

1 **EGrowth: a global database on intraspecific body growth variability in earthworm**

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12 Abstract

13 Earthworms play a key role in soil and ecosystem functioning. Predicting their abundance and spatial
14 distribution is required to understand their ecological role. There is growing evidence that
15 mechanistic models of earthworm population dynamics are promising tools to tackle this issue.
16 However, this approach requires a fair amount of data because it explicitly integrates the three
17 fundamental biological processes: growth, reproduction and mortality. Hitherto, the lack of
18 comprehensive databases on life history parameters related to these three processes hampered the
19 widespread development of mechanistic earthworm population dynamics models. As a
20 consequence, predicting earthworm abundance in a variety of conditions across species is still
21 difficult.

22 The clear bottleneck for making progress is the lack of databases on the intraspecific variability of
23 earthworm life history traits in response to environmental conditions. Data related to body growth
24 and body size are critical because body size largely determines reproduction and mortality rates.
25 Body growth is therefore the backbone of mechanistic models of earthworm population dynamics.
26 Here I present EGrowth, the first comprehensive database on intraspecific variability of earthworm
27 body growth in relation to environmental conditions. The EGrowth database contains 1073 growth
28 curves of 51 species of earthworms, representing 16002 measures of body mass. It covers
29 publications on earthworm body size from 1900 to 2016. The environmental conditions in which the
30 growth curves were produced are also reported. The database is open access and can be browsed
31 from a graphical user interface. EGrowth will be updated regularly in the future as new studies are
32 published. I propose a standardized framework for reporting future data on body growth of
33 earthworms.

34

35

36 Key words:

37 Body size; Life history traits; Interspecific variability; Intraspecific trait variability (ITV); Database;

38 Allometry

39

40 1. Introduction

41 Earthworms play an important role in soil functioning (Lavelle, 1988). For instance, they modify soil
42 structure, bulk density and aggregate stability, with direct consequences for water infiltration rates
43 and hydrological conductivity (Blanchart, 1992; Bossuyt et al., 2005; van Schaik et al., 2014). They
44 also affect nutrient and carbon fluxes through their effect on decomposition and microbial activity

45 (Pashanasi et al., 1996; Richardson et al., 2016). These modifications impact vegetation (De Deyn et
46 al., 2003; Hattenschwiler and Gasser, 2005; Laossi et al., 2009) and climate dynamics (Lubbers et al.,
47 2013; Zhang et al., 2013). A number of studies have shown that all these effects quantitatively
48 depend on earthworm abundance and traits, which are themselves constrained by environmental
49 conditions (e.g. Jouquet et al., 2008; van Schaik et al., 2014). Understanding how the environment
50 impacts earthworm abundance and traits in a quantitative way is therefore a key requisite for a
51 better grasp of their role in soil functioning. However, predicting earthworm abundance and traits in
52 a specific context is very challenging because soils are extremely heterogeneous even at fine scales.
53 In addition, ecological preferences vary among species. A major challenge is thus to develop a
54 quantitative understanding of earthworm ecology for predicting earthworm abundance and traits in
55 relation to ecological conditions.

56 A promising approach for tackling this issue is the development of process based models (Jager et
57 al., 2006; Kooijman, 2010). They have been used for a variety of purposes such as understanding the
58 spatial structure of earthworm populations, the impact of earthworms on infiltration rates, or the
59 effect of pesticides on earthworm population dynamics (Barot et al., 2007; Baveco and De Roos,
60 1996; Schneider and Schroder, 2012; Vorpahl et al., 2009). These models mimic growth,
61 reproduction and death of individuals or cohorts, in order to predict population dynamics. They
62 require a fair amount of data to parametrize the modelled processes, which has been identified as
63 the primary bottleneck for the development of such approaches (Schneider and Schroder, 2012).
64 Data on body growth variability, and thus on intraspecific body size variability (IBSV), are critical
65 because body size determines the rate of reproduction and life span (Brown et al., 2004). Indeed
66 cocoon production, cocoon hatchability, food consumption, and longevity all depend on the body
67 size of earthworms (Daniel, 1990; Michon, 1954). In turn, the population dynamics and ecological
68 effects of earthworm are also related to their body size (Brown et al., 2004).

