and theoretical reconstruction, and indicate how this distinction may help to articulate a two-ways of reasoning for history and philosophy of science. In the third section, we consider the classical discussion about the relation between philosophical claims on science, and historical case studies, and indicate some of the shortcomings of any attempt to use

historical data as evidence for philosophical claims. The fourth section argues that phenomenological reconstruction, based on text-mining, could in principle provide ways to understand the evidential/justificational role historical sequences may play for conceptions of what is scientific dynamics, and avoid some of the issues (biases, hidden assumption) that plague usual philosophical theorizing about the process of science. In the last section, we introduce the “phylo-memetic” approach as an example of such reconstruction, the “phylo-memy” being the graph of filiations between words used in paper abstracts, in a way parallel to what a phylogeny is in evolutionary biology. We present its principle, provide some examples of the phylo-memetic patterns that can be detected, and finally argue that major theses about the dynamics of science could be tested by unraveling “signatures” of the hypothesized processes detectable within phylo-memies.

2. Articulation between data-driven and theory driven research

2.1 Phenomenological and theoretical reconstructions

The articulation between observation of patterns and understanding of processes can be conceptualized in the quite generic context of theoretical thinking used in the domain of complex systems, where researchers deal with large amounts of data and huge interaction networks. The articulation between the two-ways of reasoning is dealt with the distinction between *phenomenological reconstruction* and *theoretical reconstruction* (Bourgine et al. 2009).

Theoretical reconstruction consists in proposing models and processes (formal or computational systems) that synthesize phenomenal diversity and whose generative properties make it possible to explain past phenomena, predict future events or reproduce observed structures. This is the case, for example, of the *L-systems*, a formal grammar invented in 1968 by the Hungarian biologist Aristid Lindenmayer, whose aim is to model the process of plant development or bacteria proliferation. Once the parameters of a *L-system* that most closely reproduces the patterns of a given plant species have been inferred, it is possible to simulate the growth of individuals of that species and analyze inter-individual heterogeneities by introducing variation in only a few parameters. *L-systems* are widely used, for example, in animated films to simulate realistic landscapes. In hard sciences terminology, theoretical reconstruction generally corresponds to formal and computational modeling.



Figure 1 : Figure 1: L-systems applied to plant morphogenesis. few parameters can generate a wide variety of forms that match existing plant species morphologies. Source : public domain, <https://commons.wikimedia.org/w/index.php?curid=125410>

On the other hand, when the challenge is to understand and model complex systems, intuition unaided cannot handle their intrinsic subtleties and non-intuitive properties. The task of finding a reasonably precise and concise approximation for the structure and behaviour of a phenomenon which can be grasped by the human mind is called *phenomenological reconstruction*. It is the process of pre-structuring data for a more comprehensive understanding in subsequent analyses. Ideally, phenomenological reconstruction may provide us with candidate concepts and relations, which, when integrated into a theoretical reconstruction, can then serve as a basis for the human experimental work (Bourgine et al. 2009).



Figure 4 Articulation between *phenomenological reconstruction* and *theoretical reconstruction*. *Phenomenological reconstruction* provides both inspiration for new *theoretical reconstructions* and tests for existing competing *theoretical reconstructions*. Theoretical reconstruction provides some indication of the objects to be examined in phenomenological reconstruction and predicts some patterns that might be found in the latter.

Phenomenological reconstruction is rarely thought of as a prerequisite for *theoretical reconstruction*. In fact, the name “data”, on which the models are validated, suggests entities that are directly accessible to experience and that do not need special treatment to be integrated into a conceptual model. All you have to do is to observe or measure. This is however rarely the case (see Leonelli 2016 for a detailed analysis of what data are in ‘big data science’), especially when the object of study is a complex system.

For example, if publications are one of the primary production of science, a dump of the millions of papersⁱⁱⁱ science produces annually would be a very embarrassing data-set for those who do not know how to apply a phenomenological reconstruction to pre-structure it. How such a data-set could help us to understand the structure of science? Could we say something about scientific fields and their evolution without subjectively cherry-picking the few papers that seem relevant to us? Is there a fully *bottom-up* way to identify relevant structures for the description of science evolution? Can we detect and visualize paradigm

shifts, interdisciplinary merging or emergence of new domains through the analysis of such a data-set? These tricky questions are all preliminary steps for someone asking about the regularities in the evolution of science, the influence of scientific fields on the activities of researchers, etc.

The generic output of a phenomenological reconstruction for science is a structure described with some spatio-temporal resolution (e.g. the evolution and ramifications of major research fields in quantum computing over 30 years, see below). The quality of a phenomenological reconstruction is measured by its ability to propose structures that make sense to *us* in the raw data and provide affordances for theoretical reconstruction. Although hypotheses about the underlying processes that guide the evolution could help to find the relevant phenomenological reconstruction method, a phenomenological reconstruction does not make such hypotheses. Its relevance is measured by its heuristics power in theoretical reconstruction activity and the increased capacity it gives us to process and interact with massive data sets (how to store them, how to browse them, how to retrieve them).

2.2 Phenomenological reconstruction, macroscopes and the observer

We can draw here an analogy with microscopy in biology. As well as scientific advances in the field of microscopy has helped biologists to better understand the living, the availability of digitized science productions at large scale and advances in phenomenological reconstruction will make it possible to build macroscopes, *i.e.* devices that makes it possible to observe the structures of the large socio-technical systems we live in (Rosnay 1975) and go back and forth between the raw data and high-level reconstructed structures. Phenomenological reconstructions methods, social macroscopes and historians or philosophers of science is a tripartite set required to the development of advanced theoretical reconstructions in philosophy and history of science as well as optical and image processing science, microscopesⁱⁱⁱ and biologists are tripartite sets required for the development of biological sciences.

The implementation of methods for phenomenological reconstruction into interactive macroscopes is an indispensable part of their use for scientific purposes. By this mean, the structure they identify can be analyzed (quantitatively and qualitatively) and compared to raw data (e.g. the publications). Interactive visualizations help the researcher to identify the relevant patterns but also some potential discrepancies, if any, between real data and the reconstruction (δ_1 in Fig. 4). These observations can be used either to inspire new theoretical reconstructions (triangle #2 in Fig. 4) or to compare the patterns predicted by existing models (formal or conceptual) against the phenomenological reconstruction (δ_2 on the figure). This comparison can serve as a test of the models and could help decide between several hypotheses about the processes.

For example, when describing some patterns of science from the analysis of a corpus of publications, experts must be able to match the remarkable elements of these patterns (e.g. the emergence of a new field) to some particular items in the data (e.g. the seminal papers or ideas that made this emergence possible).

For a given scientific object, scientists may specialize in one or the other type of reconstruction. However, at the level of the scientific community, the understanding of an obviously complex system such as science, which involves a large number of actors interacting over a wide range of spatio-temporal scales, should imply a two-way articulation between theoretical reconstruction and phenomenological reconstruction.

Moreover, the distinction between these two forms of reconstruction makes it possible to reconcile the hypothesis driven and data-driven approaches of science. Phenomenological reconstruction (triangle #1 in Fig. 4) is a fruitful approach for the inference of meaningful structures and patterns that characterize a complex system from unstructured data that the

system generates (for example the publications). It “provides people with candidate patterns and relations that unaided human intuition would never detect” (Bourguine et al. 2009).

