A price tag on species

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Abstract

Species have intrinsic value but also partake in a long range of ecosystem services of major economic value to humans. These values have proved hard to quantify precisely, making it all too easy to dismiss them altogether. We outline the concept of the species stock market (SSM), a system to provide a unified basis for valuation of all living species. The SSM amalgamates digitized information from natural history collections, occurrence data, and molecular sequence databases to quantify our knowledge of each species from scientific, societal, and economic points of view. The conceptual trading system will necessarily be very unlike that of the regular stock market, but the looming biodiversity crisis implores us to finally put an open and transparent price tag on symbiosis, deforestation, and pollution

Keywords

digital species, valuation of species, trading system, biodiversity, economy, informatics

Species are one of the three major elements of biodiversity, the other two being genes and ecosystems. More than 2 million species have been formally described by science so far, and another 10 million or more await formal description (Chapman 2009). Species are forming living parts of extant ecosystems and are thereby major components of the ecosystem services. These services have a monetary value. For instance, Vallecillo et al. (2019) estimated that the ecosystem services in Europe are worth €124 billion per year. de Groot et al. (2020) calculated the values of ecosystem services and estimated that the highest mean values per unit area are maintenance of genetic diversity (6,629 Int$/ha/year), waste treatment (6,552 Int$/ha/year) and recreation and tourism (4,248 Int$/ha/year). Species form a part of the Natural Capital which interacts with Human Capital and Produced Capital (Dasgupta 2021). According to Dasgupta (2021), "... many kinds of natural capital simply do not have markets. They are free to the user. So special methods have to be devised for estimating accounting prices". Species are certainly one kind of natural capital which are mostly free to use. There is clearly no standardized, generic tool to calculate the value of species across all extant taxa. This opinion paper will explore the conceptual idea of the **species stock market** (SSM), an imaginary yet impending device that will provide a unified basis to quantify the value of described as well as undescribed species.

Species are composed of physical entities called individuals. Examples of such individuals are living animals, plants, fungi and bacteria in natural habitats – but also their tissue samples in biological collections and DNA in biobanks. In addition, a single organism may have several individuals, e.g., a preserved specimen in a collection and its frozen tissue or purified DNA in a biobank. Extinct species may similarly be represented by distinct individuals through, e.g., fossil specimens or other preserved parts, although DNA data will be less common. All these individuals may be represented by one or more digital records in different databases. We could therefore argue that there are digital species (DS) composed of datasets of records on individuals (Lannom et al. 2020). These data records are increasingly being made freely available online as an open data. Well-known examples of such free resources of digital records of individuals are the International Nucleotide Sequence Database Collaboration (INSDC; Arita et al. 2021) and the Global Biodiversity Information Facility (GBIF; https://www.gbif.org/). The proposed species stock market will rely on open data records of biological individuals and metadata connected with these records. It is reasonable to divide the formation of SSM into three phases:

1. the formation of **digital species**;
2. the **valuation of species**; and
3. the **trading system for the species**.

Digital species can be created by clustering data records of individuals. Currently the most straightforward way to accomplish this is to use publicly available DNA sequences in the public sequence databases such as the INSDC. After all, DNA sequences readily lend themselves to analyses covering all extant taxa, and there is furthermore a large selection of computational tools available for the purpose (Hyde et al. 2013). Public DNA sequences range from those derived from individuals identified to species-level and lodged in natural history collections to more or less unidentified sequences derived from environmental samples such as soil, water, and air. DNA sequences identified to species level will serve as a links between digital species and the tree of life or classification. Individuals in collections typically come with ample metadata on, e.g., habitat, interactions between hosts and parasites, and functional traits. Therefore, the data records are the most valuable part of the digital species, and physical individuals can be restudied for additional, often critical information. DNA sequences from environmental samples tend to comprise both described and undescribed species since high-throughput sequencing (HTS) such as metabarcoding of samples are normally used to retrieve sequences of all individuals in any sample (Tedersoo et al. 2022). For some taxa, most or all known occurrences are in the form of DNA sequences from ecosystem studies where samples are analysed with HTS methods. Digital species might be managed further by incorporating data records of non-sequenced individuals, notably observations, older material in collections, and data from publications.

For stable communication of digital species, persistent identifiers (PID) are needed in parallel with traditional species names (Hibbett 2016, Kõljalg et al. 2016). The reason is that only formally described species have a scientific name; in addition, competing names are available for some species. Despite the shortcomings of biological nomenclature, it is still necessary to use scientific names in that they represent the major way in which species can be connected to the tree of life (Hobern et al. 2021). This tree serves to bridge biodiversity information over all data types, making it indispensable in species valuation analyses. Another important feature of digital species is their authorship. We posit that there are two principal types of authors. The first one comprises the persons who created the data records, and the second one comprises the institutions storing the physical and digital objects of biodiversity in their open archives. Such institutions include museums and botanical gardens, DNA sequence databases, and data portals. Future evaluation and funding of institutions may partly factor into this authorship. An example of a digital species as outlined in the above is visualized in Fig. 1. The compilation of datasets of this kind is explored in Kõljalg et al. (2020).

