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In defence of taxonomic governance

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Abstract

It is well known that taxonomists rely on many different methods and criteria for species delimitation, leading to different kinds of groups being recognised as species. While this state of relative disorder is widely acknowledged, there is no similar agreement about how it should be resolved. This paper considers the view that the disorder in species classification should be resolved by a system of taxonomic governance. I argue that such a system of governance is best seen as a combination of standardisation, unification and regulation, each

of which can be implemented in different forms. I investigate the forms that these three components should take for taxonomic governance by looking into two successfully governed classification systems, namely, virus classification and enzyme classification. The last part of the paper then defends the governance view against five objections.

Keywords

Taxonomic disorder
Governance
Standardisation
Unification
Regulation
Species classification
Species problem

Introduction: taxonomic anarchy

In a recent comment in *Nature*, Garnett and Christidis (2017, p. 25) write that taxonomy is in a state of ‘anarchy’. Their controversial note is only the most recent in a long series of similar opinion papers over the past decades (e.g. Crisp and Fogg 1988; Godfray 2002; Isaac et al. 2004; Mallet and Willmott 2003). At first sight, these accusations might strike one as surprising. After years of intensive debate about the definition of the species category, taxonomists are converging on the consensus that species are independently evolving lineages (De Queiroz 2007; Mayden 1997). Moreover, over the past two decades, taxonomy has witnessed an incredible increase in available data and sophisticated methods to delimit species taxa (Camargo and Sites 2013; Sites and Marshall 2004). Ironically, however, these two unmistakable signs of progress in taxonomy have contributed to the alleged anarchy in the resulting species classification. While there is consensus about defining species abstractly as independently evolving lineages, there is no similar consensus about how evolutionary independence should be operationalised to identify species taxa. As a result, different taxonomists rely on different data types and methods of analysis, often leading to competing results for the same organisms and causing different kinds of groups to be recognised as species.

In the remainder of this paper, I will refer to this situation as one of ‘taxonomic disorder’. Given the negative connotation of ‘disorder’, it should be emphasised that this situation does not constitute a failure of taxonomy. Instead, it is the inevitable consequence of the complexity of the organic world and the evolutionary processes that shape it. A group of organisms may be evolving

independently in some aspects but not in others, and different evidence types and methods pick up on these different aspects (De Queiroz 2007). Thus, the species category is not homogeneous, but is instead made up of different kinds of groups evolving independently in different ways and to different degrees. The consequence is that species delimitation sometimes takes place in a grey zone where the decision about the species status of a group is partially arbitrary and may be pushed one way or the other by the particular methodological choices of the taxonomist.

It is undeniable that the disorder in species classifications has a range of undesirable consequences. Most importantly, it negatively affects the repeatability, comparability, stability, and usability of species classification. If the outcome of species delimitation is arbitrary or dependent on the particular method or data type chosen, then different studies of the same organisms may come to different outcomes (not repeatable and not stable) that pick out groups of different kinds of groups (not comparable). In a similar way, the disorder also poses a threat to the objectivity of species classification: if the outcome of species delimitation varies depending on particular methodological choices, it seems importantly tied to the point of view of the taxonomists making those choices (Conix 2018).

The failure to meet these fundamental epistemic desiderata affects all who use the outcomes of taxonomic research. Most obviously, disorder in taxonomy affects conservation biology (Dusseix et al. 2018; Faurby et al. 2016; Oates and Ting 2015; Riddle and Hafner 1999) and conservation policy (Mace 2004). In the USA, lawyers have even petitioned for the use of the Biological Species Concept where taxonomists have failed to settle on any single definition (Schiff and Wood 2017). The incomparability of species also affects other biological research that uses species as their currency, such as studies in macro-ecology or diversification analyses in evolutionary biology and palaeontology (Isaac et al. 2004). Others have even pointed to the impact of taxonomic disorder on toxinology and public health (Carrasco et al. 2016). More generally, the disorder in taxonomy makes taxonomic information hard to use for those not familiar with the specialised literature.

It is not surprising then that both taxonomists and users of taxonomy have repeatedly urged to address these issues and proposed strategies to do so. These solutions range from getting rid of species altogether (e.g. Mishler 1999) to alternative nomenclature systems (Cantino and De Queiroz 2000), DNA-barcoding (Hebert and Gregory 2005) and minor changes to the current system (Knapp et al. 2002). One solution that has emerged multiple times over the years is the proposal to govern species classification in a fashion similar to the

regulation of nomenclature (e.g. Godfray 2002). However, as was particularly clear for Garnett and Christidis' (2017) recent proposal, this solution is usually met with extensive criticism and almost community-wide rejection (e.g. Raposo et al. 2017; Thomson et al. 2018). As a result, it has rarely been developed in any detail or defended in a systematic way beyond programmatic comments.

