The problem of defining life: a case study using family resemblance

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4	4 Jessica K. Abbott ^{1,2} & Erik Persson ³				
5	1.	Corresponding author: jessica.abbott@biol.lu.se			
6	2.	Department of Biology			
7		Lund University			
8		221 00 Lund, Sweden			
9	3.	Department of Philosophy			
10		Lund University			
11		221 00 Lund, Sweden			
12					
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16 Abstract

17 The question of how to define life has been an unresolved question in the philosophy of biology for 18 many years, but developing a definition of life that is useful in both technical and everyday contexts 19 has become more urgent as researchers around the world attempt to create fully synthetics cells in 20 the laboratory, develop more and more intelligent and autonomous robots, and search for signatures of life elsewhere in the galaxy. Developments in these areas may end up overturning our 21 22 current ideas about the distinction between life and non-life. It is therefore important to consider 23 whether it is possible to develop a definition of life that encompasses currently known lifeforms, 24 while at the same time having the potential to be applied to as-yet unknown lifeforms. Here, we 25 discuss the pros and cons of some of the current approaches to defining life, then propose an 26 alternative approach based on family resemblance. We also present preliminary data applying our 27 new approach within a statistical modelling framework, and find that although living and non-living 28 entities can be grouped according to overall similarity, it is difficult to find a single set of criteria 29 which is sufficient for defining known forms of life while at the same time being inclusive enough to 30 be useful in identifying or characterizing novel forms of life. We hope that the family resemblance 31 approach will prove to be a fruitful alternative to traditional approaches to defining life.

33 Introduction

Imagine that you are reading a book or article and come across an unfamiliar word. If it is not possible to determine the meaning of the word from the context, chances are that you would look up the definition of the word in a dictionary. A typical dictionary definition includes a description of the meaning of the word, a list of possible alternative usages with examples of each usage, and probably a list of synonyms. Even an apparently simple word such as "chair" can be difficult to define if it has many possible uses depending on context. For example, the Oxford English Dictionary's entry for the word "chair" is in fact over 5000 words long (Simpson and Weiner 1989).

41 This stands in contrast to how children learn new words when acquiring language. All humans learn 42 how to speak their first language through their interactions with other individuals, rather than by 43 looking words up in a dictionary (MacWhinney 1999). The child's mother might say "sit down on the 44 chair", and use a gesture to help indicate her meaning. In this sort of situation, the child receives 45 information not only about how a "chair" looks, but also what it's used for. Over time, the child will 46 see many examples of different types of chair and learn what they all have in common (MacWhinney 47 1999). Eventually, the child becomes able to recognize even rather unusual examples of chairs as 48 chairs (Figure 1).

This sort of learning process works well for words used in everyday situations, but what about more abstract concepts such as "life"? Technical and scientific definitions of the word "life" are necessary in various biological and chemical research fields, such as the origin of life (Pross 2016), but how well do these definitions align with a layperson's definition of life that builds on personal experiences of life and death? Does it even matter if the technical and layperson definitions don't align very well?

54 Although the question of how to define life has been an important issue in the philosophy of biology at least since Aristotle (Barnes 1984), it is becoming increasingly relevant as a result of current 55 56 technological developments. Researchers around the world are now engaged in attempts to create fully synthetic cells in a laboratory setting (e.g. Gibson et al. 2010, Hutchison et al. 2016), and 57 58 coordinated efforts are being made to try to detect signatures of life elsewhere in the galaxy (Seager 59 2014). Developments in these areas may end up overturning our current ideas about the distinction 60 between life and non-life. It is therefore important to consider whether it is possible to develop a 61 definition of life that is useful in both technical and everyday contexts, while at the same time having the potential to be applied to as-yet unknown lifeforms. We will begin by discussing pros and cons of 62 63 some current approaches to defining life, then propose an alternative approach, and finally present 64 preliminary data applying our new approach.

65 Types of definitions

66 The two examples of the definition of the word "chair" discussed above – an adult who looks up an 67 unknown word in the dictionary, and a child who learns new words through personal experience and 68 interactions with other people – exemplify not only two different ways of acquiring information, but 69 also two different approaches to defining objects and phenomena. In the first case, the dictionary 70 definition, it is assumed that an exhaustive list of criteria can be made which must be fulfilled in 71 order for an object to be considered a member of the category "chair". This is typically called a de re 72 definition (Føllesdal et al. 1988, Lübcke 1988, Bernadete 1993, Retana-Salazar and Retana-Salazar 73 2004, Thompson 2008). "De re" is Latin and can be translated as "about the thing"; it is often 74 contrasted with "lexical", or "de dicto" (lat. "about what is said") definitions (e.g. Gayon 2010). A de 75 re definition therefore attempts to capture the essential properties of a phenomenon, while the de 76 dicto reference aims to capture how a term is commonly used. De re definitions are common in 77 dictionary definitions of everyday objects, as well as in technical definitions of objects and 78 phenomena within the natural sciences (it is, for example, possible to unambiguously define an atom 79 of gold based on the number of protons contained in the nucleus of the atom).