69 In order to build mechanistic models of body growth, we need to estimate the effects of the
70 environment on growth patterns. For this we need databases that document the respective effect of
71 a variety of environmental factors. This kind of data is typically available from experiments in
72 controlled conditions, where only the factor(s) studied vary. A large number of studies have
73 reported this type of experiments on earthworms. However, as far as I am aware, there is no
74 comprehensive database compiling data on the effect of the environment on intraspecific body size
75 variability in earthworms.

76 Building a database on IBSV that covers a wide spectrum of earthworm species is challenging in
77 several aspects. The first inherent difficulty is that the shape of body growth curve varies among
78 studies (Grimm et al., 2014). In particular, growth curves can be non-monotonic because body size
79 can regress, present oscillations or can follow a staircase shape (Lakhani and Satchell, 1970; Michon,
80 1954; Tondoh and Lavelle, 1997). Hence, data on body size without reference to the shape of growth
81 pattern have limited utility for modelling the effect of the environment on body size. The ideal
82 structure of a global database should include this diversity of growth patterns, and should enable
83 generalization to species for which growth form has not been measured so far. A simple way to
84 achieve this is to build IBSV databases on body growth curves – i.e. ontogenetic growth. Body
85 growth curves are measures of body mass at different times on the same individual or on the same
86 population. This approach allows the modelling of body growth and the calculation of a variety of
87 body growth parameters that can be compared among ecological conditions and across species
88 (West et al., 2001).

89 A second difficulty for building databases on IBSV is the retrieval of the conditions during growth.
90 Having this information is critical for identifying the drivers of IBSV, and to quantify their effect on
91 body size. This information also allows parametrizing reaction norm functions, which are
92 mathematical models that predict body growth in relation to environmental conditions such as
93 temperature (Angilletta et al., 2004; Gillooly et al., 2001; Ray, 1960). Retrieving environmental

94 conditions in reports on body growth of earthworm is however challenging because there are no
95 standardized guidelines to present this type of information. As a result, these data are often missing
96 or dispersed within the documents.

97 Lastly, the data by themselves are difficult to access because they are scattered in many articles, in
98 different journals and in different kind of reports. The title and summary of the documents often do
99 not reveal the presence of data on body growth. Growth curve data were often published in early
100 articles that are not recorded in search engines and not available in electronic format. Data are
101 usually difficult to reuse because they are presented only in graphical form, without the
102 corresponding raw data. This implies a manual digitalization of the figures to reuse the data.

103 Furthermore, centralizing existing data on body size and growth of soil animals is necessary, not only
104 for making these data easily reusable, but also to ensure that these data will not be definitively lost
105 in the future.

106 In this paper, I present the EGrowth database. The database compiles existing data about body
107 growth of 51 species of earthworm. It actually contains more than 16000 body mass measures,
108 representing more than 1000 growth curves. The database is open access and can be accessed in a
109 variety of manner. It can be downloaded or accessed through a Graphical Interface (GUI) from R or
110 from internet. This database will be updated in the future with new studies. In order to facilitate this
111 process, I propose a standardized framework for reporting future data on body growth of
112 earthworms.

113

114 2. Material and methods

115 2.1 Database construction

116 Data were searched in articles published in peer reviewed journals and in PhD theses from 1900 to
117 2016. Articles were searched in different ways, with the goal to be as exhaustive as possible. An

118 intensive internet search was carried out through different databases, mainly Web Of Science,
119 Scopus, Google Scholar and Researchgate. References cited within the articles were also searched
120 for online and in various libraries in France (MNHN and IRD Bondy) and USA (UCSB and Stanford).
121 Key words such as earthworm growth rate, body size, and ones related to earthworm ecotoxicology
122 - a field which offers a large amount of data- were used to retrieve publications. In addition, all
123 issues from the most relevant journals – Pedobiologia, Soil Biology & Biochemistry, Biology and
124 Fertility of Soils, Applied Soil Ecology and Megadrilogica were checked manually through table of
125 contents for articles containing data about earthworm growth rate. Articles that were not available
126 in a digital format were scanned, and the text was extracted through an OCR process (Optical
127 character recognition). Then figures and tables with relevant data were extracted, digitalized with
128 the software DataThief, and exported into spreadsheets. Point data from figures were reported with
129 their associated error bars when available. Error bars were converted to Standard Error bars.
130 Metadata such as the number of measures per point, temperature and treatments were searched
131 for manually in the text and included in the database, when available. The authors of the articles
132 with missing data were contacted in order to complete the database. All articles were stored as pdf
133 files in an online folder and can be accessed upon request.