The aim of this paper is to provide a systematic defence of the governance of species classification as a solution to the problem of taxonomic disorder. To do this, section "The governance view" argues that the governance view can be disentangled into three crucial aspects: standardisation, unification and regulation. Together, I argue, these can address the problems of repeatability, comparability and objectivity. Section "Enzymes and viruses" briefly discusses two fields where a governance system has been successfully implemented, namely, virus classification and enzyme classification, and considers the implications of these cases for the governance of species classification. Section "Objections and responses" then addresses the main objections raised against the governance view. Most of this paragraph (between, 'To do this' and 'raised against the governance view' is redundant and does not really seem to be in the style of the journal. If this can be done without approval from the editor (it does not change the content at all!), I think it would be better if the first sentence ('The aim of this paper is to provide a systematic defense of the governance of species classification as a solution to the problem of taxonomic disorder') is moved to the end of the previous paragraph, and the rest is deleted.

The governance view

Despite the recent controversy, the governance view is rarely spelled out in detail. I argue that it consists of three distinct aspects: standardisation, unification and regulation. As each of these can be implemented in different ways, it is helpful to distinguish between them when evaluating the governance view. This section discusses each of these aspects in turn.

Standardisation

By the standardisation of species classification, I mean the adoption of common standards for recognising groups of organisms as species. Such standardisation can be implemented on at least three levels. First, we can standardise the species concept. There has, of course, been extensive debate about this among both philosophers and biologists, resulting in an emerging consensus that species are independently evolving lineages (De Queiroz 2007; Mayden 1997). In this respect, then, standardisation on a very abstract level seems already on the way. Second, we can standardise the outcomes of species delimitation in the shape of

a list of accepted species. Such regularly updated lists already exist or are in the making for some taxa, but not all.

Finally, we can standardise precise criteria and methods used for species delimitation. This has been proposed by some, for example in the shape of a criterion of diagnosability (Groves et al. 2017) or a combination of genetic, morphological and geographic distribution data (Shanker et al. 2017). However, large-scale standardisation seems far away in taxonomy, as the diversity of species taxa across different higher taxa makes it unlikely that a single criterion for species status can be agreed upon. For this reason, standardisation may only be possible within certain higher taxa and with different standards in place for different taxa. In line with this, a set of qualitative and quantitative standards for subspecies delimitation in marine mammals has recently been proposed, along with a call for standardisation to improve consistency (Taylor et al. 2017a, b).

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It is clear that standardisation provides a solution for some of the problems of disorder in taxonomy. Most obviously, standardising the species concept and operationalization could increase the repeatability, comparability and objectivity of species classification. Universal adoption of a single species concept or set of criteria for species delimitation would make it likely that different taxonomists recognise the same species when given the same data or set of organisms. Such species would also be comparable at least for the properties targeted by the standardised concept and criteria. The standardisation of outcomes (i.e. a species list) has different epistemic benefits. Most importantly, it would greatly improve the usability of species classification for other biological disciplines, policy-makers and legislators. In addition, taxonomy could benefit too, as creating such a list requires extensive debate and cooperation between specialist, extensive review of existing work and potential follow-up research when experts disagree.

Unification

The unification of species classification is the counterpart of standardisation on the organisational side and can come in many different forms: collecting all information in one place, representing all information in the same format, centralising authoritative organisations, adopting a single procedure for classificatory changes or new species and adopting a single and homogeneous naming system. Note that while such unification is logically distinct from standardisation, they fit well together in practice because standardised criteria and species lists are easier to represent in the same format, collect in one place, regulate by the same organisation and be adapted by the same procedures. Such unification already exists to some extent in the shape of the Codes for

nomenclature. Further significant steps towards unification over the last two decades include the establishment of databases such as Zoobank, WoRMS and CephBase, and species lists such as the List of Marine Mammal Species and Subspecies. Useful and important as these initiatives are, however, they remain limited to certain taxa, and in some taxa (e.g. birds) multiple competing species lists exist. Moreover, registration of new species in these databases is not in all cases forced by the nomenclature commission. Thus, further unification in taxonomy is still possible.