80 In the second case discussed above, similarities in form and function can be used to create an 81 internal list of properties that a chair usually fulfils. A list of properties or criteria of this type is more 82 fluid than in a de re definition. Not all criteria need always be fulfilled, the list of criteria can be dynamically updated, and criteria can be weighted differently depending on their relative 83 84 importance. This more fluid type of definition makes it possible for us to recognize non-standard 85 examples of chairs as long as they have enough in common with other types of chair we have 86 previously encountered (Figure 1). This is an example of a family resemblance approach, where 87 objects are understood based on their overall similarity rather than a list of necessary criteria 88 (Wittgenstein 2001). Studies of language acquisition have shown that we generally use this type of 89 approach when learning our native language (Medin and Schaffer 1978). The idea of family 90 resemblance as a linguistic phenomenon was first developed by the philosopher Ludwig 91 Wittgenstein (1889-1951) while working at the University of Cambridge in the early 1900's. He 92 wanted to investigate how we describe and understand complex phenomena such as art or games. 93 A game is a deceptively simple concept. Everyone knows what a game is, but to create a list of 94 criteria shared by all games, while still excluding non-game phenomena (i.e. a typical de re definition) is likely impossible. The diversity of different types of games is simply too large; there are 95 96 board games, ball games, card games, video games, role playing games, games that are played 97 alone, games that are played as a group, cooperative games and competitive games, etc. The only

98 things that all these different types of games could perhaps be said to have in common is that they 99 are entertaining and include some sort of element of competition (it must be possible to "win" the 100 game, either by defeating the other team, the other players, or the game itself). But the same could 101 be said of other types of phenomena, such as a structured debate, and it is not clear whether these 102 properties apply to all sorts of games. This makes it difficult and perhaps even impossible to define 103 games as a group in the same way as we define an atom of gold.

104 Some writers have therefore suggested that we should instead use the family resemblance approach 105 for constructing definitions (Neuman 2012, Pennock 2012), not simply considering it as an 106 interesting linguistic phenomenon. Using a family resemblance approach, one could use the 107 properties of the majority of games to create a more intuitive definition (although we will not 108 attempt this here). Under such a definition, not all criteria would need to be fulfilled, as long as the 109 overall similarity is sufficiently high. For example, solitaire could be recognized as a game using a 110 family resemblance approach even though most games require multiple players, based on its overall 111 similarities with other types of card game.

112 "Fuzzy" definitions in biology

Biology encompasses many phenomena that are difficult to define. What is a gene, or a species? In 113 114 both cases different definitions are used in different contexts, because it is difficult to develop a 115 definition that works in all contexts (Dupré 1995, de Queiroz 2005). When it comes to defining species, there are a number of different widely-applied species concepts, and introductory 116 117 textbooks in evolutionary biology typically include several different variants, each with its own pros 118 and cons (e.g. Ridley 2003). One of the most common is the so-called biological species concept, 119 which states that individuals that can successfully mate and produce fertile offspring are members of 120 the same species (Ridley 2003, de Queiroz 2005). However this definition is not useful for organisms 121 that do not reproduce sexually, such as bacteria or parthenogenetic organisms (which reproduce 122 clonally via unfertilized eggs; Dupré 1995). It also does not take into account the fact that there are 123 many plants and animals which can hybridize with other closely-related individuals when given the opportunity. For example, tigers (Panthera tigris) and lions (Panthera leo) can hybridize to produce 124 125 partially fertile offspring (female hybrids are sometimes fertile but males are not), but this does not 126 occur under natural conditions since the two species are found in different parts of the world (Li et 127 al. 2016). Although these two species could therefore potentially be classed as different populations 128 of the same species according to the biological species concept, this solution is not embraced by 129 biologists due to their divergent morphology, non-overlapping ranges (Asia versus Africa), 130 adaptation to different habitats (mainly forest versus mainly savannah), and different social

structure (solitary versus social; Castelló 2020). This simple example illustrates why many biologists
embrace a pluralistic approach to defining species, where multiple possible definitions of what
constitutes a species are acceptable, with different definitions being used in different contexts
(Stanford 1995, de Queiroz 2005).

135 One reason why finding a single definition of a species is so challenging is because life is so diverse, 136 and different groups of organisms can have completely different ways of living and reproducing. But 137 this is not the whole story. Speciation is also a gradual process, which means that differences in 138 morphology and behaviour can sometimes arise long before two populations become so genetically 139 different that they can no longer hybridize (Li et al. 2016). This makes it very difficult to pinpoint any 140 specific time when organisms cross the boundary from being two populations of the same species, 141 to becoming two different species. There are therefore considerable similarities between the 142 problem of defining species, and the problem of defining life. If anything, defining life is even more challenging since the origin of life is so difficult to study, and there are many entities which may in 143 144 some sense be considered borderline between living and non-living, including viruses, intracellular 145 parasites, or semi-autonomous components of organisms such as sperm.