2.3 Epistemological red flags

It is important to highlight that phenomenological reconstruction is never autonomous from theoretical reconstruction insofar as it already implies some minimal conceptual models of what we are looking for that help us determine which part of the data should be collected and processed for subsequent analysis. Again, the analogy with the design of a microscope is useful. What wavelength should it focus on? What is the observation protocol? What are the relevant resolutions? All these dimensions must be explored by biologists in order to construct the appropriate microscopes for their object of study while different types of microscopes will provide knowledge on different aspects of the organisms studied.

Besides, any phenomenological reconstruction selects a subsets of observables to be processed and makes some particular choices in its control parameters to produce a human-readable artifact. Consequently, the output of a phenomenological reconstruction is necessary a projection, in the mathematical sense and in a small dimensional space, of the properties of an object that lives in a large dimensional space. As well as different projections are necessary to fully grasp the properties of an object (ex. Fig. 5), we should expect that different methods for phenomenological reconstruction are needed to fully grasp evolution of science (for example analyzing semantic space, citations network, co-authors network, PhD parentages, etc). The different kinds of reconstruction will make it possible to highlight processes of different natures that take place in the evolution of science.



Figure 5 : Example of projections of a three dimensional object into two 2-dimensional spaces.

Moreover, a good ergonomy is a crucial feature of a good macroscope, that should makes it possible to easily vary the parameters of the phenomenological reconstruction to explore the different angles of projections it make it possible.

To conclude this section, we claim that a *bottom-up* phenomenological reconstruction of the structure of science from its productions (publications, proceedings, patents, labs notebooks, etc.) is essential to pre-structure the data in order to conceptualize meaningful models of science evolution. Moreover, these phenomenological reconstructions should be implemented in *macroscopes*, e.g. technology devices that make it possible to interact with scientific production through these reconstructions.

In this paper, we will focus on a type of phenomenological reconstructions that addresses the question of understanding the evolution of ideas and scientific fields from the point of view of the evolution of the academic vocabulary. This approach is complementary to other methods that rely on other types of data, such as citation data or co-authorship. It has some specific advantages that are discussed below.

3. History of science, case studies and philosophy of science.

Before we develop on how phylomemories provide a way to detect features highly relevant for both the pattern and process questions described in §1, let us consider what are the main issues with “unidirectional” philosophy of scientific change (unidirectional, in the sense that the analysis goes only in one way between the two kinds of reconstructions), and what are the reasons that have prevented philosophers from engaging fully in two-way thinking between the two types of reconstruction (or between patterns and processes).

In most cases philosophers start from a previous conception of the scientific processes and activities and draw their account of the pattern of scientific progress - its continuous or discontinuous character, its rate of increase etc. - upon a conception of how science works, of how theories are elaborated and revised. However, it is not obvious that only one account of how science proceeds should be correct for all sciences. And, moreover, those accounts are sensitive to the way one defines science. This is all the more important that the very notion of science is historically changing : alchemy or music would at some point have been considered as sciences, while they no longer have this status. And philosophers know well that a set of necessary and sufficient criteria to capture what ‘science’ is will remain out of reach (Gayon 2016) because of this historicity of the definitions of scientific practices, as well as the dependence of science upon the technical, sociological, etc., conditions of what could be done in terms of scientific enquiry (for instance, one could argue that ‘experiments’ do not enter into the notion of science for the Ancient Greeks since almost no experimental device was available; while experiments may be part of the current definition of natural science if a random scientist is asked today).

Starting from a conception of how science changes, in order to make sense of the patterns of change, thus raises the problem of the dependence upon prior notions of science. Therefore competing views of the progress of science may be affected by this underlying issue regarding the accounts of scientific processes that ground them.

Moreover, philosophical theories of how science is done often differ regarding the level of analysis they focus on. When philosophers look at science, they can focus on many kinds of things: statements (e.g., the law of perfect gases), hypotheses (e.g., the “hypothesis of natural selection”, Gayon 1998), theories (e.g. the theory of quantum electrodynamics, or of sexual selection), models (e.g. the Fisher-Wright model in population genetics), experiments, texts (Newton’s *Principia Mathematica*), observations or data points - all those things are deemed as scientific. Then, many activities are involved: writing, computing, observing, experimenting, teaching, lecturing, reading, drawing graphs and diagrams, programming... Among all this, considering what belongs to the very nature of science, and what is sociologically contingent, is not obvious; actually a claim for science studies is that all differences between those items is arbitrary or conventional, and one should turn to a descriptive approach integrating all those elements (Latour 1988).

Considering philosophy of science at the highest level of generality, it appears that philosophical accounts of science generally chose one set of items and practices, and elaborate on this basis their account of how science proceeds and progresses. Popper mostly considered hypotheses, the way they are tested, and the consequences this has upon the growth of science. He arguably worked in the tradition of the Vienna Circle, where the basic units of philosophical and logical analysis were statements (or propositions). Hull (1988) considered mostly theories as units of the Darwinian process he sees in science, and intended to draw analogies with Darwinian phylogenies; the equivalent of natural selection is the set of interactions between scientists and scientists vs. the world which lead to differential representation of various theories among scientists. Kuhn focused on theories,

but forged a new concept to define the relevant level of analysis, indissociably conceptual and philosophical, namely the “paradigm” (Kuhn 1962). In any case, the differences between the levels of analysis imply that different patterns of scientific progress are allowed to coexist, since they will be constructed by considering these different levels. It is logically possible that the evolution of theories is discontinuous whereas the evolution of hypotheses or concepts or models is more continuous, for example.

For now we surveyed the solidarity between the claims about the process of science, and those about the patterns of scientific progress. Most philosophical claims about scientific evolution concern the latter but often rely on the former. Given that philosophers, and especially those we cited here (Popper, Kuhn, Lakatos, Hull) disagree on the two issues - patterns, processes - , the obvious problem arising here is the nature of the tests one could use to decide between competing views. How to test, for example, Hull’s claim that scientific process is Darwinian, or Kuhn’s claim that science is a discontinuous process of normal science and disruptive revolutionary paradigms ?

What we expressed here in terms of patterns and processes of scientific change – or of phenomenological and theoretical reconstructions - can be related to a tradition lamenting the lack of testing of philosophical theories of scientific change. This tradition has generally formulated the problem in the terms of a relation between philosophy of science and history of science. The first attempt at a rigorous historical testing of philosophical theories of scientific change has been developed in the 1980s by Larry and Rachel Laudan and Arthur Donovan with the “Scientific Change” project at Virginia Polytech Institute (VPI project). In the 1960s and 1970s, with Kuhn, Laudan and others, philosophy of science has famously undergone a shift away from the picture of science developed by logical empiricists, which was thus designated as the “received view” of science. This shift was motivated partly by philosophical problems, such as the divide between theory and observation, and with the possibility of testing hypotheses in isolation (questioned by the so-called Duhem-Quine thesis, among others), and partly by the mounting evidence that the “received view” was inadequate to describe actual historical episodes of scientific change. The historical school of philosophy of science - following Kuhn’s work - argued for the necessity for philosophical theories of scientific change to be informed by the history of science. However, with many theories emerging from this school, historical examples were “illustrative rather than probative” (Donovan et al., 1988, p. 5). That is, even though these theories were built with a concern for history and with a reliance on some historical examples, the confrontation to the historical record was not systematic and thorough enough to claim that the theories had been properly tested.