The unification of taxonomy has no direct epistemic benefits for species classification but is again likely to reduce the impact of taxonomic disorder for the users of taxonomy. If there is one location where all state of the art taxonomic information is collected, in one format, and with references to major databases and authoritative publications, this information can be used by non-specialists without having to delve into the taxonomic literature first. This way, unifying taxonomy could have indirect epistemic benefits for biology. To the extent that taxonomy benefits from the insights gained in neighbouring disciplines, further unification would also lead to indirect epistemic benefits for taxonomy.

Regulation

By the regulation of species classification, I mean the adoption of an authoritative body or set of mechanisms and rules that guides species classification and determines what concepts, operationalizations and/or outcomes should be used. Such regulation is currently only in place for the naming of taxa, and not for their classification. The nomenclature commissions publish and revise naming rules and provide rulings on individual problems of nomenclature. The success and general acceptance of these commissions suggest that regulation constitutes a suitable tool for at least some aspects of taxonomy. Like standardisation and unification, such regulation can come in different shapes: it may be top-down, by an authoritative body, but can also be more community-driven and bottom-up with the main decisive power for each taxon in the hands of an expert committee, periodical community meetings or voting system. While regulation thus limits the classificatory freedom of taxonomists, these limitations can be self-imposed rather than external.

The regulation of species classification is not epistemically or practically valuable for species classification per se. Hence, it is not a goal in itself, like standardisation or unification. Instead, its potential benefit for taxonomy lies in its ability to bring about these other two aspects. The desirability of regulation thus depends on its efficacy of bringing standardisation and unification about,

and on the efficacy of other methods for doing this. In that respect, there is a straightforward justification for regulation: there are countless taxonomic traditions, different methods, data-types, species concepts and criteria for species delimitation. In addition, there are countless governing bodies, institutions, databases, web-portals and publication channels. It seems unlikely that anything like standardisation or unification will come about naturally. Indeed, the evolution of taxonomy over the past decades suggests that further splintering of the taxonomic community is likely to occur as methods get more complex and specialised. All this suggests that standardisation and unification are only likely to happen if it is driven by a dedicated authoritative body or system.

While the regulation of species classification would mostly benefit taxonomy by enabling standardisation and unification, there are some indirect epistemic benefits connected to it. First, the procedures through which standardisation and unification are enabled by regulation are likely to benefit the resulting classifications too. This is because these procedures involve the establishment of expert committees, mechanisms for feedback from the community, explicit debates about the concepts and values involved, frequent revisions and clear and fixed procedures for implementing changes. It is agreed among philosophers of science that such social mechanisms are crucial for scientific objectivity (Longino 1990). And while some of these, such as peer-reviewed journals, are already well in place in taxonomy, the instalment of regulatory mechanisms for standardisation and unification would inevitably require more of these. Second, a regulatory system could complement the informal social mechanisms currently in place to act effectively against taxonomic vandalism (e.g. Williams et al. 2006). Finally, a regulatory body could enforce certain standards for taxonomic research, such as explicit declaration of the species concept used or registration of new species in online databases. While these are simple measures that could make classifications more user-friendly, they are hard to implement without a regulatory body.

Enzymes and viruses

The previous section has distinguished between three components of the governance view and argued that each of these can take different shapes. This raises the question of which shape of governance would be best for species classification. Given the enormous complexity of the century-old system of species classification, this is hard to foresee. To overcome this difficulty, this section considers two fields where a governance system was implemented to deal with a situation of disorder similar to that of species classification. The first concerns the classification of enzymes (section “Enzyme classification”) and the second the classification of viruses (section “Virus classification”). After

discussing these, I consider what conclusions can be drawn from these cases for the governance of species classification (section “Implications for species governance”).

Before doing this, an important caveat has to be made. Both virus and enzyme classification are practice-oriented in a way that does not straightforwardly apply to species. Moreover, both these domains are smaller than taxonomy and studied by fewer distinct groups of scientists. It follows that there are substantial differences between governance of classification in these fields and governance of biological taxonomy and that solutions that work in the former might not in the latter. For this reason, an in-depth discussion of a governance system in some branch of biological taxonomy could have been more insightful than the cases discussed here. However, while there are good examples of regulation, unification and regulation in various parts of biological taxonomy, these are never implemented together and on a large scale. For such examples, we can only turn to neighbouring disciplines. As we will see below, there are striking similarities between the problems faced by biological taxonomy and the problems that those neighbouring disciplines solved by adopting a governance system. Thus, while the success of governance systems in these cases does not guarantee the same for biological taxonomy, they are still informative and provide reasons to consider similar solutions for species classification.