146 Although we will not discuss it in any further detail, it is worth mentioning here the issue of "life" and "living" as the opposite of "death" and "dead". Defining "living" versus "dead" is a question of 147 148 individual status as alive or not, and is outside the scope of this work. Here, we are interested in 149 being able to distinguish "living" from "non-living", i.e. all organisms that currently exist, have 150 existed, or may exist in the future, compared to objects or entities that have never been alive and 151 never will. All non-avian dinosaurs are currently extinct, but they were alive while they still existed 152 on earth. In contrast, a stone is not alive and never will be, so it would be nonsensical to call it "dead". Nevertheless, some of the criteria that are traditionally associated with defining life versus 153 154 non-life are also associated with defining living versus dead, making it difficult to discuss these issues 155 completely independently of each other. For now, we intend to leave an analysis of the overlap 156 between them to future work.

157 How to define life? Problems and potential solutions

158 Properties that are typically associated with life include, for instance, energy use, growth,

reproduction, the ability to sense and react to the surrounding environment, and the ability to adapt

to this environment (e.g. Solomon et al. 1993, Audesirk and Audesirk 1999). There are a number of

161 biological systems that have some but not all of these properties, of which viruses are likely the most

162 familiar. However other examples include transposable elements (DNA sequences which can copy

themselves between different parts of the genome) or prions (proteins which can transform other

164 proteins into the same configuration), both of which could be considered to carry out a form of 165 reproduction. Apart from the difficulties arising from known cases such as this, the challenge of 166 defining life is multiplied when trying to develop a definition which could extend beyond the known 167 forms of life. It is only a matter of time before we will have to deal with practical problems 168 associated with alternative lifeforms, such as autonomous robots, general artificial intelligences, or 169 synthetic cells (Persson et al. 2019). More speculative, but still within the realm of possibility, is the 170 discovery of extra-terrestrial lifeforms, for example microorganisms under the surface of Mars. We 171 need to be able to recognize these alternative forms of life even if they may be very different from 172 currently known lifeforms. This is unlikely to be possible using a de re approach. If we cannot agree 173 on a set of criteria to define known lifeforms, how much more difficult will it be to find a unique set 174 of criteria which unify robotic, synthetic, and extra-terrestrial life?

175 There are several potential ways to move forward given these difficulties. We might decide to simply 176 try harder, under the assumption that at some point we will have gained enough knowledge to 177 construct a correct and all-encompassing definition of life. A problem with this approach is that all 178 currently known life has a single origin (Pross 2016), which means that it may not be possible to 179 determine which criteria are universal to all life and which are a contingent result of a common 180 evolutionary history (Gould and Lewontin 1979). A second approach could therefore be to wait and 181 see, i.e. put off trying to develop a single all-encompassing definition until we know what alternative 182 forms of life it must include. Finally, we might decide to treat the definition of life in the same way as 183 the species concept, and simply accept that life is too diverse for a single definition to be adequate. 184 In this case different technical definitions of life could be developed depending on the context, such 185 as the origin of life. The earliest biological systems probably lacked some of the criteria typically 186 associated with modern lifeforms, such as the ability to sense the external environment (Pross 2016, 187 West et al. 2017). Definitions of life that are used when researching the origin of life therefore tend to include broad criteria such as "energy use" and "dynamic equilibrium" (Pross 2016), rather than 188 narrow ones such as "composed of cells" (Bedau 2010) or "contains information encoded in DNA" 189 190 (Koshland 2002, Lazcano 2008, Bedau 2010). Given the ongoing discussion in the literature of the 191 problem of defining life (Persson et al. 2019), none of these approaches seem to be particularly 192 satisfying. We discuss why in more detail below.

193 Try harder

Although it may be valuable to continue searching for universal criteria for defining life, the question is how likely it is that this approach will succeed. Philosophers have attempted to define life at least since Aristotle (Barnes 1984), and if anything, the difficulties have increased over time rather than diminished as our knowledge has increased (Zimmer 2021). For example, whether viruses should be 198 considered living has been unclear since their discovery, and is still controversial among biologists 199 today (Choi 2008, Hegde et al. 2009, López-Garcia and Moreira 2009, Ludmir and Enquist 2009, 200 Moreira and López-Garcia 2009, Navas-Castillo 2009, Forterre 2010, Herrero-Uribe 2011), even 201 though most introductory textbooks state that they are not living because they do not have a 202 metabolism and cannot reproduce outside of a host cell (e.g. Solomon et al. 1993, Audesirk and 203 Audesirk 1999). Proponents of the view that viruses should be considered living tend to consider the 204 ability to reproduce and adapt via evolution, as well as evidence of their relatedness to the rest of 205 the tree of life, to be more important criteria (Hegde et al. 2009, Ludmir and Enquist 2009). An 206 informal survey of 40 professional biologists of all career stages at Lund University revealed an 207 almost exact 50-50 split on this issue (Abbott, unpublished data). Recent research has not helped to 208 clarify the issue.