The **valuation of species** can be based on non-anthropogenic as well as anthropogenic values. It is clearly problematic to quantify the non-anthropogenic value of species over all taxa in one and the same way. If we start to quantify the value of nature, it becomes anthropogenic immediately. Therefore, it seems reasonable to initially set one and the same, identical base value to all species, ranging from *Homo sapiens* Linnaeus to parasites and pests. The anthropogenic value of species is based on diverse traits, including ecosystem services, which ideally can be quantified precisely. The main requirement, however, is that such traits can be digitized according to accepted data standards and connected to the data records of the digital species. This will allow automated book-keeping of the digital species, automation being the only feasible approach as the numbers of species runs into the tens of millions or more. One such trait would be the citation rate of the species name (or PID of the digital species) in publications. This requires that publishers, data portals, and species identification pipelines use the same or linked species PID systems. The number of high-quality data records per digital species is another useful trait in the valuation process. To avoid inflation of data records, some kind of weighting or filtering approach may be needed. Millions of DNA sequences of some single species or tens of thousands of observations of popular bird species are examples of where down-weighting may be called for. Protected, threatened, and keystone species should receive higher a value, but a valuation standard of such species is needed. Funded research that produces data records of the digital species is another useful measure. Species whose underlying research is better funded should potentially be assigned a higher value. As a consequence, parasites and disease agents may become the species with the highest values. The funding parameter can also be used in the opposite direction, namely to find species of high value but that are not covered by well-funded research efforts.

The value of the species and datasets of the digital species become the foundation of the species stock market. The **trading system** we envision is conceptually very different from the normal stock market. Just like the regular stock market, though, the species stock market seeks to provide an instantaneously updated estimate of the value of each and every item in its holdings. However, unlike the regular stock market, the species stock market does not seek to transfer ownership rights of species among shareholders. Instead, the concepts of buying and selling will have to assume new forms. The act of turning a natural meadow into an industrial site – thus effectively terminating a specified or estimated number of individuals of a set of species – could be compared to selling on the species stock market. The species stock market would be able to put a price tag on this transaction. The price could be thought of as an invoice that the seller needs to settle in some way that benefits global biodiversity, such as through a donation to a pre-approved, biodiversity- or climate change-oriented welfare organization. Conversely, taking some action that benefits biodiversity as estimated through individuals of species would be akin to buying on the species stock market. Buying, too, has a price tag on it, but the price should probably be thought of in goodwill terms. The species stock market would thus make it possible to valuate actions such as reforestation of an industrial site or restoration of a polluted habitat. The species stock market we envision will not allow greenwashing, that is, buying some set of species with the act of subsequently selling others in mind. Transactions would essentially be unidirectional.

Indeed, the species stock market we envision is an endeavour where no human being will make any direct monetary profit, and yet one from which all of biodiversity – including humans – benefit. We argue that the time has come to design and develop such a platform, because ecosystem services and nature protection need well-founded prices for the species in specific habitats or areas (Hungate et al. 2017, Mosberg 2018). The system must cover all extant and extinct species, both described and undescribed. The creation of the SSM is probably best orchestrated by the international associations of taxonomists and economists. These are disciplines that perhaps are not accustomed to working together, but we see no other way out of the looming biodiversity crisis than entering the primary unit of biodiversity – species – into a monetary system subject to public trade. This will, finally, put a price tag on species – and a cost on logging, pollution, climate change, and so on. Money is, somehow, a language that everyone seems to understand, and if we need to transpose the intrinsic value of biodiversity into monetary terms for everyone to appreciate it, then we feel that this is what biology must seek to do.

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Conflicts of interest

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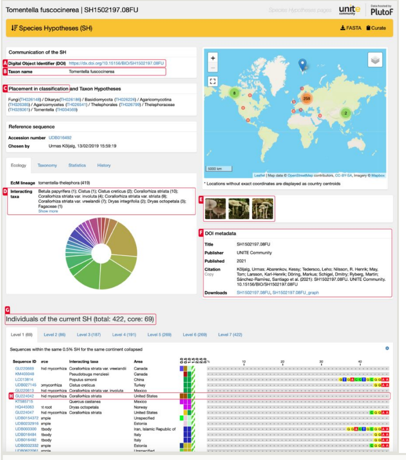

Figure 1.

A mycological example of a Digital Species (DS). It is based on so-called Species Hypotheses (SHs) published by the UNITE Community (https://unite.ut.ee). The SH paradigm offers stable identification and communication of described and undescribed species. They include several essential elements of the DS as follows: (A) Digital Object Identifier (DOI) is a collective identifier for all individuals included in this taxon; (B) Taxon name connects the SH with (C) classification (i.e., the tree of life); (D) individuals of the SH often accompanied by rich ecological data like – in this case – the interactions of the fungal SH with plant species; (E) individuals may include multimedia to visualise different features and traits of the DS; (F) DOI metadata feature information on who (and when) published the current SH and provides downloading options for the dataset; (G) the largest data panel includes all individuals and their associated data in browsable mode; and (H) single individual with Sequence ID as a link to the GenBank nucleotide archive. The interacting taxon is an orchid species - *Corallorhiza striata* - found in United States. The row ends with DNA sequence data which can be browsed to the right.