Enzyme classification

Enzymes are macromolecules that catalyse chemical reactions in organisms. The complexity of enzymes and their classification arguably matches that of species: enzymologists commonly classify enzymes on the basis of criteria as diverse as evolutionary history, structure, reaction mechanism, location in the cell, overall reaction catalysed and biological role in the metabolic pathway (McDonald and Tipton 2014; Montella et al. 2012). Like in species classification, this complexity sometimes requires arbitrary decisions in enzyme classification. Given this arbitrariness, it is perhaps not surprising that after a series of important breakthroughs in enzymology in the first half of the twentieth century, the naming and classification of enzymes were in a state of chaos (Tipton and Boyce 2000).

The case of enzymes is relevant to the topic of this paper because the chaos in enzyme classification has been resolved by a system of governance. The resulting Enzyme Commission (EC) classification is, in the first place, a unified system of nomenclature that regulates the common and scientific name of all enzymes and assigns a unique and informative four digit number to each enzyme (NC-IUBMB 2018). In addition, all recognised enzymes are published in a

central database that collects all relevant information on the enzyme (McDonald et al. 2007) and links it to important publications and entries in the main protein, enzyme and gene databases (McDonald and Tipton 2014).

Parallel to this process of unification, EC enzyme classification is also standardised. While there are many scientifically interesting criteria for the classification of enzymes, the EC system is based only on the overall reaction catalysed. A set of more fine-grained concepts determines in which of the six main classes each enzyme is classified, and in which of the subclasses and sub-subclasses enclosed in these classes (McDonald and Tipton 2014; Montella et al. 2012; NC-IUBMB 2018). Unlike the abstract concepts, the operationalization of these concepts is not standardised. Thus, enzymologists use a wide range of different methods to decide in which of the various classes a particular enzyme should be classified. Because the abstract concepts leave substantial room for interpretation, the choice between multiple operationalizations and, hence, conflicting classifications, is sometimes arbitrary. In such cases, the EC system is geared towards optimising the consistency of the system. Finally, the outcomes of enzyme classification are standardised in the shape of an official list of recognised enzymes.

The standardisation and unification of enzyme classification did not come about naturally and was should be 'were' the result of a community-driven regulation of nomenclature and classification. After several preliminary attempts to construct a unified enzyme classification, the International Union of Biochemistry (IUB) established an International Commission on Enzymes in 1956 to address the chaos described above (Tipton and Boyce 2000). This commission consisted of 12 specialists from different continents and universities and was in frequent contact with many more biochemists (Webb 1993). This resulted in the first Enzyme List (IUB 1961) and classification (Dixon and Webb 1964), both of which have been regularly updated and extended ever since. Today, there is an automatized online procedure to propose new enzymes and changes in classification, which are then evaluated by a specialised subgroup of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology. Once considered by this committee, the proposal is published online for public review and subsequently added to the Enzyme List and database.

The unification and standardisation of the EC classification have allowed it to remain relevant even though insight in enzymes has changed dramatically since it was established. Today, the EC number is used in all publications discussing enzymes, acting as an unambiguous identifier over a range of different disciplines and contexts. Moreover, the EC number figures in the main

biological and biochemical databases and is used to connect proteins and genes to their physiological function in biochemical databases and the important Gene Ontology (a system that unifies the representation of genes and gene-products and enables easy access to genetic data). The usefulness of the EC classification is regularly emphasised by enzymologists and bio-informaticists, who refer to the EC system as ‘incredibly useful’ (Rahman et al. 2014, p. 17 [3](#)) and should be ‘...137), a ‘solid basis’, and ‘an indispensable tool’...’ a ‘solid basis’ and ~~is~~ ‘an indispensable tool’ (Omelchenko et al. 2010, p. 10).

Virus classification

It is generally accepted among virologists that there is no single uniquely natural classification of viruses. Hence, any classification of viruses requires ‘scientific judgment and pragmatism’ (Adams et al. 2017, p. 1443). Given that virus classification has to serve many goals and viruses have several features relevant to classification, it should be no surprise that there are often multiple good ways of doing this. To avoid the chaos that is likely to follow from this, virologists have adopted a governance system for classification.