209 There are three main hypotheses about the origin of viruses (Krupovic et al. 2019). One of the 210 earliest hypotheses was that viruses are remnants of the most ancient lifeforms on earth, a 211 transitional form between non-living organic molecules and living cells. Support for this hypothesis 212 has decreased over time since it is hard to see how an entity that is completely dependent on living 213 cells for reproduction could arise before the existence of such cells (Krupovic et al. 2019). A second 214 hypothesis is that viruses arose from transposable elements that acquired the ability to transmit 215 themselves horizontally (i.e. between unrelated individuals, rather than exclusively from parent to 216 offspring). This hypothesis is fairly widely accepted since there are a number of structural and 217 biochemical similarities between retroviruses and transposable elements (Biémont 2010, Krupovic et al. 2019). A third hypothesis is that viruses arose from bacteria or other intracellular parasites that 218 219 lost more and more of their genetic material and independent functions as they became more 220 dependent on their hosts (Krupovic et al. 2019). If this hypothesis is true, then this implies that 221 viruses have evolved from living to non-living over time, which may be problematic for definitions of 222 life that consider metabolism to be an essential criterion (Koshland 2002, Boden 2003, Bedau 2010). 223 Recent work suggests that all three processes may have contributed to the origin of viruses 224 (Krupovic et al. 2019), again making it problematic to definitively classify viruses as either living or 225 non-living. Similar issues apply to mitochondria and chloroplasts, cell organelles with a bacterial 226 origin – when does a symbiont transition from autonomous lifeform to cell component (George et al. 227 2020)? We are therefore sceptical that the problem of defining life will be resolved if we simply 228 collect more data.

229 Wait and see

As mentioned above, one of the reasons why it is difficult to define life is because we currently only
have information about life on earth. We therefore cannot conclusively distinguish between

232 properties that are truly essential or universal from those which are specific to our kind of life. For 233 example, some definitions of life include the criterion that individuals should encode information in 234 DNA (Audesirk and Audesirk 1999), or be composed of cells (Solomon et al. 1993). It is relatively easy 235 to imagine that another type of molecule could be used to encode information rather than DNA 236 (Pinheiro and Holliger 2012), but less clear whether it is possible for lifeforms to exist that are not 237 composed of cells. Experiments with synthetic lifeforms may be useful in helping to investigate these questions, but these synthetic lifeforms will likely be highly influenced by existing life, partly because 238 239 it is most convenient if they can be kept under ordinary lab conditions, but also because existing 240 lifeforms are often used as templates for synthetic organisms (Osbourn et al. 2012). For example, 241 Syn-3.0, a synthetic bacterium created by Hutchinson et al. (2016) is a highly modified version of the 242 bacterium Mycoplasma mycoides, an intracellular parasite of cattle and goats. Synthetic biology is a 243 fast-developing field, yet it is unclear how long it will take to develop synthetic lifeforms that are 244 radically different from known life.

245 Because of this, it would actually be much more valuable if extra-terrestrial life with a completely 246 independent origin is eventually detected. But whether this is even feasible is currently unclear. 247 Although it might be technologically feasible to bring back samples from Mars, either now or in near 248 future, there is a history of traffic between the earth and Mars both through natural (meteorites) 249 and artificial (probes) means, which means that should life be detected there then there is no 250 guarantee that it will have an independent origin (Sullivan and Baross 2007). It is also conceivable 251 that lifeforms based on different chemistries could exist in other parts of the solar system, and be 252 accessible for direct study at some point in the future (Sullivan and Baross 2007, Petrowski et al. 253 2020). But here we end up in a catch-22 of sorts. Without a definition of life that goes beyond 254 currently known types of life, how are we supposed to recognize these novel lifeforms? We can 255 therefore conclude that although we will surely learn much if and when we create or discover 256 completely new types of life, we cannot wait until then to develop a better definition of life.

257 Accept that there cannot be a single definition

258 Another option is to abandon the search for a single all-encompassing definition of life (Jeuken 1975, 259 Oliver and Perry 2006, Mix 2015), similar to the plurality of species concepts that was discussed 260 above. Such an approach would result in the development or refinement of multiple technical 261 definitions of life, each of which would be most useful within a specific context. Different criteria 262 could be included depending on whether the definition was to be relevant for the transition from 263 pre-biotic chemistry to living organism during the origin of life, when an autonomous robot or 264 artificial intelligence could be considered alive, or what minimal properties a potential extra-265 terrestrial lifeform might need in order to qualify as such. The advantage of this approach is that it

reflects the fact that life is a dynamic process which is difficult to capture using a limited set ofcriteria.