134 Overall, 414 publications were analysed, from which only the ones with at least four monitoring
135 dates were retained. As a consequence, many articles, in particular the ones that used Instantaneous
136 Growth Rate (IGR) - the difference of (log) body mass between two dates -, were not considered.
137 Studies that used adults at the beginning of the experiments were also discarded. At the end 162
138 publications were used to build the database. The list of articles is given in supplementary material.

139

140 2.2 Database structure

141 The database is organized in three tables (Fig. 1), which are described in detail in supplementary
142 material.

143 [Figure 1]

144 2.2.1 File "curves.txt"

145 This table stores the growth curve data points (16002 entries, 4 columns). Each entry is the
146 individual or average biomass of a batch of earthworms at a given time in a given experiment, with
147 the standard error of the mean of the biomass, when available. Each growth curve has a unique
148 identifier called "CURVE_ID". All points with the same CURVE_ID belong to the same growth curve.
149 Be aware that the column "time" is in most cases not the age of animals but the time since the
150 beginning of the experiment.

151 2.2.2 File "curves_md.csv"

152 This table (1073 entries, 30 columns) describes the environmental conditions in which each growth
153 curve was produced. This table is linked to the "curves.txt" file through the CURVE_ID field. This field
154 allows the user to retrieve the environmental conditions in which each curve was produced. For
155 each curve the name of the species studied, the types of factors that were tested in the experiment,
156 the level of the factors, the intra and eventually interspecific earthworm density in the container,
157 the room temperature, the soil moisture, the geographic origin of the individuals, the food and the
158 substrate can be obtained. In experiments with fluctuating temperature, the average temperature
159 was reported. There is also a "REF_ID" field that indicates the source of the data. This field is used to
160 join this table to the file "references.csv".

161 2.2.3 File "references.csv"

162 This table describes the documents from which the growth curves come from. It is linked to the
163 "curves_md.csv" file through the "REF_ID" field. It contains also the DOI of sources, when available.

164 This file is essential for tracking the origin of the data and for reproducibility of analyses. Only
165 published data were included in the database. There are 162 entries and 7 columns in this table.

166 2.2.4 Database access

167 The database is open and can be accessed in a variety of manners that are presented in details in the
168 user guide provided in supplementary material.

169 You can access it through a Graphical User interface from internet at [http://www.jerome-](http://www.jerome-mathieu.com/open-data/egrowth)
170 [mathieu.com/open-data/egrowth](http://www.jerome-mathieu.com/open-data/egrowth) or from the R software console by typing:

171 [code]

```
172 if (!require('shiny ')) install.packages('shiny');
```

```
173 library(shiny);
```

```
174 runGitHub("EGrowth", "JeromeMathieuEcology")
```

175 [end of code]

176

177 Alternatively you can download the database in your computer from Zenodo

178 <https://zenodo.org/record/1039952#.WrEX7ZdrzRY>, DOI <http://doi.org/10.5281/zenodo.1039952>

179 and access it through R.

180

181 A minimal example of the database usage is presented now.

182 This example assumes that the database (the three files "curves.txt", "curves_md.csv" and
183 "references.csv") are stored in the R working directory.

184 The first step is to read the data.

185 [code]

186

```
187 growth <- read.table("curves.txt", h = T, na.strings = "na", sep = "\t")
```

```
188 EGrowth_metadata <- read.csv2("curves_md.csv", h = T, na.strings = "na", sep = ",", dec = ".")
```

189 [end of code]

190

191 Then one way to proceed is to merge the tables based on field "CURVE_ID", which is the growth

192 curve unique identifier:

193 [code]

```
194 EGrowth <- merge(growth, EGrowth_metadata, by = "CURVE_ID")
```

195 [end of code]