Laudan and colleagues in the VPI project envisioned the process of testing as a relation between philosophical theories and historical cases studies. This method was preferred to alternatives sources of testing drawing on contemporary science: the experimental method was deemed impractical; surveys, ethnomethodological studies or laboratory studies were considered valuable but ill-suited to study the processes of scientific change, which can span over large timescales and involve whole scientific communities. The value of empirical testing itself, as well as the related search for general patterns in science and for consensus among philosophers of science, were simply justified by appealing to the success of these methods in the natural sciences. They construed philosophy of science as an empirical science of science rather than an enterprise relying on a priori standards (see Hull, 1992; Scholl, 2018). Three principles guided the VPI project: 1) testing the empirical support of theories should be done comparatively rather than in isolation; 2) The different theories should not be tested as wholes but broken down into claims or theses, some of which should be extracted and tested; 3) Just like in natural sciences, hypothetico-deductive methods are more fruitful than inductive methods. One should test claims rather than start with the historical record in order to formulate new theoretical claims.

In order to proceed to this comparative testing, Laudan and colleagues picked the most cited theorists, Thomas Kuhn, Paul Feyerabend, Imre Lakatos, Larry Laudan, they then extracted theses from their publications and reformulated them in a neutral language. Thus, Kuhn's "paradigms", Feyerabend's "global theories", Lakatos' "research programs" or Laudan's "research assumptions" were all equated and reformulated as "guiding assumptions", defined as long-lived conceptual structures that are the most important units in the process of scientific change. Case studies were then undertaken each with the goal of testing a subset of the philosophical theses. Most of the case studies retained belonged to the history of physics, which the editors justified by the fact that the philosophical theories under test were formulated with mostly physics in mind.

Even though the VPI project was short-lived, it elicited multiple reactions. Some saluted its spirit while being virulently critical regarding the details of its design (e.g. Dumouchel, 1991)^{iv}.

Others have formulated more general problems with this approach to the relation between philosophy of science and history of science:

- History of science might not provide the right kind of data to test philosophical theories because historians are interested in the particular. This is especially relevant in recent decades when the interests of historians has moved away from methodological and foundational aspects of science, towards questions of practice, social context, material culture etc. This worry was formulated by Larry Laudan himself (1989) and others (e.g. Pinnick and Gale, 2000) who advocated for a properly philosophical method of developing historical case studies.
- Another concern has been formulated as the "dilemma of case studies" (Pitt, 2000; see also Faust & Meehl, 1992). If one works according to a "top-down" approach, following the hypothetico-deductive method like the VPI project, there is a risk of selection bias in the choice of the case studies, that is, there is a risk of cherry-picking the case studies that confirm theoretical claims rather than those that do not. Conversely, if one works "bottom-up", starting from case studies and trying to infer general claims from them, it falls prey to a form of the problem of induction: how many case studies are sufficient to justify a general claim?
- A third concern regards the "theory-ladenness" of case studies. Even if methodological solutions to selection bias are implemented, there is a deeper sense in which case studies are influenced by theory. The historical record is not a repository of data readily informed for the testing of theories. To investigate historical case studies and make sense of the historical material, researchers must rely on conceptions of scientific activities. The theories that they explicitly or implicitly endorse influence the constructions of their historical narratives. This compromises the status of case studies as empirical evidence (see Hull, 1992; Nickles, 1995; Richards, 1992).

Some have deemed the difficulties insurmountable. For example, Schickore (2011) has rejected what she called the "confrontation model", the conception of the relation between philosophy and history of science inspired by the natural sciences and illustrated by the VPI project. Instead she has defended a hermeneutic model in which history of science is not used to test philosophical theories. Rather, researchers engage in a process of transformation of philosophical concepts through historical investigations that takes the form of an interpretive circle. Others have endorsed the confrontation model and have provided different refinements or modifications in order to overcome the dilemma of case studies and theory-ladenness (see Burian, 2001, 2002; Haufe, 2016; Hull, 1992; Scholl, 2018).

Thus, concern for the testing of philosophical theories of scientific change has been repeatedly expressed over the last few decades, and debates regarding the appropriate methods for such testing are still ongoing. However, this literature concentrates on historical case studies as the main empirical resource for the testing. The potential contribution of the phenomenological reconstructions provided by text-mining analyses for the formulation and testing of philosophical theories has not been taken into account in this debate. It is not the purpose of this chapter to adjudicate whether or not historical case studies can ultimately be a valuable source of data for philosophical theories of scientific change. Rather, we wish to argue that phenomenological reconstructions produced by phylomemies provide another form of data that mitigates several of the problems attached to historical case studies that we just mentioned, and that give insights into the evolution of science that historical case studies cannot give.

4. Interest of using phenomenological reconstruction to question science evolution.

Pursuing the analogy with the science of complex systems introduced in §2, one could expect here that first a phenomenological reconstruction of the data could be proposed, in order to make sense of the underlying patterns, and warrant the theoretical reconstruction of the processes.

Our claim is that traditional historical methods should be completed with bottom-up approaches to provide phenomenological reconstructions. Let us expand on why it is so by saying more about “theory-laddeness”, selection biases and other problems that we introduced above. We will then show how data-mining methods, and phylomemies in particular, can solve or avoid these issues.

Historians of science classically proceed by reading materials, sometimes by interviewing scientists or other people involved if it is recent history. The issue here is that those tests are of course limited by the sample of documents considered. In effect, when one says that scientific progress is discontinuous, the evidence appealed to consists in a small sample of texts, analyzed in a way that the conceptual discontinuities are made salient. That’s for instance how Kuhnian philosophers proceed when they argue in favor of this thesis (Kuhn 1977).

This sample is generally biased towards papers or books written by ‘important scientists’, namely, scientists like Newton or Darwin whose work has undoubtedly provided major changes in our understanding of the natural and social world. This bias is not arbitrary, if one wants to focus on what evolves in science; however, what doesn’t change, or doesn’t change much, is also part of the scientific evolution, exactly like stasis is an important aspect of biological evolution (Brandon 2006).

Since the beginning of the 20th century, reading (let alone mastering) the whole scientific literature in any field of study has become an impossible task for any historian

Thus, the choice of samples raises a major issue for any attempt to test a general claim about the patterns in the progress of science or of a given scientific fields. Distinct choices of documents constitute different sets of evidence and may support opposite claims about patterns. For instance, it may be that Kuhnian discontinuities established by looking at major innovative texts disappear when one takes into account many more documents. The lack of a robust phenomenological reconstruction here raises an issue for evaluating theoretic models of processes.

Inversely, one may consider that the choice of documents implicitly assumes a metric about

what is more or less significant in science. Such a metric may be explicated and in turn we would have reasons for choosing this or that metric, and the robustness of the claims about patterns would rely on those reasons for a metric regarding scientific importance. Testing claims about patterns of science evolution would boil down to assessing conflicting arguments about metrics for scientific 'importance', and it is likely that this conflict cannot be settled, because all sides assume distinct conceptions of what is valuable in science (accuracy? explanatory breadth? predictability? generality? etc.), conceptions in turn involving a whole philosophical view of science. The point here is that starting from the theories about processes underlying scientific activity faces the risk of admitting multiple biases in the constitution of the phenomenological model of data itself.

Moreover, quite relevant to philosophy of science is the following fact: science writes its own history while it progresses. For instance, most presentations of relativistic physics would start by showing the progress accomplished since Aristotle by Galileo and then Newton (and his absolute space), before highlighting the aporia faced by physicists (constant speed of light vs. relativity of motion) and showing that restricted relativity is the proper solution to them. Through teaching, this narrative of how science evolved is shared by scientists, and often philosophers would rely on it. Historians may carefully deconstruct such narratives, by showing for instance the bifurcations, contingent decisions, or the existence of unconceived alternatives that could later on play a role (e.g. Kuhn 1957; Shapin, 1996; Kyle Stanford 2006). However, the point is that those narratives often have a strategic importance for scientists themselves, since they provide a sort of justification for their claims. Showing that some idea was there in Darwin's books, yet forgotten, and has been reactivated and developed by current scientists is a powerful way among evolutionary biologists to argue in favor of new ideas (e.g. Mallet 2008). It's plausible that those agendas by scientists shape some of the philosophical views. Thus, the sample biases here invoked - mostly, the 'great authors and great books' bias - are often even more entrenched because of this protowriting of history by scientists on duty.