268 However there are also disadvantages with this approach. For one thing, a single common definition 269 of life would be very useful when discussing the challenges associated with novel forms of life. A 270 definition of life which is broadly applicable and understandable for laypersons and policymakers as 271 well as experts, would be an advantage during public debate of issues related to novel forms of life. 272 This does not mean that a broad definition would necessarily replace the various technical 273 definitions within a given field, but it might make interdisciplinary communication more successful. 274 Another potential problem with existing technical de re definitions of life is that many of these 275 definitions include criteria at different hierarchical levels of organization. For example, a typical 276 textbook definition of life might include the criteria "energy use", "growth and development", 277 "reproduction", "homeostasis" (the ability to maintain a consistent internal state), and "evolutionary 278 adaptation" (Campbell et al. 1987). Of these criteria, the first four can be applied to the individual 279 organism, but the last one can only be applied to a population of organisms (Persson 2013). A 280 population cannot undergo development from embryo to adult (other than via its component 281 organisms), while a single individual cannot undergo evolutionary adaptation. This leads to an odd 282 situation where this definition cannot sensibly be applied in its entirety to *either* a specific individual 283 or to a specific population of individuals, calling its general utility into question.

284 Some authors have attempted to resolve this problem by developing definitions of life in terms of 285 systems rather than individuals, circumventing the issue of criteria which are applicable at different 286 hierarchical levels (Ruiz-Mirazo et al. 2004, Weber 2010, Pross 2016). Since evolutionary adaptation 287 is usually considered one of the most important properties of life compared to other dynamically 288 stable non-living systems (such as a self-driving car, or the earth's system of ocean currents), this 289 means in practice that the system must be defined at the population level or higher. The advantage 290 of such a definition is that it is more internally consistent, but this usually comes at the expense of 291 being more complicated, imprecise, or unintuitive (Ruiz-Mirazo et al. 2004, Weber 2010, Pross 292 2016). The question is whether the problems discussed above are because defining life is impossible, 293 or are they a result of the traditional fixation on a de re definition?

A case study of a family resemblance approach

We would like to suggest that continuing to search for a broadly applicable de re definition of life is unlikely to be fruitful, and that it would be better to try a new type of approach which can accommodate the complexity of life as we know it. In our view, a family resemblance-based approach has better potential to achieve the aim of producing a broadly applicable and intuitive definition of life, since such a definition would be based on overall similarities across lifeforms and
allow for occasional exceptions from specific criteria. A family resemblance approach could also
allow for different weighting of criteria, for example if metabolism is considered to be a more
important property of life than evolutionary adaptation (or vice versa).

A potential weakness of the family resemblance approach to definitions is that it is not sufficiently objective. What if we cannot all agree on what or how much two entities need have in common, in order for both to be classified as alive? This is of course a problem, but not, we would argue, an insurmountable one. We have attempted to use statistical modelling to determine which criteria are most useful for describing life as we know it, while excluding criteria that are uninformative. Using this information, it may be possible to develop a definition of life that builds on specific combinations of criteria, rather than a single exhaustive list. Here we present preliminary results

310 from a case study illustrating how this type of approach might work.

311 Methods

312 First, we compiled a list of suggested criteria for defining life from the primary literature, as well as 313 from introductory textbooks in biology (see table 1). Descriptions of a phenomenon were considered 314 to be equivalent to specific terms with the same meaning, such that "maintenance of their 315 functional systems" (Allaby 1991) was considered equivalent to "homeostasis" (Campbell et al. 316 1987). This resulted in approximately 30 individual criteria, some of which were variants on a similar 317 theme; e.g. "evolves", "adapt to environment", and "natural selection" were considered separate 318 criteria since evolution can occur through purely neutral processes and does not necessarily require 319 adaptation to the environment or natural selection (Ridley 2003). We then selected a number of 320 living organisms and other entities (including objects, processes, and organismal components) which 321 were intended to span the boundary between living and non-living (see table 2). Next, we attempted 322 to determine whether these entities fulfilled the criteria in table 1 or not. This resulted in the 323 production of a data matrix where 1 indicated that the criterion was fulfilled for that entity, and zero 324 indicated that it was not. Note that it was not always obvious how a given criterion should be 325 applied to a specific entity (e.g. does a bacterium have purposiveness?), but we discussed these 326 cases thoroughly and attempted to use our best judgement. We also scored each entity according to 327 whether it is usually considered to be living or not (see table 2). This classification as "living" or "non-328 living" is of course also open to interpretation, so in the cases where the answer was ambiguous 329 (e.g. plastids or viruses), we carried out two sets of analyses – one more inclusive analysis where all 330 ambiguous cases were classified as "living", and one more conservative analysis where all ambiguous 331 cases were classified as "non-living".