196 We can plot all curves of a species of interest.

197 Example with *Drawida willsi*:

198 [code]

```
199 if (!require('lattice ')) install.packages('lattice');
```

```
200 library(lattice)
```

```
201 with(EGrowth[EGrowth$species == "Drawida willsi",], xyplot(bm~time | CURVE_ID,
```

```
202                               type = c("p", "smooth"), pch=20, cex = 1.5, col="grey20",
```

```
203                               ylab="Biomass (mg)", xlab="Time (days)", layout=c(4, 2),
```

204 `par.settings=list(strip.background=list(col=c("grey80")))`

205 `)`

206 [end of code]

207

208 [Figure 2)

209

210 Then you can retrieve the environmental data by typing:

211 [code]

212 `EGrowth_metadata[EGrowth_metadata$species == "Drawida willsi",]`

213 [end of code]

214

215 More examples and the code of all the analyses presented in this paper are given in the User Guide.

216 The code of the GUI is provided in the GitHub repository:

217 <https://github.com/JeromeMathieuEcology/EGrowth>

218

219 3. Coverage of EGrowth

220 At the present time, the EGrowth database contains 1073 growth curves, made of 16002

221 measurements of biomass. These data come from 162 publications.

222 3.1 Temporal dynamics of publication

223 No data were found between 1900 and 1953. The production of data on earthworm body growth
224 started in 1954, with the seminal PhD thesis of Jean Michon (Michon, 1954). From this time
225 onwards, the number of published growth curves increased exponentially until the 90's (Fig. 3a).
226 During this period, five other theses focused on earthworm body growth and life history traits. After
227 the 90's, the publication rate of growth curves slowed down. The last past ten years showed a
228 dramatic reduction in the production of new data. In particular the number of species covered has
229 not increased since 2011 (Fig. 3b).

230 [Figure 3]

231 3.2 Species covered

232 Growth curve data on 51 species are included in EGrowth (Fig. 4). The most documented species
233 were by far *Eisenia foetida* (n=244), *Lumbricus terrestris* (n=131), *Eisenia Andrei* (n=87),
234 *Aporrectodea caliginosa* (n=74) and *Lumbricus rubellus* (n=70) (Fig. 4). The criteria for studying a
235 specific species was rarely reported, except for *E. foetida*, which is a model species in ecotoxicology
236 (OECD, 1984). In the top five studied species, two are considered as global invasive species (*L.*
237 *terrestris* and *L. rubellus*). Overall, only one endemic species (*Hormogaster elisae*, Spain) was
238 studied. There are no data for endangered species such as *Megascolides australis*, the giant
239 gippsland earthworm from Australia (Van Praagh, 1992), or *Driloleirus americanus*, the giant Palouse
240 earthworm from USA (Sánchez-de León and Johnson-Maynard, 2009).

241 [Figure 4]

242 3.3 Locations covered

243 Growth curves in EGrowth were issued from 86 different sites spread around the world (Fig. 5). Most
244 of the data were produced in Europe and in India. At the moment, no dataset is available from
245 Russia, China and central Africa. Data from Russia and China probably exist, but were not found

246 because they are not yet available in English. There are much more body growth curves from
247 temperate areas (n=693) than from tropical (n=283) or from Mediterranean climates (n=97).

248 [Figure 5]

249 3.4 The general shape of body growth curves in earthworm

250 The shape of body growth curves from birth to death has been poorly documented so far. The most
251 complete work regarding this topic is the PhD of Michon (1954). He compared the pattern of body
252 growth of 14 species, from birth to death, with extremely frequent measures of body mass. He
253 identified several stages in the life cycle of earthworm based on the shape of the logged body mass
254 growth curve. In particular, he showed the existence of a senescence phase, which has been poorly
255 documented since then. From this work and from more recent ones, we can define a general pattern
256 of earthworm growth shape (Fig. 6a).

257 After birth (B), juveniles (J) usually follow a lag phase, then a steep, exponential or linear, growth. In
258 long living species, the J phase can show a staircase shape pattern (Lakhani and Satchell, 1970).
259 When sexual maturity is attained, adults enter the reproduction stage (R) and growth is strongly
260 reduced and sometimes becomes negative. After some time, adults enter a senescence stage (S),
261 during which time body size decreases and sexual organs disappear.