Virus classification is highly unified in several respects. Most importantly, there is a single system of nomenclature for all viruses (ICTV 2018a). In addition, there is a regularly updated Master Species List (King et al. 2018) and a regularly updated Virus Report (ICTV 2018b) which provides an extensive and authoritative summary of the main characteristics of all recognised viruses along with important publications. Importantly, all entries in the report follow a standard format which requires virologists to be explicit about the criteria for species (and family and genus) delimitation. This means that, unlike the situation in biological taxonomy, it is always clear whether different virus species are comparable. Further unification of virus classification was realised by the establishment of a single organisation responsible for regulation, a single journal that publishes summaries of revised virus taxa, a single procedure for proposing taxonomic changes and a single web-portal that hosts all these services (Adams et al. 2017; Lefkowitz et al. 2018).

This unification goes hand in hand with the extensive standardisation of virus classification. There is a single accepted abstract definition of species for all viruses. Similarly, there are loose definitions of higher taxonomic levels that are applied across virus taxonomy (ICTV 2018a). While the operational level is also standardised in the shape of criteria for species delimitation, these criteria have a limited scope. That is, even though similar criteria are applied to all viruses, the precise thresholds or operationalizations of these criteria are only fully determined on the level of the genus or the family (ICTV 2018b). Finally, the

outcomes of virus classification are standardised in the shape of the Master List (King et al. 2018).

The standardisation and unification of virus classification are implemented through centralised regulation by the International Committee on Taxonomy of Viruses (ICTV). This committee was founded in 1966 by 43 virologists representing the different national microbiological societies with the explicit aim of regulating both the nomenclature and classification of viruses. An executive committee elected by all members then proposed a set of rules and established subcommittees and study groups with specialists to propose classifications for the different main groups of viruses. The proposed classification was then discussed by the subcommittees and ultimately approved by the ICTV in the first Report (Wildy 1971). To this day, the regulation of virus taxonomy occurs through a similar system of specialised study groups and subcommittees that propose changes to the ICTV, which then rejects or accepts by majority vote (Adams et al. 2017; Lefkowitz et al. 2018). Importantly, any virologist, even if they are not a member of a study group, can propose changes to the classification. All proposed revisions can be accessed online, and everyone is invited to contribute to the debate before changes are accepted. As all these debates as well as all changes in classification are available online, the process of revision is fully transparent (Adams et al. 2015).

~~Importantly,~~ this if the 'Importantly' is removed, this word needs a capital system of governance is not only used to adapt virus classification, but also to adapt the standards and rules of classification and nomenclature. For example, species classification was implemented in the seventh Report (Regenmortel et al. 2000) and the definition of species was subsequently adapted in 2013 after extensive debate concluded by majority vote (Adams et al. 2017). Similarly, after a dedicated workshop, the ICTV has decided recently that it should be possible to recognise virus species only known through metagenomic data. To accommodate this change, the ICTV then decided to develop new tools for submitting the relevant data and new data standards appropriate to viruses recognised on the basis of metagenomic data (Simmonds et al. 2017).

The ICTV virus classification is an excellent example of highly successful governance. Its classification system is extensively used, and the Master List and Virus Report are generally accepted as the authoritative sources on virus taxonomy. Moreover, the unified organisation of virus taxonomy allows the community to react quickly and efficiently to challenges and new insights.

Implications for species governance

While the classification of organisms is of course substantially different from that of viruses and enzymes, there are at least four conclusions we can draw from these cases about the governance of species classification: (1) concepts and outcomes should be standardised, (2) the standardisation of operationalization should leave space for variation, (3) classification should be as unified as possible and (4) standardisation and unification should be implemented by bottom-up community-based regulation.