332 Once the data matrix was complete, we analysed it in various ways. All analyses were carried out in 333 the R Statistical Programming environment (R Core Team 2020). First, we checked whether our evaluation of all criteria produced a useful descriptive result by carrying out a cluster analysis 334 335 (Ward's method using the hclust() function; Legendre and Legendre 2012, R Core Team 2020). We 336 expected that successful scoring would result in living organisms clustering separately from other 337 entities. Next, we carried out linear discriminant analysis (using the Ida() function in the MASS package; Venables and Ripley 2002) to determine if it was possible to accurately assign entities to 338 339 the classes "living" and "non-living" using the full set of criteria. If so, this might suggest that a de re 340 definition is feasible after all. Finally, we checked which criteria were most highly correlated with 341 classification as "living" using Spearman rank correlation (using the cor.test() function; Keough and 342 Quinn 2002, R Core Team 2020), in order to determine which criteria may be most useful in 343 constructing future definitions of life.

344 Several of the criteria were found to produce exactly the same result when evaluated across all 345 entities. For example, entities that fulfilled the criterion "metabolism" invariably also fulfilled the criteria "growth" and "stimulus response" (at least within this particular dataset). We therefore 346 347 collapsed perfectly correlated criteria into single variables in order to reduce the dimensionality of 348 the dataset for the linear discriminant and correlation analyses. The full (unreduced) dataset was 349 used for the cluster analysis, in order to preserve complete information about relative similarity. 350 However results were qualitatively similar when carried out on the reduced dataset (data not shown). 351

352 Results

353 The cluster analysis revealed that non-living entities generally did not cluster with living entities (see 354 figure 2). However both main clusters included some ambiguous cases; for example, red blood cells 355 and sperm clustered together with living intracellular parasite species, and viruses clustered 356 together with non-living entities. This means that even using a more conservative classification of 357 viruses as non-living, it is still difficult to clearly separate (more or less) autonomous living organisms 358 from their component parts. The linear discriminant analysis confirmed this. For the inclusive classification dataset, entities were correctly classified as "living" only 44% of the time (14/32 cases -359 360 4 correctly predicted as "non-living" and 10 correctly predicted as "living"). Entities which were 361 classified as "living" in this dataset tended to be misclassified as "non-living" in the analysis more often than the reverse (14 living organisms incorrectly predicted as "non-living" compared to 4 non-362 363 living entities incorrectly predicted as "living"). For the conservative classification dataset, the criteria "feed" and "homeostasis" correctly predicted all cases. 364

365 The criteria that were most and least highly correlated with our classification as "living" are 366 presented in table 3. Results were somewhat different for the inclusive and conservative 367 classification datasets. The only criteria that were among the top 5 best predictors in both datasets were "autocatalytic cycles" and "enzymes". Poorly-performing criteria across both datasets were 368 369 more consistent, and included "mutation", "reproduction by self or non-self", "order", "adapt to 370 environment", and "natural selection". These results suggest (1) that exactly which criteria are best for defining life depend on the specific set of lifeforms we wish to define, and (2) that criteria which 371 372 are likely to be most useful for identifying novel forms of life (e.g. "reproduction by self or non-self", 373 "order" or "adapt to environment") are unlikely to be sufficient for classifying known forms of life.

374 Conclusions

375 Consistent with our expectations, living organisms tended to cluster separately from non-living 376 objects and entities in our proof-of-concept analysis. However the distinction between cell 377 components and intracellular parasites was not particularly clear, consistent with our expectation 378 that defining life based on a single set of criteria is not easy (figure 2). In addition, the poor 379 classification results in the linear discriminant analysis of the inclusive dataset suggest, as discussed 380 above, that simply adding more information does not necessarily help to resolve problems with 381 separating life from non-life. Interestingly, there seems to be a trade-off between accuracy and 382 broad applicability when attempting to define life. Very general criteria such as "natural selection" 383 or "order", which are expected to be most useful in the context of the origin of life or extra-384 terrestrial life, were poorly correlated with classification as "living" or "non-living" in this dataset 385 (table 3). This suggests that although it might be possible to develop a de re definition of life that 386 encompasses all currently living organisms on earth, such a definition is unlikely to be useful in the 387 context of understanding and characterizing novel lifeforms.

388 This case study only includes a limited number of entities and criteria, and this will of course affect 389 the outcome of the analyses to some extent. For example, correlations between criteria and 390 classification as living will likely change depending on exactly which combinations of criteria and entities are included in the analysis. The differences in outcome between the inclusive and 391 392 conservative classification datasets reflect this. Similarly, how each criterion should be interpreted 393 with respect to a given entity is not always straightforward. For example, does a red blood cell have 394 genetic control of development? Yes, in the sense that our genes control the development of our red 395 blood cells, and that the maturing cell itself must actively express these genes in order to develop 396 normally (Moras et al. 2017). But it would also be reasonable to argue that the answer should be no, 397 in the sense that the red blood cell does not itself contain any genes when it is mature, and

therefore cannot produce any new red blood cells via genetic control of development (Moras et al.
2017). The specific results presented here should therefore be considered preliminary, and it might
be necessary to reach some sort of consensus with respect to the evaluation of the criteria in order
to obtain robust results.