262 [Figure 6]

263 3.5 The variety of monitoring schemes of earthworm body growth curve

264 In most of the publications, growth was monitored only during a fraction of lifespan. Three broad
265 monitoring schemes can be identified (Fig. 6b).

266 The type 1, called Instantaneous Growth Rate (IGR), is the most often used. It is calculated as the
267 difference of (usually log) body mass between two dates (e.g. Eriksen-Hamel et al., 2009). The
268 monitoring generally occurs during the juvenile stage. The exact age at the beginning and at the end

269 of the monitoring vary among studies and is often not reported. This kind of data was not included in
270 E-Growth database because it is not suitable for fitting growth rate models.

271 The monitoring scheme type 2 is the most common after type 1. It refers to cases where biomass was
272 measured on more than four occasions, the first measurement being during the juvenile stage, but
273 not at birth. Monitoring ends either during the juvenile stage (J monitoring scheme) or during
274 reproduction stage (JR monitoring scheme). Measures were rarely taken until senescence (JS
275 monitoring scheme) or until death (JD).

276 In the third broad monitoring scheme, monitoring started at cocoon hatching. This monitoring
277 scheme is the most informative because the age of the individuals is known. Unfortunately, this
278 monitoring scheme is also the least frequent, probably because of the fact that obtaining a batch of
279 synchronized hatchlings with the same age is difficult. Some techniques such as storing cocoons at
280 low temperature has been proposed to solve this difficulty (Bouwman, 1998). However, it still
281 requires to breed the individuals in advance, to wait for cocoon production and for hatching. This
282 can be a severe difficulty in species with slow population dynamics. Within this monitoring scheme,
283 a variety of monitoring length also exists. A number of studies only cover the juvenile stage (BJ).
284 These studies are particularly useful to estimate the age of the individuals in the monitoring scheme
285 type two, in which age at the beginning of the monitoring is not reported. However BJ data are
286 usually not sufficient to estimate the shape of the growth curve without making strong assumption
287 about the shape of the growth curve. In BR monitoring scheme, individuals are monitored until their
288 mature stage, before senescence occurs. In this case, the growth curves are usually monotonic:
289 there is no decrease in body mass. This is the most frequent sampling design in monitoring scheme
290 type three. A very limited number of studies monitored growth rate from birth to senescence (BS) or
291 from birth to death (BD). These monitoring schemes are however the most informative as they give
292 estimates of life span and the complete shape of the body growth curve.

293 Overall, the great majority of studies in EGrowth lasted between 100 and 200 days (Fig. 7a), but
294 some lasted over 900 days (e.g. Mulder et al., 2007). Most sampling frequency fell into one of the
295 three following classes: every week, every two weeks, or every month (Fig. 7b).

296

297 [Figure 7]

298

299

300 3.6 Drivers of body growth

301 Nearly all studies were performed in controlled conditions in the laboratory. Only seven growth
302 curves, all from temperate areas, were obtained in the field (Table 1). In the laboratory, by far the
303 two most frequently documented factors are the type of food provided (368 curves) and the toxic
304 effect of a variety of products (330 curves). These experiments typically come from studies on
305 vermicomposting and from ecotoxicology. The effect of air temperature (140 curves) and density
306 (134 curves) are also well studied. All other factors are much less well studied. Surprisingly, the
307 effect of soil properties on earthworm growth has been poorly studied (48 curves), whereas it would
308 greatly help to understand the distribution of earthworm species in nature. Overall, 172 curves
309 comes from experiments that tested two or more factors.

310 [Table 1]

311 In ecotoxicology studies, the most frequent treatments are related to the type of waste used as
312 substrate for growth, manure being the most studied (Table 2). The effect of copper and cadmium
313 are the most documented among metals, while Moxidectin, Glyphosate and Dieldrin are the most
314 studied among pesticides.