- (1) Both the abstract classificatory concepts and the outcomes of virus and enzyme classification are standardised. Standardisation of the concept determines a theoretical framework within which the scientists individuate the relevant units, and ensures that the resulting classifications yield units that are to some extent comparable. Given the growing consensus in biology that species are independently evolving lineages, a similar standardisation would probably be relatively easy to implement. Standardisation of the outcomes, on the other hand, is particularly important for the users of enzyme classification or virus classification. The EC enzyme list and the Master List of viruses provide an updated list reviewed by experts in the field that allows non-specialists to easily and quickly access information. It is no surprise then that both lists are widely used and well-received.
- (2) Both enzyme classification and virus classification are successful without fully standardising the operational criteria for classification. The EC enzyme classification only fixes a relatively abstract concept for the class, subclass and sub-subclass to which an enzyme belongs, but not the criteria to determine the most fine-grained level of classification. Similarly, virus classification does not adopt a discipline-wide criterion for species status. This does not mean, however, that these two classification systems do not standardise the operational level at all. In the case of enzymes, scientists are required to take into account the consistency of the various classes and, thus, the limits set by previously recognised enzymes. In the case of viruses, there are family-wide or genus-wide criteria for species delimitation which ensure comparability on those levels. Moreover, the criteria used across different families are still broadly similar. More generally then, both systems seem to have found a balance in the trade-off between standardisation and the scientific freedom that is necessary to adapt classificatory practices to the particular enzyme or virus under investigation. This could be an attractive solution for species classification too, as it would allow taxonomists to adapt their criteria to the taxa under investigation while at the same time increase comparability to the highest degree possible.

- (3) The extensive unification of enzyme classification and virus classification is crucial to the efficiency and success of these classification systems. For example, this unified structure allowed virologists to quickly adapt to the increasing availability of genomic data and the opportunities this offers. The ICTV now recognises viruses only known through such data and is adapting its revision system appropriately (Simmonds et al. 2017).¹ Similarly, the unified structure of virus taxonomy allowed it in 2000 to implement the species-level relatively easily and to adapt the definition of species in 2013 by majority vote. This is in stark contrast to biological taxonomy, where the debate about species concepts has been going on for a long time and disorder continues to hamper its efficacy (Zachos 2016).
- (4) Both in enzyme classification and virus classification, regulation played a crucial role in establishing standardised concepts and outcomes, and in unifying the organisation of the discipline (Adams et al. 2017; McDonald and Tipton 2014). Moreover, the same regulatory bodies also continue to play a crucial role in maintaining and revising the existing classification and classificatory principles. In both cases, regulation is not top-down, but bottom-up with an important role for committees drawn from specialists in the various relevant subfields. Moreover, community feedback and peer review play an important role in both systems. Any changes to the existing classification are only accepted after they have been open for review from the community. Final decisions are then made either by the community or by a committee that represents the community. A similar system in biological taxonomy could ensure that the input from all subfields of taxonomy is taken into account and that any restrictions of scientific freedom are self-imposed and open to change.

Objections and responses

To finish the paper and further substantiate my points, I consider five objections that have been raised against the governance view. I argue that the case-studies in section “Enzymes and viruses” as well as the analysis of the governance view in section “The governance view” strongly mitigate these objections.

Scientific freedom and the hypothesis-based nature of taxonomy

One particularly common objection to the governance view is that it is incompatible with the scientific freedom that is required for a hypothesis-based science like taxonomy (Bremer et al. 1990; Lambertz 2017; Raposo et al. 2017; Thomson et al. 2018). The idea is that regulation and standardisation would limit

this freedom and thus hinder progress. Taxonomy would then be reduced to a mere labelling discipline at the service of its users.

The considerations raised in this paper suggest that this objection is misdirected. First, this objection conflates standardisation and regulation with stability and resistance to change. However, both standardisation and regulation are perfectly compatible with frequent changes in classification or classificatory principles when new evidence or conceptual change require this. Thus, even regulated standards and the species recognised by these standards are fallible and subject to change. Indeed, mechanisms for change and the community feedback necessary for this are a crucial component of the regulated classifications of enzymes and viruses. Thus, one could even argue that the regulation of taxonomy can streamline this fine-tuning of hypotheses by establishing efficient systems of review, expert discussion and subsequent revision.

Second, the discussion above suggests that regulation and standardisation need not strongly inhibit scientific freedom. For one, they only affect the application of the species concept and in no way restrict what research taxonomists should do or what hypotheses they raise about the evolutionary relations between groups. Moreover, I have argued above that some degree of scientific freedom is necessary in the operationalization of standards, even in systems as strongly standardised as virus taxonomy. It is also worth pointing out that the system of regulation can be constructed and adapted bottom-up, by the community itself. Thus, one could argue that the regulation of taxonomy is in fact the taxonomic community exercising its scientific freedom to solve an important problem.