402 As presented here, our approach is mainly descriptive. However we do not feel that this is a major drawback. For one thing, any useful definition must be able to reflect our intuitions about life, which 403 404 means that describing these intuitions is an important first step towards being able to construct a 405 broad definition of life. An advantage of this approach is that it can also be applied iteratively, 406 dynamically updating our descriptions of life as new information is obtained. In addition, further 407 work could build on these results to help us get closer to a broadly-applicable definition of life. For 408 example, which combinations of criteria best describe each cluster within figure 2? What happens if 409 we include hypothetical examples of novel forms of life? Some authors have suggested that life 410 might be a matter of degree, rather than a binary property (Hazen 2009, Bedau 2010, Jager op 411 Akkerhuis 2010, Tirard et al. 2010). Would it then be more useful to include additional levels of classification than simply "living" versus "non-living"? There are many outstanding questions and 412 413 possible directions to explore. Nevertheless, we hope that this case study of a family resemblance approach to defining life shows the potential which this approach provides. 414

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- 560 Table 1: List of criteria defining for defining life obtained from the literature and from introductory
- textbooks in biology.

Criterion	Source		
Adapt to environment	(Wingo 1963, Campbell et al. 1987, Solomon et al. 1993,		
	Mader 2001)		
Autocatalytic cycles	(Morowitz 1992, Fenchel 2002, Macklem and Seely		
	2010)		
Boundary	(Campbell et al. 1994, Greener 2008, Macklem and		
	Seely 2010, Pennock 2012)		
Can die	(Hansen 2008)		
Cells	(Solomon et al. 1993, Campbell et al. 1994, Fenchel 2002. Sadava et al. 2008)		
Chromosomes	(Wingo 1963)		
Decrease in entropy	(Wingo 1963, Morowitz 1992, Fenchel 2002, Moore		
	2012, Pennock 2012)		
Development	(Campbell et al. 1987, Solomon et al. 1993, Gould and		
	(Campbell et al. 1994, Audesirk and Audesirk 1999		
	Fenchel 2002)		
Enzymes	, (Lawrence 2000, Fenchel 2002, Sapp 2003)		
Evolves	(Wingo 1963, Campbell et al. 1987, Solomon et al. 1993,		
	Gould and Keeton 1995, Audesirk and Audesirk 1999,		
	Fenchel 2002, Sapp 2003, Greener 2008, Sadava et al.		
	2008, Pennock 2012)		
Feeding	(Greener 2008)		
Genes	(Gould and Keeton 1995, Strickberger 2000, Sapp 2003,		
	Sadava et al. 2008)		
Genetic control of development	(Pennock 2012)		
Genetic material isolated from	(Pennock 2012)		
Crouth	(Wingo 1062, Comphall at al. 1087, Allahy 1001		
Growth	Cwingo 1963, Campbell et al. 1987, Allaby 1991,		
	and Audesirk 1999 Lawrence 2000 Strickberger 2000		
	Fenchel 2002. Greener 2008. Pennock 2012)		
Homeostasis	(Campbell et al. 1987, Allaby 1991, Solomon et al. 1993,		
	Audesirk and Audesirk 1999, Sadava et al. 2008)		
Metabolism	(Wingo 1963, Morowitz 1992, Solomon et al. 1993,		
	Campbell et al. 1994, Gould and Keeton 1995, Lawrence		
	2000, Strickberger 2000, Greener 2008, Sadava et al.		
	2008, Pennock 2012)		
Movement	(Solomon et al. 1993)		
Mutation	(Pennock 2012)		
Natural selection	(Greener 2008)		
Nucleic acids	(Lawrence 2000)		
Order	(Wingo 1963, Campbell et al. 1987, Gould and Keeton		
	1995, Raven and Johnson 1996, Mader 2001, Sapp		
	2003, Moore 2012)		
Organic molecules	(Audesirk and Audesirk 1999, Fenchel 2002, Pennock		
	2012)		

Protoplasm	(Wingo 1963, Sapp 2003)	
Purposiveness	(Pennock 2012)	
Regulatory mechanisms	(Raven and Johnson 1996, Korzeniewski 2001, Macklem	
	and Seely 2010, Pennock 2012)	
Related	(Sadava et al. 2008)	
Replicate chemical information	(Fenchel 2002, Moore 2012, Pennock 2012)	
Reproduction by self or non-self (not	(Campbell et al. 1987, Allaby 1991, Solomon et al. 1993,	
specified)	Gould and Keeton 1995, Raven and Johnson 1996,	
	Lawrence 2000, Strickberger 2000, Mader 2001,	
	Fenchel 2002, Greener 2008, Moore 2012, Pennock	
	2012)	
Reproduction by self-replication	(Wingo 1963, Morowitz 1992, Audesirk and Audesirk	
	1999, Sadava et al. 2008, Macklem and Seely 2010)	
Stimulus response	(Wingo 1963, Campbell et al. 1987, Morowitz 1992,	
	Solomon et al. 1993, Raven and Johnson 1996, Audesirk	
	and Audesirk 1999, Lawrence 2000, Mader 2001,	
	Greener 2008, Pennock 2012)	
Use external substances	(Campbell et al. 1987, Allaby 1991, Audesirk and	
	Audesirk 1999, Lawrence 2000, Mader 2001, Fenchel	
	2002, Greener 2008, Sadava et al. 2008)	