Hence, besides the philosophical debate of delineating what science is, it appears that one of the issues preventing philosophy of science from smoothly articulating phenomenological and theoretical reconstructions is that there is no method for phenomenological reconstruction that has been proposed independently of any hypothesis on the process of science and which output is rich enough in terms of patterns and structure to serve as test bed for different theoretical reconstructions.

In other words philosophy of science has mostly focused on the activity of theoretical reconstruction without fully investigating phenomenological reconstruction. We attribute this shortcoming to the lack of data about scientific processes or the impossibility to address these data as a whole. In effect, even though one wants to achieve a phenomenological reconstruction of let's say *quantum computing* between 1990 and 2018 in order to theorize the processes of constitution of this scientific domain, it is not possible to read the corpus, as we said - no more possible than it was possible to access to the fine-grained structure of genes (namely DNA) before the existence of some microscopes, and then to access to the architecture of genome and genomic networks before PCR and late sequencing technology.

We claim that a technical and methodological shift, due to computation tool, existence of accessible databases of scientific journals (PubMed, Arxiv, Web of Science, etc.) and the development of text-mining methods and complex networks analysis makes now possible a phenomenological reconstruction of scientific evolution in the same way as postgenomic techniques made possible a science of genomic networks and architectures (Richardson and Hallam 2015).

Thus, here enter data-mining and automated methods considering very large data bases of documents. Because they do not focus on a small sample of 'significant' papers, they do not

assume those arguments about metrics, significance, etc. The obvious difference however is that they consider papers in a non-semantic way, they do not read the propositions, theorems, statements, they do not understand models. But in principle they do not suffer all the biases we indicated concerning the establishment of patterns in scientific evolution. Whether science progresses continuously or discontinuously, whether it's a Darwin-style process or not, one can arguably think that those methods in general may offer good tests for the hypotheses philosophers of science elaborated regarding the history of science.

Before turning to the specific data-mining we'll use, namely phylomemy reconstructions, we will say a word about the general approach it instantiates, and then distance it from classical scientometrics, which cannot answer the question about patterns that interest philosophers.

In contrast with most of the arguments by philosophers of science, which consider together the process of science and the patterns of scientific evolution and often infer the latter (as detected on small samples) from the former, data mining applied to large journals databases makes it possible to start from detected patterns in large literature and then infer possible processes. Thus, pattern detection is the first task, and on this basis one can directly test claims about the general shape of scientific evolution. If science is discontinuous, at some level this should appear in the general data-mining approach to science evolution - provided that the algorithm used is likely to reveal relevant aspects of scientific dynamics. Additionally, it can also reveal at which level, scale or grain these discontinuities exist, a question that was often not considered by traditional philosophy of science, which often deals with general claims about how evolution of science should be, assuming some notions of what scientific activity is.

In a second step, an automated phenomenological reconstruction would allow one to couple patterns and processes, in a way similar to some analyses in evolutionary biology. Namely, patterns detected may be seen as signatures of some processes.

Appealing to an analogy we used before with evolution, notice that the concept of signature is pervasive in ecology and evolutionary biology. For instance, molecular evolutionists scrutinize populations' genomes in order to detect patterns of variation that will signal the effect of natural selection or, inversely, the effect of stochastic processes ("random genetic drift") acting on gene pools^v. The signature of a process is the pattern which very probably is there because of such a process; even if the process cannot be detected, the pattern can reliably indicate its existence. A proper phenomenological reconstruction can therefore allow one to detect a signature in the data, provided that signatures of specific processes have been characterized, in the same way evolutionists can characterize the signatures of selection, drift, or hitch-hiking. Regarding scientific evolution, one will expect also that some patterns displayed by the change or stability of scientific concepts, hypotheses, propositions of theories (more later on the grain of analysis) may feature signatures of specific processes.

To sum up, a quantitative data-mining approach therefore would optimally provide us with two things : ways to test philosophical claims about science evolution while mitigating the sample biases and grain issues above-mentioned; characterizations of 'signatures' of various kinds of processes that could allow one to assess theoretical reconstructions about scientific processes by inferring processes from these typical detected signatures present in the phenomenological reconstruction.

5. Analysing the evolution of science through text mining

5.1 Principles of scientometrics analysis

Scientometrics, the quantitative analysis of science (and in a second stage, of its evolution) is a field which can be traced back to the 1950s (Garfield, 1955) and has its first applications in the fields of communication and information science and management science. It began with the study of citation patterns, which used two main methods: the *bibliographic coupling* index, which looks at how two publications can have common references (Kessler 1963), and *co-citation analysis* (Garfield, 1974), which examines how articles are cited jointly. These methods were initially focused on the question of information retrieval and the identification of articles relevant to a given request. They were not intended to reach general conclusions on the structure of science and its evolution.

Until now, most scientometrics studies has been turned toward the evaluation and management of science with a focus on measures of scientific activity : quantifying the quality and impact of scholars - based on citations, patents, funding, etc. - (Abbasi et al. 2011, Sinatra et al. 2016), measure of the prestige of journals (West et al. 2010), description of the scientific landscape (Börner et al. 2003, Kawamura et al. 2017), detection of hot or emergent topics and prediction of research landscape developments.

A second branch of quantitative analysis of science has developed in sociology around the analysis of co-occurrence of terms in documents or *co-word analysis* (Callon et al. 1983, Zitt 1991). Co-word analysis first of all, starts with some metrics allowing one to say whether two scientific contents (the nature of this is deliberately left vague here) *A* and *B* are closer between one another than with content *C* ; second, it provides ways to construct evolution patterns captured at several levels of grain and scale (theories, concepts, hypothesis, models), based on what the analysis of words in texts (provided by data mining algorithm) can feature, given that 'words' is the basic material handled by the algorithms.

This approach was explicitly oriented towards the analysis of the dynamics of science from a sociological perspective, for which co-citation analysis was considered insufficient and limited. In addition to some well-known weaknesses of co-citation analysis (e.g., low sensitivity - or *recall* - in the identification of recent domains, fragmentation of some identified communities, cf. Braam, 1991a,b or Callon et al. 1983), Callon argued that citation as a social practice is not well defined and can cover meanings as diverse as allegiance, recognition, reciprocity, etc. This makes it difficult to interpret the cognitive structures that this methodology highlights. Moreover, as these same authors have pointed out, the practice of citation is absent in some knowledge production contexts and, in the contexts where it is present, it may have very different meanings. Citation analysis is therefore not relevant for a generic study of the contexts of scientific production, which Latour and Woolgar (1986) have proposed to group under the concept of *literary inscription*, and which includes scientific articles, but also reports, projects, patents, etc.

Over the last decade, fostered by the availability of very large academic archives, scientific dynamics has received increasing attention (Börner 2004, Chen et al. 2009, Zeng 2017). Some work focused on citation network reconstruction (Börner et al 2004), other relied on top-down categorization of scientific fields from editors to compare their semantic diversity and evolution (Dias et al. 2017). Most of these researches try to qualify scientific articles rather than scientific production as a body of knowledge: which are the key paper of a field, how papers can be clustered, which are the potential seminal papers, etc. Following mainstream scientometrics, the main goal is either to evaluate the scientific production and its producers, or to improve scientific information retrieval systems. Very few papers are interested by the tracking of the conceptual innovations within fields, the extinction or emergence of concepts, or the conceptual bifurcations and merging, as it is required by any attempt to capture patterns of scientific evolution. That is why we will turn to approaches that are not in the pure tradition of scientometrics, namely the phylomemy reconstruction (see

5.2) as a method for the phenomenological reconstruction of science dynamics.