Finally, while taxonomy is indeed an empirical and hypothesis-based discipline, arbitrary decisions can never fully be avoided due to the tension between the discreteness of classification and the continuous nature of evolutionary processes. However, this does not mean that there is an ineliminable tension between the user-oriented and hypothesis-based aspects of taxonomy. While there is a short-term trade-off between stability and the frequent adaptation of classificatory hypotheses, on the long term, these two sides of taxonomy can only benefit from each other. Deep and accurate insight in ~~the~~ evolutionary groups is likely to increase long-term stability and usefulness of classifications, thus benefitting all who rely on these classifications. Similarly, a taxonomic system more geared towards its users is likely to lead to more funding and increased respect for taxonomy, which in turn could contribute to resolving the taxonomic impediment.

Small changes and continued effort will do the job

A second objection holds that the governance view is too drastic and costly a solution for a problem that can also be resolved by minor tweaks to the current system (Cotterill et al. 2017; Knapp et al. 2002; Thomson et al. 2018). The idea is that continuing on the same track with relatively small changes such as improvements in the education of new taxonomists, better fund-raising and better use of databases could resolve the problem while at the same time avoiding the complete overhaul of the system. As Newman (1989, p. 24) puts it, refinement might be a better solution than ‘a monkey wrench thrown into the gears of an entire system’.

Two remarks are in place here. First, many of the small changes suggested to improve the current system are also compatible with the governance view. Indeed, some of these changes are a crucial part of the governance view, such as making the species concept explicit or better use of databases. Second, it is doubtful whether simply continuing taxonomic efforts in the current system is likely to resolve the disorder problem. While taxonomy has made significant progress over the past 250 years, this progress has not been in the comparability or repeatability of species classifications. Indeed, while our insight in the evolutionary relations of groups has increased dramatically, the disorder in taxonomy has remained constant over the past decades, and some even argue that it has increased (Isaac et al. 2004). It seems then that more of the same will not do the job, and the ‘costly medicine’ of an overhaul of the system is required (Buckeridge 2017, p. 600).

An arbitrary pick is not a solution

~~Yet,~~ a Another objection holds that philosophers and taxonomists have debated the species concept for centuries without coming close to a substantial agreement (Thomson et al. 2018). The idea is that arbitrarily settling on one particular concept or standardisation, as the governance view seems to do, is no satisfying philosophical or scientific resolution to this problem and gives up on the progress that has been made in this debate.

It is true that the governance view implies that some taxonomic decisions are not made solely on the basis of empirical considerations. However, it is wrong to see this as an unsatisfactory solution to a problem that could be resolved with continued scientific and philosophical effort. As many have pointed out (De Queiroz 2007; Zachos 2018a), it is inevitable that in some cases, there are multiple competing species classifications that are empirically acceptable. Indeed, the recognition of this arbitrariness is itself the result of increased insight in the organic world. Importantly, all of this does not mean that species classification is arbitrary in all respects. Even if the world does not fully

determine which classification is best, there are other factors we can rely on to make these decisions. Species classification is an important tool for many scientific and non-scientific fields and impacts everybody in society. If there are several good but competing options, taxonomists should simply choose the option that is most useful for these fields, or that is most consistent with the rest of the classification system and thus makes the system more useful in general. This is also the idea behind Garnett and Christidis' (2017) claim that lawyers, sociologists and anthropologists should be involved in the regulation of species classification.

In short, the arbitrariness in the regulation view is not problematic: on the one hand, it reflects our increased insight in the organic world , and replace by ';'..... on the other hand, it provides an opportunity to make species classification as useful as possible for those who rely on it.

Values should not influence taxonomy

The claim that some decisions in taxonomy should be made on the basis of the various purposes of species classifications raises another popular objection. This objection holds that neither value-judgments nor lawyers or legislators should influence biological taxonomy (Raposo et al. 2017; Thomson et al. 2018).

The response to the previous objection suggests that this objection is misdirected. It is true that there are many decisions in taxonomy in which value-judgments should not play a role. For example, the decisions whether there is gene-flow between two populations, whether a particular trait is under selective pressure or whether a particular phylogenetic tree fits the data should not be influenced by considerations about what would be best for users of taxonomy. However, as discussed above, not all taxonomic decisions are fully determined in this sense. For those decisions that cannot be settled by only empirical considerations, taxonomists should choose the option that is most desirable given the particular set of goals and values we have. For example, if splitting a group into two species would lead to conservation policy that increases the chances of inbreeding depression, this may be a good reason to recognise the group as a single species (Frankham et al. 2012).