Table 2: List of entities included in the analysis of life. Entities indicated as "Yes/No" were considered

ambiguous, and analysed separately as both living and non-living in order to see how this influenced

the outcome of the analysis.

Entities	Classified as living?
Arabidopsis thaliana (thale cress)	Yes
Caenorhabditis elegans (nematode)	Yes
Chlamydomonas reinhardtii (single-celled alga)	Yes
Clay crystals	No
Colloids	No
Danio rerio (zebrafish)	Yes
DNA virus (e.g. herpes simplex)	Yes/No
Drosophila melanogaster (common vinegar fly)	Yes
Escherichia coli (intestinal bacterium)	Yes
Gallus gallus (domestic chicken)	Yes
Homo sapiens (human)	Yes
Hydra vulgaris (freshwater polyp)	Yes
Liposome (phospholipid bilayer vesicle)	No
Macrostomum lignano (flatworm)	Yes
Memes	No
Mus musculus (house mouse)	Yes
Plastids (cell organelle, e.g. chloroplast)	Yes/No
Poecilia formosa (Amazon molly)	Yes
Prion (e.g. CJD-causing)	No
Red blood cell	Yes/No
Ribozyme (catalytic RNA)	No
Rickettsia typhi (intracellular parasitic bacterium)	Yes
RNA virus (e.g. HIV)	Yes/No
Saccharomyces cerevisiae (brewer's yeast)	Yes
Snowflake	No
Sperm	Yes/No
Synechocystis sp. PCC 6803 (cyanobacterium)	Yes
Transposon	No
Viroid (e.g. tomato chlorotic dwarf viroid)	Yes/No
Virophage (viral parasite on other viruses)	Yes/No
Wolbachia (intracellular parasitic bacterium)	Yes
Xenopus tropicalis (western clawed frog)	Yes

567

- 569 Table 3: Criteria which are most (white rows) and least (grey rows) strongly associated with a priori
- 570 classification as living versus non-living. Criteria with equal correlation coefficients are presented on
- 571 the same row. A) Results when ambiguous cases are classified as "living". B) Results when
- 572 ambiguous cases are classified as "non-living". Significant correlations are indicated in bold.

573	A)
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Criteria	Correlation coefficient	P-value
Autocatalytic cycles, Chromosomes, Genes	0.833	3.23*10 ⁻⁹
Enzymes	0.832	3.59*10 ⁻⁹
Movement	0.762	3.95*10 ⁻⁷
Nucleic acids, DNA	0.745	9.87*10 ⁻⁷
Reproduction by self-replication	0.698	8.96*10 ⁻⁶
Mutation	0.494	0.00417
Reproduction by self or non-self (not specified)	0.462	0.00773
Purposiveness	0.361	0.0423
Order	0.149	0.415
Adapt to environment, Natural selection	-0.149	0.415

575 B)

Criteria	Correlation coefficient	P-value
Feed, Homeostasis	1.00	0
Movement, Protoplasm	0.939	1.96*10 ⁻¹⁵
Cells	0.881	3.03*10 ⁻¹¹
Growth, Metabolism, Simulus response, Regulatory mechanisms,	0.825	6.52*10 ⁻⁹
Genetic material isolated from the environment		
Autocatalytic cycles, Enzymes	0.770	2.50*10 ⁻⁷
Nucleic acids, Evolves, Replicate chemical information	0.511	0.00278
Mutation, Can die, Related	0.458	0.00837
Organic molecules, Adapt to environment, Natural selection	0.402	0.0224
Order	0.342	0.0551
Reproduction by self or non-self (not specified)	0.275	0.128



- 578 Figure 1: Spontaneous learning of the word "chair". After seeing multiple examples of a given type of
- 579 object, we learn to identify the important properties associated with this type of object. This later
- allows us to recognize non-standard examples of chairs. (All images obtained from Wikimedia
- 581 commons.)



Entities

583

Figure 2: Results of cluster analysis. Non-living entities generally cluster together at the right-hand
side of the plot, and living entities at the left-hand side of the plot. However both main clusters
include some ambiguous cases; red blood cells and sperm cluster together with intracellular parasite
species on the left-hand side of the plot, and viruses cluster together with non-living entities on the
right-hand side of the plot.