In what follows, we will focus on methods based on co-word analysis to illustrate how far we can go with the mere analysis of textual content. Undoubtedly, as highlighted in conclusion of section 2, this type of analysis would then benefit from being combined with other quantitative approaches such as citation analysis or co-author analysis and it has already been demonstrated that this combination is valuable in the perspective of bibliometric evaluation (Noyons et al. 1999) or information retrieval (Braam et al 1991a,b).

We will consider for our examples the Web of Science (WoS) meta-data database as a proxy for the digitized production of Science. We assume that there is a consensus on the fact that peer reviewed papers referenced by the WoS are part of the body of knowledge that Science produces. We should however acknowledge that this database is only partially covering Science productions and that the access to analysis of only titles and abstracts of scientific papers can only lead to a partial phenomenological reconstruction compared to what can be done with the full text. As we will show, phenomenological reconstruction on partial data nevertheless gives a fairly accurate picture of Science dynamics as a whole. One might however pose the question of the strategic importance, for the study and development of Science, of the public large scale availability for text-and data mining purposes of the scientific corpora we collectively produce.

5.2 From words to the macro-structures of Science

The most basic level of vocabulary analysis is probably the mere quantification of the popularity of terms in the literature, *i.e.* the evolution of the volume of publications that mention these terms. The figure 6 depicts for example the evolution of the number of records mentioning one of the following keywords in the Web of Science database (33,500 records in total until 2018): *quantum computer*, *quantum computing*, *quantum processing*, *quantum algorithm* or *quantum communication*

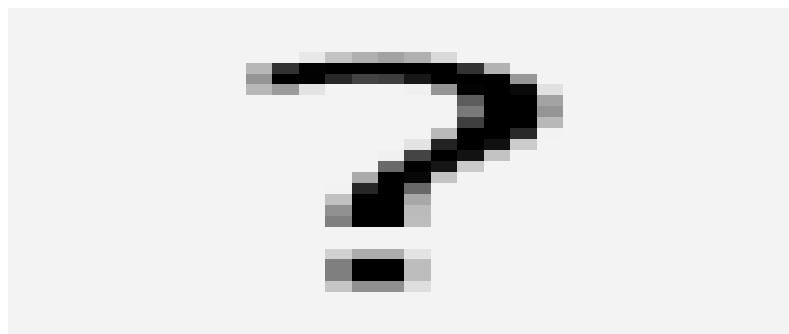


Figure 6 : Number of records in the Web of Science database for the query “quantum computing”.

Apart from the fact that the field of quantum computing seems to have emerged around 1994 and that it has experienced some acceleration (in 2002, 2008 and 2016) and evolutionary plateaus, little can be said about this curve. In addition, the term “quantum computing” itself may have referred to different concepts over time, a phenomena that cannot be revealed by this plot.

In order to get the higher-order organization of the science of “quantum computing”, that we will call the *meso-level*, we need to analyze how this term has been linked by scholars to other terms like “entanglement”, “optical lattices”, “quantum matter”, etc.

Callon et al. (1991) pioneered this approach with what they called *co-word analysis*. Its methodological foundation is the idea that “the co-occurrence of key words describes the contents of the documents in a file”. At that time, they were analyzing the key words

provided by editors or authors of a paper. This led to limitations and biases as they had no control over the process of associating key words to documents. Since then, advances in text-mining made it possible to mine directly documents of a corpora to uniformly extract key words from their plain text according to some chosen metrics of relevance. This has enlarged the reach of co-words analysis that now addresses the question of what can be said about a set of documents from the mere quantitative analysis of its textual content *i.e.* when the only ones observable are text strings. As already pointed out by Callon et al. (1991) “a simple counting of co-occurrences is not a good method for evaluating the links between co-words” and more sophisticated metrics should be used in order to reveal the relational structure between terms. As emphasized in section 2.3, the choice of these metrics, as well as the choice of the metrics of relevance for key word extraction are of utmost importance for the interpretation of the final analysis.

Given these metrics, the scientific objects that we deal with are words networks: for a given set of documents, we have on one side a list of text strings or n-grams (nodes) and on the other side their relations expressed as association strengths in the chosen metrics (links). Now on, we can apply graphs and networks theories to identify relevant structures within these words networks. These structures will be sub-networks with particular properties and the choice of the properties to be searched for, and therefore of the associated network clustering algorithms, is an other component of the methodological approach to be discussed. The end result however is the identification of groups of terms and their relational structure that, in the corpora considered, define some scientific issues like for example the set “*qubit manipulation, quantum information science, quantum thermodynamics, superconducting nanocircuits, microtraps, trap array, quantum gate*”.

Phenomenological reconstruction is about finding objects that make sense to us. The cognitive hypotheses in co-word analysis is that the meaning of a word (text string) is revealed by its patterns of interactions with other words (for example the meaning of “match” is perceived completely differently when it co-occurs with “gas cooker” and “kitchen” than when it co-occurs with “soccer” and “goal”). These patterns of interactions provide a context for the interpretation of a word and a word could have different meanings if it takes part to distinct interactions patterns. It should be noted that this approach doesn’t exhaust what can be said about the meaning of words in a text. More sophisticated methodologies like pragmatic sociology (Chateauraynaud 2003), argumentative analysis (Palau & Moens 2009) or sentiment analysis (Liu 2015, Pang & Lee 2008) can be complementary to the co-word approach.

A network of relations between a set of words, that defines the interpretation context of each word in the set, is a building block of the meso-level of a phenomenological reconstruction based on vocabulary. Its size can range from describing a very specific problem to a long list of related issues depending on how generic or specific is the desired point of view (that will depend on the choices of metrics and clustering algorithms).

What we have described so far holds for any set of documents. When documents are dated, as is the case for scientific production, the phenomenological reconstruction of the meso-level elements can be performed over different periods of time and their composition and hierarchical organization is likely to evolve. Chavalarias & Cointet (2013) proposed a method called *phylogenomy reconstruction* to analyze such evolution.

For dated corpora, the output of a co-word analysis of a subset of documents from a given period of time leads to the identification of the main scientific fields of that period, defined in terms of words networks. Phylogenomy reconstruction is the operation that defines temporal slicing methods of the corpora and then compute the inter-temporal similarities between the corresponding scientific fields in order to reveal their conceptual kinship. It is a phenomenological reconstruction of the macro-level of science semantic networks that

highlights how meso-level entities evolve through time at different scales of observation. The resulting multi-level organization this method defines (see Fig. 7) is a set of lineages of scientific fields arranged within phylomemetic branches. Each branch describes how fields of a given domain have strengthen, merged, split or weaken over time.



Figure 7 : Multi-level organization of phylomemetic networks. *Left:* from the micro-level of terms occurrences evolution to the evolution of the macro-level scientific fields, passing by the meso-level of keywords local networks describing some domain of interest. *Right:* the lineage of scientific fields arranged into phylomemetic branches. Each circle represents an element of the meso-level in the left part of the figure (a network of keywords computed over a given period that describes a scientific field). Vertical links between circles stand for conceptual kinship detection. Times flows top-down. The part of the branch highlighted by the caption is the domaine of *rehabilitation engineering* detailed in 5.3.