It is important to note that arbitrary decisions in taxonomy are already influenced by value-judgments concerning the cost of certain methods, ethical restrictions on the sampling of organisms, conservation consequences and even the location of sampling (Harris and Froufe 2005; Isaac et al. 2004). Thus, the main difference between the current situation and the governance view is that these value-judgments would be debated explicitly and subsequently fixed in standardised concepts and operations, instead of playing their role implicitly.

Given that taxonomy affects the whole of society through its impact on trade legislation, biodiversity conservation and agriculture, the preferences of all stakeholders in society should be taken into account when making ‘arbitrary’ decisions. Doing this ensures that one set of value-judgments is not inappropriately favoured over another.

Together, these considerations suggest that rather than raising an objection to the governance view, the involvement of values in taxonomy is one of its strengths: by making the role of value-judgments in arbitrary decisions more explicit, the governance view can ensure that the interests of all relevant parties are taken into account while at the same time avoid that unwanted value-judgments creep in.

Too much bureaucracy and practical problems

The strongest objection against the governance view is that it is inefficient and practically not feasible. Most importantly, it would add another layer of bureaucracy to the already inefficient institutional structure of species classification (Hollingsworth 2017; Thomson et al. 2018). Such additional bureaucracy would be costly, and it is unclear where funding could be found to support it. The shortage of taxonomic specialists for most taxa also suggests that it would be difficult to form committees with the required expertise. Finally, it seems likely that a governance system would slow down classification, as new species would have to await approval by the relevant committee before they can be recognised.

The force of this objection is hard to evaluate as it depends on the comparison of the practical and bureaucratic loads of the current system and a governance system yet to be developed. To avoid engaging in such counterfactual debates, it is helpful to turn to the case-studies of regulated classification in section “Enzymes and viruses”. These cases suggest that even though the establishment of committees, subcommittees and a working group is costly and takes up valuable time of experts, there are also various gains in efficiency. First, the unification of classification can increase efficiency by merging distinct but similar initiatives with a narrow scope. For example, the establishment of one standardised master-list means that various competing lists or classifications could be merged. This is precisely what happened in the case of virus classification, where multiple associations and classifications were in place before the establishment of the ICTV (Fauquet and Martelli 2013). Second, a unified and well-regulated taxonomy could also attract funding that is currently not available to taxonomy. For example, the ICTV and its virus classification are supported with dedicated grants and staff hired to maintain the system (Adams et

al. 2017). This means that funding and manpower need not be drawn away from actual research on virus taxonomy. Finally, it is worth pointing out that a new taxonomic system could be implemented gradually depending on the funding available. For example, revisions for the new Virus Report do not happen simultaneously, but are implemented taxon per taxon, over the course of several years (ICTV 2018b).

Nevertheless, it is hard to deny that implementing a regulation system would require funding and time, and it would take some time before the system becomes as efficient as the current one. However, this does not mean that such a system is not viable. There are drawbacks to every solution to the species problem, and to keeping the current system. The point is that these have to be weighed off against the benefits of these solutions. While this can only be done by developing a governance system in more detail, I argue that the benefits of such a system are considerable and thus may well outweigh the costs of additional bureaucracy.

Conclusions

This paper has presented the governance view as a solution to the problem of disorder in biological taxonomy. More precisely, I have argued that the standardisation, unification and regulation of species classification can increase the comparability, repeatability, objectivity and usability of this classification. I have substantiated this by analysing each of these three components in detail, by drawing the parallel with enzyme classification and virus classification and by responding to five important objections.

It goes without saying that more work is needed to develop the most appropriate governance system for taxonomy and fully evaluate the viability of that system. Moreover, it is also clear that the governance of taxonomy is not the only viable solution. Others have proposed to adopt multiple parallel classification systems, the abolishment of the species rank (Mishler 1999) or changing conservation law and policy (Doremus 2010). Zachos (2018b), finally, suggests that focusing on the underlying data rather than the species rank could help to avoid the threshold character of ranks and select the resolution that is suitable for the particular case at hand. At this point, it is crucial to continue the debate and take all viable options into serious consideration in a constructive debate.

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¹ To the extent that there is governance in the classification of bacteria and archaea, it has been slow to react to the similar challenges posed by environmental screening and metagenomic data in these fields. The International Code of Nomenclature of Prokaryotes (Parker et al. 2015) still requires a pure culture submitted to at least two collections before a new species can be named, but this rule is controversial as there is a wealth of taxonomic information available on candidate species that have not been cultured (Breitwieser et al. 2017; Hedlund et al. 2015; Konstantinidis and Rosselló-Móra 2015).