315

316 [Table 2]

317

318 4. Nine recommendations for reporting body growth curves

319 The absence of a general framework to report data on growth has resulted in a heterogeneity of
320 available information among studies in the EGrowth database. This has occasionally resulted in the
321 discarding of growth curves because of the absence of critical information. It has also resulted in
322 missing values in the database, which limits the possibilities of disentangling the effect of different
323 factors, like temperature and humidity. This issue could easily be avoided in the future if simple
324 guidelines were followed systematically when reporting results. The general good practices on how
325 to report data for their reuse in meta-analyses have been proposed in various articles and are
326 summarized by the FAIR principle: Findable, Accessible, Interoperable and Reusable (Gerstner et al.,
327 2017; Penev et al., 2017; White et al., 2013; Wilkinson et al., 2016). Here I focus on the specific
328 aspects in reporting growth curves for their easy re-use and integration in databases. I propose a
329 tentative template for reporting such type of results, accompanied by a To Do checklist
330 (Supplementary material).

331 4.1 Reporting the experimental design

332 It is critical to clarify as much as possible the experimental design. For this, four components need to
333 be clearly explained: 1° the type of treatments that vary between curves, if any (e.g. temperature or
334 food). 2° the treatment levels for each treatment (e.g. for temperature: 5°C, 15°C, 25°C). If there are
335 more than one factor, the combination of levels covered (full factorial, incomplete design) must be
336 specified. 3° the number of independent measures (replicates) per level of treatment. This is usually
337 the number of containers per level of treatment. 4° the number of individuals per replicate: density
338 within containers (e.g.: 3 ind.replicate-1).

339 If you will allow it; I would like to remind you here of a few points on experimental design. First,
340 individuals in the same container cannot be considered as independent because of block effects.
341 Using the individuals' data without accounting for this block effect leads to pseudo replication
342 (Hurlbert, 1984). Indeed, all individuals in the same container are affected similarly by any variation
343 of the container, and hence are not independent. When it is possible to track individuals separately,
344 we can use the raw data and integrate a block effect (i.e. container) in the analysis. However, for
345 earthworms, this is generally not possible without using tags (Mathieu et al., 2017). The correct
346 procedure in general is thus to use the averaged biomass by replicate, but this results in a significant
347 loss of statistical power. In order to circumvent this problem, a solution is to distribute individuals in
348 as many as possible separate replicates, rather than grouping them in a limited number of replicates.
349 This maximizes the power of the study without increasing its cost (the number of individuals does
350 not change). Following these lines, it is more efficient to put only one individual per container rather
351 than several ones. Beyond improving the power of statistical tests, it removes all effects of density
352 dependence such as competition and reproduction, which can interfere with the treatments, and
353 which can vary according to species (Uvarov, 2009). In the end, it gives a better picture of the effect
354 of treatments on growth, all other things being equal. Replicates with only one individual per
355 container thus facilitate the comparison among studies and among species.

356 4.2 What is biomass and how to report it

357 Reporting biomass is not as trivial as it can seem at first. Indeed biomass can change significantly
358 with body moisture, gut content, and fat content, without having an ecological or evolutionary
359 significance. Hence, it is important that the type of biomass reported is clearly mentioned. The ideal
360 unit for comparing studies is dry weight of gut voided individuals. This removes the issues of body
361 moisture and gut content, which represent a large proportion body weight and which can vary
362 substantially regardless of dry biomass. However, this unit is not practical because it requires gut
363 voiding then killing a fraction of the individuals at each monitoring event.

364 A good compromise is to report fresh biomass of non-gut voided individuals, and to measure
365 separately, on a batch of individuals of varying size, gut content as a function of fresh biomass (e.g.
366 Bolton and Phillipson, 1976; Curry and Bolger, 1984), and the relationship between the biomass of
367 fresh gut voided and dry gut voided individuals (Saussey, 1966).

368 Whatever the type of biomass reported, it is crucial to clearly define it, and to use appropriate
369 terminology and units. For instance, in a number of publications the word "growth" is used instead
370 of biomass. Growth is a variation of biomass over a period of time (units can be mg.day.⁻¹), not a
371 biomass at a given time (units: mg).

372 4.3 Reporting age rather than time

373 Ideally, body growth curves relate body biomass to age. This permits one to estimate growth
374 parameters that depend on age, such the age at growth spurt - the maximum growth rate (Parks,
375 1982). These kind of parameters are sometimes the only ones affected by a treatment. For instance,
376 a particular treatment can produce a shift in phenology such as a decrease of age at maturity, and
377 change population dynamics, without impacting maximal body size.