To summarize, the workflow of phylomemy reconstruction starts from a large set of publications as the raw data and ends with the production of a structure characterizing the transformations of large scientific domains at a given spatio-temporal resolution (cf. Fig. 8). In between, it applies sophisticated methods of text-mining, co-occurrence indexation, transformations of temporal co-occurrence matrices into a proximity matrices and complex networks analysis on the resulting graphs (see Fig. 8). We invite the reader to refer to Chavalarias and Cointet (2013) and Chavalarias et al. (2020) for technical details.



Figure 8: Workflow of phylomemy reconstruction from raw data to global patterns. The output is a set of phylomemetic branches where each node is constituted by a network of terms describing a research field. These nodes are a proxy of scientific fields and can have different statuses : emergent, branching, merging, declining. Source: Chavalarias and Cointet 2013.

The concept of phylomemy (or *phylomemetic networks*) has been proposed by analogy with the concept of the phylogenetic tree: a formal object that represents some aspects of cultural evolution through the analysis of its digital traces. It relies on the notion of *meme* understood as “cultural information that passes along from person to person, yet gradually scales into a shared social phenomenon” (Shifman 2013). However, it is important to emphasize where the analogy begins and ends. Phylomemy reconstruction is a concept that belongs to a phenomenological reconstruction approach. Consequently, it does not imply any particular

hypothesis on the nature of the phenomena that have generated the reconstructed pattern (here the social learning processes that govern the diffusion dynamics), which should be elaborated and tested in a theoretical reconstruction step. The notion of *meme* must therefore be understood in its broad sense, without any particular hypothesis on the ontological nature of memes or on the nature of the media in which they spread; nothing commits phylogenetic reconstructions to memetics, understood as the view of cultural evolution initiated by Dawkins. The only property we retain from the definition of *meme* is that it is something that is transmitted non-genetically, with some variation, from one person to another. The phylomemy reconstruction method could be applied to any kind of meme, from images co-occurring in web pages to technical artifacts co-occurring on archeological sites. A phylomemy of science aims to study how researchers' practices in the use of terms spread across a population and change over time. From a theoretical perspective, it is important to note that the formal object which represents inheritance patterns in phylomemies is a lattice, contrary to the traditional phylogenetic approach that deals with trees. This avoids any a priori hypothesis on the nature of these diffusion processes. It accommodates horizontal transfer of terms between distinct clusters of terms, in a way parallel to lateral gene transfer in phylogenetics.

5.3 Example of phylomemy reconstruction

Before highlighting the advances that this method brings for history and philosophy of science, let's present a concrete example of what it leads to. We won't be interested here into the technical details but rather in the nature of outputs that can be produced with this methodology.

In the framework of a collaboration with the European Commission^{vi}, we had access to about 5000 authors keywords of projects submitted to the Future and Emerging Technologies funding Scheme between 2009 and 2010 (FET Open). The co-occurrence matrix of these keywords has been processed from the full Web of Science Database between 1990 and 2010 (about 29M documents) and then the phylomemy reconstruction workflow (steps 2 to 4 in Fig. 8) was applied (Chavalarias and Cointet, 2013b, Chavalarias 2016). The goal was both to identify the science behind FET Open projects and to get insight on how it has unfolded through time (Fig. 9).

Figure 9: Sample of phylomemetic branches of the reconstruction of the domain of future and emerging technologies. The branch of quantum computing (cf. Fig 10) has been framed in dotted lines. This phylomemy has been generated with the WordsEvolution, a program developed by David Chavalarias.

One of the branches of this phylomemy depicts the domain of *quantum computing* (Fig 10). This domain of research can be defined by terms such as *quantum computing*, *quantum computers*, *quantum processing* or *quantum algorithms*. An example of sub-field from this domain is the relational network formed by the terms "*qubit manipulation*, *quantum information science*, *quantum thermodynamics*, *superconducting nanocircuits*, *microtraps*, *trap array*, *quantum gate*".



Figure 10: phylomemetic branch of *quantum computing* from the phylomemy reconstruction of the scope of FET Open projects between 1994 and 2007. Each square in the phylomemy is a set of terms defining a scientific field. As example, the details of fields 1 and 2 are given. Field that contain terms appearing for the first time in the phylomemy have a red header, those that contain terms not directly inherited from parent fields are have an orange header and fields that only contain terms borrowed to their parents are have a green header. This reconstruction highlights the reconfiguration of the fields around 2000 at a moment where two negative results have challenged mainstream approaches. We can clearly observe too phases of development involving many vocabulary innovations, with the pace of innovation slowing down in-between at a moment where major negative results where published. Source : Chavalarias, 2016

The domain of *quantum computing* is particularly interesting from the point of view of phylomemy reconstruction for several reasons:

1. As it can be observed in figure 10, this field has emerged in the 1990s, which means that its production is very well covered by digital archives which coverage largely increased in the early 1990s;
2. This field is extremely well defined: it corresponds to an exotic branch of computing based on a new physics with a very specific vocabulary;
3. This is an area where theory and experience must go hand in hand, each of these activities being well represented in the publications, hence the phylomemetic reconstruction has good chances to capture all relevant aspects of the field's dynamics;
4. This is an area of high societal and strategic importance. For some tasks, quantum computers are theoretically billions of times faster than conventional computers, which would allow them to "break" all the cryptographic protocols

currently used. The first nations that produce a quantum computer will have a major technological advantage over others, with access to all private or confidential data, which is why the U.S. military became involved in this area early on.

The quali-quantitative analysis of this branch is very revealing of the different phases of development of this domain of research in its first 20 years^{vii}. The sub-fields that feature brand new concepts from the perspective of this structure (*i.e.* terms that appear for the first time in these sub-fields) are highlighted in red.

The morphology and the pace of innovation displayed by this branch alerts the reader that the domain of quantum computing may have undergone a reconfiguration around the 2000s. Indeed, two negative results have challenged mainstream approaches precisely at that moment, with Noah Linden and Sandu Popescu (2001) proving that the presence of entanglement is a necessary condition for a large class of quantum protocols, which coupled with Braunstein's 1999 result, called the validity of the main quantum computer approach, NMR quantum computation, into question.

Both phases of development (1990-1999 and 2001-2007) involve many innovations and a diversity of approaches reflected by the number of distinct sub-fields. On the contrary, the pace of innovation (as indicated by the frequency of red labels) seemed to have slowing down around the negative results with a lower variety of fields. This description of the evolution of this domain is radically different from what can be inferred from the mere volume of publications (figure 6) that is regularly increasing over this period.

By studying this branch in greater depth, we would be able to determine the details of this reconfiguration, the respective importance of technological and theoretical innovations, the role of the turnover among the academic community, etc. What appears here is a specific profile of interrelation between science and technologies that is proper to this field but that could be compared to what happens in other fields (*e.g.* bioscience in relation to biotechnologies, statistical physics in relation to modeling and computing techniques, etc.). Thus the philosophical questions regarding the dependence between science and technique - the reason why Gaston Bachelard, highly aware of the dependence between the two domains, coined the word "phénoménotekhnique" - can be dealt with on the basis of compared patterns of such dependencies detectable in phylomememes.

Without aiming at exhaustiveness in the taxonomy of phylomemetic patterns, in addition to the case of domain reconfiguration, we briefly present two other examples that illustrate the possibility given by this methodology to do cross-domains comparison of evolutionary dynamics: *domain hybridization* and *abrupt domain emergence*.

Domain hybridization happens when a research domain incorporates research results and theories from another research domain. This is the case for example for the domain of *rehabilitation engineering*. Initially focused on concepts such as *orthosis*, *amputation*, *prosthesis*, *bone*, etc. in the early 1990s, this domain has incorporated the work from cognitive sciences on *mirror neurons* and *brain-computer interface* to evolve toward *brain-machine interfaces* and *neural prostheses* for *active orthosis*. In addition to highlight the hybridization of these two domains and its timing, this phylomemetic branch also reconstructs the main conceptual emergences with a good precision (Chavalarias and Cointet 2013b): the term neuroprosthesis becomes part of the phylomemy in 1994, two years after the seminal paper of Kovacs et al. (1992), the merging of the two branches takes place in 2000, one year after the first workshop on Brain-machine interface supported by the Eastern Paralyzed Veteran Association, the terms *retinal prosthesis* appears in 2000 which correspond when the first clinical trial of permanently implanted retinal prosthesis took place. We can see here that morphological and semantics transformations of this phylomemetic

branch synthesize the main transformations of this field during 20 years of research.



Figure 11: The phylomemetic branch of *rehabilitation engineering*. This branch has progressively evolved to incorporate the work in cognitive science on mirror neurons and brain-computer interfaces.

Abrupt domain emergence happens when suddenly a sustainable domain including a large amount of sub-fields appears after a conceptual or technology innovation. This is the case for example for the research on *massively multiplayer online games* (Fig. 12) that has been first mentioned in 2002 in Web of science (2 publications) and appears in the phylomemy in 2003 as a sustainable branch, with lots of new terms (red labels) pointing to conceptual innovations.



Figure 12: Phylomemetic branch of *massively multiplayer online games* that has emerged abruptly in 2003.

The morphological analysis of phylomemetic branches can be coupled with a statistical analysis of the content of the fields. For example, Chavalarias and Cointet (2013) have demonstrated that the position of a field in a phylomemy of science (a field can be emergent, steady, declining, etc., cf. fig. 5) is strongly correlated with cohesion measures on the terms that make up the field. In particular, it has been observed that a non-emergent field with a low cohesion measure is much more likely to disappear in the next period than any other non-emergent field. Thus a phylomemy conveys important information about the dynamics of the science domains it describes that should be taken into account in a theoretical reconstruction.

We take advantage of this example to insist on the fact that a phylomemy is a formal structure that is a phenomenological reconstruction and consequently it makes no particular assumptions about the nature of the phenomena that generated the reconstructed pattern. It however makes choices on the data and the values of the parameters that are used in the reconstruction and, as stressed in 2.3, the output result is only a *projection* of the global complex structure of science in the form of a visualization that can be grasped by the human mind. If we had chosen other parameters, the displayed structure might have been different, illustrating other important aspect of the dynamics of the domains under study and conversely, structures that hold for a large range of parameters will likely be core structures of science dynamics. In addition, the reader must have noticed that even these projections are intrinsically multi-level and that one would have to be able to zoom in and out on the overall structure to fully understand it. For this reason, the implementation of phylomemy reconstruction methods into macrosopes like Gargantext is of utmost important to unleash they heuristic power (Delanoë and Chavalarias forthcoming, Lobbé et al. forthcoming).

6. Discussion

The study of phylomemies paves the way for a quali-quantitative study of science evolution which would no longer rely solely on simple numbers and their trends (number of publications, quotations, h-factors, etc.) but also on elements of morphology of the branches of science ; and the different types of relationships these branches have with each other and the lower levels of terms dynamics.

A first sense of 'level', here, includes usual hierarchy in complexity : terms, concepts, hypotheses, models, theories, are distinct levels. Terms dynamics, in this method, is the lowest level. Clusters of terms will match with concepts, and theories will match with clusters of higher order (clusters of clusters). 'Topics' are clusters that sit on the same level as concepts, but are defined and labelled within the phylomemy. Since one can consider the diachronic changes in those clusters, and sets of clusters, descriptions of the evolution of science can be given at several levels. Each one needs however to include a discussion of the relation between the level of terms and the other levels, and the assumptions used to define this relation.

Another major descriptive concept regarding phylomemies is 'scale', which has also been used throughout this chapter. Scales can be defined in terms of time intrinsic to the process (defined by the rate of change of terms), and in terms of space in the phylomemy (namely, considering either a discipline, a set of disciplines, etc.) Phylomemies therefore allow for analyses at various scales and on various levels, which explains why they could be used to assess philosophical claims about the dynamics of science (those claims having been defended at several levels and scales), as we'll suggest it now.

The relationships between phylomemetic branches may be of distinct types such as: hybridization, thematic divergence, conceptual or methodological borrowing, etc. The various processes hypothesized by philosophers to account for scientific dynamics at various levels - Kuhnian, Hullian, Lakatosian, Popperian processes - can be discovered within the phenomenological reconstruction, to the extent that signatures of those processes can be characterized in the terms of the phylomemies.

For instance, a scientific process as hypothesized by Lakatos (1978), namely the elaboration of a core set of hardly modifiable views and methods surrounded by a "protective belt" of concepts, models and methods, that will be more likely to be revised, may correspond to specific patterns where two kinds of scientific contents can be distinguished according to two different rates of change. In turn, this can be detected by determining a ratio of red vs orange vs green labels (see figures), which measures the introduction of new terms.

A philosophical discussion should be given here of the relations between terms, concepts and topics (as defined in the phenomenological reconstruction) but it would not change the method of measuring those differential ratios, in order to find out the signature of a "protective belt/ varying periphery concepts and tools" mechanism proper to Lakatos' view of scientific dynamics as a dynamics of "research programs" progressively negotiated.

In turn, Kuhnian views of "scientific revolution" would correspond to signatures where a large discontinuity occurs, and spans across several thematic fields; it also implies that a "normal science" period should be detected by its very low rate of change compared to short periods of revolution.

This low rate of change will also appear as a relative conservativity ratio of terms, and possibly as a conservativity of topics through branching processes (which indicates that sub-fields develop, but that a same way of using core concepts, methods, references, exemplars etc, is conserved through the branching). The "abrupt domain emergence" (described above) may indeed be part of the signature of a Kuhnian revolution, however the rapidity of

the sweep has to be measured against its extension (which *is not very wide* in the case of *massively multiplayer online games for example*) in order to talk of a genuine Kuhnian revolution. Here philosophical arguments are required to determine this ratio (intensity of sweep/ extension of range), but the method of inferring back from pattern signatures to processes is still adequate.

Thus, regarding the very general philosophical question about the process of science sketched in §2, the preliminary findings pointed out above show already some lights.

- a) First, patterns appearing in phylomemies parallel known patterns in speciation study : rapid speciation, branching, fission ... If it were confirmed by more extensive analysis of science phylomemies, this might be one argument in favor of a Darwinian viewpoint as Hull (1988) advocated it,
- b) Second, not all patterns are signatures. Think again of evolutionary biology here. Gould and Eldredge (1972) famously proposed that biological evolution is not gradual, as Darwin and classical Darwinians from the Modern Synthesis believed it (based on the fact that most non-deleterious mutations are small), but discontinuous^{viii}. Yet, assuming that punctuated equilibrium is sometimes the correct view; when it is, does it imply a revision of our view of processes ? Some argued that it does (Erwin 2000; Gould 2002), especially because selection for small mutations cannot account for punctuations, and stasis along immense periods of time in very varied environments cannot be accounted for by stabilizing selection (Hansen and Houlié 2004) - but importantly those inferences are not necessary. Complex selective scenarios involving positive feedbacks, episodes of isolation and allopatric speciation, quick genetic revolutions, are likely to account for punctuated patterns^{ix} without invoking novel processes unknown to classical Darwinians^x.