378 Reporting age is also needed for comparing growth models across studies. Indeed, parameters in
379 growth models are often age dependent. Hence, they can only be correctly estimated if age is given
380 in data, rather than time since the beginning of the experiment. This is particularly important when
381 the study do not start from the birth of the individuals. In such case, if the age at the beginning of
382 the growth curve is not given, it is difficult to translate the time axis into age. This is particularly true
383 for studies based on IGR. Without age and weight, it is not possible to integrate IGR data in growth
384 curve databases.

385 In conclusion, reporting age offers a lot more possibilities for modelling and for comparison across
386 studies. If age is not known, then reporting the biomass of juveniles at hatching or at the first date of
387 monitoring can be very helpful to rescale the time axis into age.

388

389 4.4 Reporting phenology

390 Phenology is an important aspect of body growth patterns. Indeed a number of standard indicators,
391 such as biomass at maturity, are defined in relation to the stage of the individuals. Changes in stages
392 can be indicated by arrows on curves (Klok and de Roos, 1996) or directly as a table giving the
393 proportion of individuals at each stage, at each date (e.g. Elvira et al., 1996). When data are
394 presented in an aggregated way, the most useful information is the age at which 50% of the
395 individuals reached a given stage. Reporting the death or quiescence of animals is also interesting
396 because it allows computing the mortality curve, and to take into account density dependent
397 processes. This can be indicated by a sign such as stars on graphs, or directly in the raw data.

398 4.5 Reporting taxonomy

399 The correct identification of species is critical for comparing data and building databases. However,
400 taxonomy is still being actively updated, with sometimes major revisions. Most earthworm
401 classifications has been developed on morphological or anatomical traits, and recent molecular
402 studies are revising many taxa (e.g. Csuzdi et al., 2017; Domínguez et al., 2015). The problem is
403 particularly accurate for growth experiments because identifying living individuals is very difficult,
404 and in most cases not possible until maturity. This might not be problematic to compare treatments
405 within a study, but it becomes a matter of importance when comparing results across studies and
406 across species. Most taxonomical errors probably consist in aggregating different species into a
407 single species, because of cryptic species. This leads to artificially increasing intraspecific variability
408 while decreasing interspecific differences. The problem occurs even in the most studied species such
409 as *E. foetida*, *L. terrestris*, and *A. caliginosa*, whose taxonomical status has been revised several
410 times. As it is almost impossible to check the identification of species in previous studies, caution
411 should be taken in any comparative analysis. The only option to circumvent this difficulty in future

412 studies is to systematically store a few individuals from each study in pure alcohol, and to check
413 identifications with molecular techniques. This is necessary to reach a homogenous and
414 standardized classification across studies.

415 4.6 Reporting the conditions of the experiments: the need for metadata

416 Understanding the drivers of IBSV requires that environmental conditions in which data were
417 acquired are reported. This information should cover at minimum the air temperature, the soil pH,
418 soil moisture, expressed in clear units, the number of individuals per container, and the dimensions
419 of the container. Soil humidity in particular is often poorly reported although it is a critical condition
420 for earthworm growth. The type of food, its amount, and the frequency at which it was provided
421 should also be mentioned. These data should ideally be given for each curve and, if possible, for
422 each measurement date. Indeed the conditions such as temperature or the number of individuals
423 sometimes vary during the experiments.

424

425 4.7 Reporting raw data

426 An obvious limiting factor for building databases on body growth curves is that data are usually only
427 presented graphically. Extracting data from graphs is tedious, time consuming and needs to be done
428 by a careful and experienced worker. In addition, digitalizing growth curves is sometimes not
429 possible when data overlap, or when artwork resolution is too low. A much more efficient way
430 would be to publish the data also in tables. Ideally, data should be stored in long term repositories
431 such as Zenodo or Figshare, which offer four key features to reuse data in the future: long term
432 storage, easy identification and citation of data through unique identifiers (DOI), easy finding of
433 datasets through key words in metadata, and easy download of data. Alternately, raw data can be
434 presented in supplementary material associated with the manuscript. In both cases, it is critical to

435 use non-proprietary format such as comma separated text (.csv) or tab separated text (.txt), because
436 they will always be readable from all platforms.