In the same way as punctuated equilibria, many phylomemetic patterns by themselves are equivocal. Signatures, as we argued, are particular patterns that point to specific generative processes in a more unambiguous way than just patterns. Hypothesizing specific signatures and searching for them in phylomemies (and not only detecting patterns) is what allows for deciding between rival philosophical theories of scientific processes at a given scale and level. Considering differential ratios of colored labels in phylomemies, as we just hypothesised, defines three different signatures that would indicate Kuhnian, Lakatosian or Popperian patterns of scientific evolution. detecting the signature of process requires to consider tests of selection designed by evolutionary biologists. Those compare haplotypes variation due to drift and due to selection, and (Kreitmann's test), and the difference regarding variation patterns signals sequences under selection. An analogous of this test would detect Hullian processes in science dynamics.

- c) Third, fields and scientific domains generally display very different evolutionary dynamics according to phylomemies. The patterns seen may therefore be signatures of very diverse processes; for instance the "abrupt emergence" described in our last domain might be analogous to what evolutionary genetics calls "selective sweep" (Hermisson and Pennings 2005), where the selection on a locus actually incorporates all neighboring loci and induces a rapid genomic change. But other domains may rarely witness such signatures. This calls for further investigation, and especially, analyzing differential social structures of domains and their respective relations to technology - the former requiring other data than what is required for phylomemies. In any case this may indicate that there is not one process of science, but various science-producing

processes, whose integrated theory has yet to come. It gestures towards a pluralistic view of science processes. At some scale - time scale, or disciplinary scale - Hullan the signature of a Darwinian process may dominate, while at another scale the dynamics of science would provide a signature of a Popperian or Kuhnian process. It might also be that at depending upon the level analyzed - be it theories, or models - the signatures are not the same, and therefore, the dominant processes are not the same. What phylomemetics allows is therefore a test of hypotheses about the general dynamics of science at several scale and several level : differences in signatures at scales and levels would define a pluralistic view of science dynamics.

CONCLUSIONS

We argued in this chapter that phylomemetics provide an example of the kind of phenomenological reconstructions required for a bottom-up approach to the dynamics of science that would make possible a search for domain-characteristic processes of science in a robust manner. We mean by "robust" the fact that biases proper to usual philosophical reconstructions can be attenuated.

Of course, biases still exist and their neutralization requires to multiply the points of view through cross-analyses (for instance, changing the notion of terms proximity in the reconstruction, the notion of clustering in the detection of scientific fields, the text-mining methods that delineate a specific vocabulary, etc.). Experts of the field should also take part in the control of phylomemetic reconstructions by a back and forth movement between maps, expert knowledge and phylomemetics.

Moreover, we do not claim that all controversies in philosophy of science can be solved by appealing to phylomemetics - which would first ignore that no data set is immune to some philosophical characterization (for instance about the role of publications in the process of science), and second, bypass the need (acknowledged above) of a philosophical reflection on the relations between concepts, terms, tags, topics, in order to fine-grain what "signatures" should be.

Last, no philosophical theory of a scientific process can emerge directly from the phenomenological reconstruction. Our claim is rather about a complementarity than a revolution in the philosophy of science.

To conclude we should indicate on the basis of the previous developments that, with the help of this new methodology, several questions about the evolution of science can be revisited:

- How can we characterize the multi-level structure of science, its organization in disciplines and sub-disciplines and its dynamics ? What are different regimes of science? Are there patterns of concepts emergence and disappearance within branch of science that are characteristic of some particular domains? How heterogeneous are the timescales of science evolution between disciplines?
- What does mostly influence the evolution of a branch of science: Conceptual or methodological innovation? The arrival of a new generation of scientists? The capitalization of results steaming from another branch of science? A technology innovation?
- How scholars flow through the global structure of science? How heterogeneous are scholars with respect to their role in building the phylomemy? Do we have

contributors specialized in developing emerging branches, other consolidating mainstream ideas and some building the interdisciplinary bridges that open-up new directions of research ?

The methodology of phylomemy reconstruction is still at its early development. Scientists in computational social sciences and complex systems must collaborate with the philosophers and historians of science to identify the different types of reconstructions relevant to the study of the evolution of the sciences. These reconstructions will constitute as many projections of the complex object named *Science* that will provide access to particular aspects of the evolution of the sciences.

We are confident that this approach can be brought to a point where the morphological and quantitative features of branches of science will reflect the types of research regimes that take place within them. The detailed and cross-domain characterization of these typologies will open-up new perspectives for comparison with the science regimes predicted by authors from philosophy of science.

We also expect phylomemy reconstruction, and similar methodologies, to be game changers in our relation to science production, introducing empirical observations and testable hypothesis at the core of history and philosophy of science.

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- i Medline, the biomedical database alone had more than 1,28M new records in 2019.
[https://www.ncbi.nlm.nih.gov/pubmed?term=\(%222018%2F01%2F01%22%5BDate%20-%20Create%5D%20%3A%20%222019%2F01%2F01%22%5BDate%20-%20Create%5D\)](https://www.ncbi.nlm.nih.gov/pubmed?term=(%222018%2F01%2F01%22%5BDate%20-%20Create%5D%20%3A%20%222019%2F01%2F01%22%5BDate%20-%20Create%5D))
- ii
- iii Microscope could be replaced here with any other observation and measurement methodology like DNA arrays for example.
- iv Dumouchel criticized:
- The opacity of the process of extraction of the theses.
 - The recasting of normative claims in terms of descriptions of the expected behavior of scientists.
 - The fact that many of the theses selected were shared among theorists, so that the project was not a comparative test of the relative success of different theories of scientific change but rather a test of a general shared model of scientific change.
 - The vagueness (“usually”, “largely”) and ambiguity (“novel predictions”) of some of the terms used in the theses compromised rigorous empirical testing.
 - Discrepancies between case study authors and editors in the assessment of the relations between the case studies and the philosophical theses.
 - The assumption of the importance of “guiding assumptions” in the design of the test.
- v In effect, natural selection tends to constrain genomic sequences - since genomic sequences decreasing mean fitness are counter-selected - while stochastic processes assume equal fitness and therefore, all alleles being indifferent to reproductive success, all of them can be there and the amount of variation across the population regarding the focal sequence may be higher. Many tests have been designed (McDonald and Kreitmann 1991; Tajima 1989), but the very idea is that, the fact that selection or drift acts upon populations produce different patterns of genomic variation, thereby, and inversely, detected patterns signal the underlying processes.
- vi EU FP7 FET OPEN TINA project n°245412, PI David Chavalarias.
- vii See https://en.wikipedia.org/wiki/Timeline_of_quantum_computing for a timeline.
- viii According to them and against Darwin’s own view, the fossil record should be taken at face value, and the fact that it displays very long periods of morphological conservatism (“stasis”) and short periods of huge change in body plans’ (“punctuations”) is a reliable indication of what actually occurred in phylogenies. The controversy between orthodox gradualists and supporters of punctuated equilibria is still open (Jablonski 2000), and as in our case of science (point (b) above), the most plausible view is that some parts of the evolution of some clades were gradual while others displayed punctuated equilibria.
- ix Similarly, stasis is likely to be explained by the same type of scenarios involving selection processes.
- x Gould and Eldredge themselves actually started by providing explanations for the punctuations very akin to Mayr’s classical theories of speciation (Gould and Eldredge, 1972).