437 4.8 Report individual growth curves

438 It is much more useful to publish the raw data of each growth curve or each replicate, rather than
439 their average. It clarifies the experimental design. It gives more power to analyses and simplifies
440 them. Indeed, it is much straightforward to include all data in analysis than using aggregated data,
441 which must be weighted by error bars and sample size. In addition, it reduces the digitalization
442 errors, particularly when data overlap in graphs.

443 4.9 Report error bars and their unit

444 Despite previous reminders about the necessity of reporting error bars in graphs (e.g. Cumming et
445 al., 2007), they are still absent in a number of publications. When reporting averaged data is the only
446 possibility, it is vital to show the error bars of the mean. It is also critical to clearly mention the type
447 of error bar that was used (e.g. standard error, standard deviation, confidence interval) and the
448 sample size, otherwise errors bars cannot be used.

449 Conclusion

450 The EGrowth database shows that a large amount of data on earthworm body growth is already
451 published. By centralizing these data, EGrowth should help the development of process based
452 models of earthworm ecology. EGrowth also reveals knowledge gaps that challenge the applicability
453 of such models to real situations in nature. In particular, there is a clear lack of data from the field.
454 This kind of data is critical for assessing the performances of models. In addition, the effect of critical
455 environmental factors for earthworm growth, such as soil properties and soil humidity, have been
456 little studied so far. Lastly, little is known about rare species that are not dominant, particularly
457 regarding large or endemic species. In order to integrate new data, EGrowth will be updated in the
458 future. For this, a framework to report future data on earthworm body growth is proposed.

459

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463

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589

590

List of publications used to build the EGrowth database on earthworm body growth variability

Contact: Jerome.mathieu@upmc.fr

a) List of publications from which data were included in the EGrowth database

1. Addison, J.A., *Safety testing of tebufenozide, a new molt-inducing insecticide, for effects on nontarget forest soil invertebrates*. Ecotoxicology and Environmental Safety, 1996. **33**(1): p. 55-61.
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Checklist for reporting growth curves of Earthworms

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1 Experimental design

- The treatments are clearly defined.
- The treatment levels are clearly defined.
- The number of replicates per treatment is clearly indicated.
- The number of individuals per replicate is clearly indicated.

2 Biomass

- The type of biomass is clearly mentioned (dry vs fresh biomass).
- The gut content status is mentioned (void gut vs non voided gut).
- The unit of the biomass is given.
- "Growth" and "biomass" are used appropriately.
- The biomass at hatching is reported.
- The biomass at first date of the survey is given numerically (not only on graphs), with the error bar.

Bonus

- Gut content was estimated.
- Body moisture was estimated.

3 Age and time

- The age of the individuals at the first measurement is clearly given.
- The meaning of the X axis (age or time since the beginning of the measures) is defined.
- The units of the time/age axis are clearly mentioned (e.g. days, weeks).

If IGR (Instantaneous growth rate) only is reported,

- Its formula is mentioned.
- The absolute biomass are also reported.
- The age at each measurement is reported.

4 Phenology

- Full clitellum development is indicated.
- Death of individuals is indicated.

5 Taxonomy

- A couple of individuals are stored in alcohol for molecular identification.

6 Conditions of the experiments (metadata)

All these information are reported:

- Geographical origin of the specimens.
- Geographical coordinates in decimal degrees.
- The system of coordinates.
- Country where specimens were sampled.
- Species name, with the descriptor.
- Air temperature (°C).
- Soil or substrate pH.
- pH measurement type (e.g. H₂O, KCl).
- Container volume.
- Substrate mass or volume.
- Soil and substrate moisture.
- Type of moisture measurement.
- Type of food given.
- Amount of food given.
- Sampling scheme (I,II or III, see figure 4).
- Stages covered by the monitoring (B,J, JR,JRS,JRSD and so on, see figure 4).

7 Data

- Raw data and metadata are available either as supplementary material or in a data repository.
- Data are presented in txt or csv files.
- Data are given at the highest resolution possible (either by individual or by replicate) rather than as average per treatment.
- Error bars are given if averaged data are presented.
- The nature of errors bar is clearly stated.