

## PROCEED v6.0

Changes made in PROCEED database version 5,

both TimeSeriesDB and RatesDB

Original version:

**RatesDB:** PROCEED Rates DB v5 for upload 2021-11-25.csv (GitHub)

**TimeSeriesDB:** Harvesting Time Series 2021\_10\_20.csv

Who made these changes:

Lucas D. Gorné

Postdoctoral fellow at Brock University 2021-10 to 2022-10

Under supervision of Kiyoko Gotanda (Brock University)

Co-supervised by Andrew Hendry (McGill University) and Fanie Pelletier (Sherbrooke University)

## Changes

- (RatesDB) There were two pending issues columns ("pending\_issues" and "pending.issues"). I joined comments from both in only one column "pending\_issues"
- (RatesDB) Spaces, dashes, brackets and other symbols in column names can create issues in importing and processing data. I edited some column names as follows:

Native Response to Invasive -> resp\_introduced  
Landscape Change -> landscape\_change  
Climate Change -> climate\_change  
Reference comments -> reference\_comments

- (RatesDB) I reordered some columns for convenience. The new order of variables is:

es\_ID  
ref\_ID  
sys\_ID  
species  
taxa  
taxa\_fine  
system  
comments\_on\_system  
sex  
sample1  
sample2  
sample1.latitude  
sample1.longitude  
sample2.latitude  
sample2.longitude  
coordinate.means  
coordinates.notes  
landmark  
design  
genphen  
years  
gtime  
gtime.notes  
generations  
trait\_description  
Roff\_Mousseau  
Kingsolver\_Diamond

data.type  
 new.data.type  
 data.scale  
 outlier  
 n1\_r  
 n2\_r  
 mean1\_r  
 mean2\_r  
 sd1\_r  
 sd2\_r  
 n1\_ln  
 n2\_ln  
 mean1\_ln  
 mean2\_ln  
 sd1\_ln  
 sd2\_ln  
 out\_in  
 urban\_disturbance  
 driver  
 old\_disturbance  
 new\_disturbance  
 Introductions  
 Other  
 resp\_introduced  
 Hunting\_Harvesting  
 landscape\_change  
 Pollution  
 climate\_change  
 time.series  
 tserieshandling  
 comments  
 DOI  
 reference  
 reference\_comments  
 copyright  
 who  
 repeated\_systems  
 pending\_issues

- (RatesDB) I changed spelling in "new\_disturbance" = "Hunting/Harvesting" to "new\_disturbance" = "Hunt\_harv"

- (RatesDB) In situations where a population is released from the hunting/harvesting disturbance, I changed: "new\_disturbance" = "Hunt\_harv" to "new\_disturbance" = "Other"

Those populations under this situations are two systems (first: "new\_disturbance"="Hunt\_harv"; second: "new\_disturbance"="Other"). So when needed I split this in two systems.

I added two variables, "released\_sys" (keeps information of the system previous to being released) and "released\_es" (keeps the information of the change and/or time series for a specific trait and system previous to being released).

- (TimeSeriesDB) There was a comment in the last, non-named column (\*\*Confirm Pairwise groups from here\*\*). I added a column named "obs" for general observations.
- (TimeSeriesDB) I replaced "Rate\_ID" with "es\_ID". This variable is a unique identifier for each time series and it is related to a specific rate in the RatesDB. Each time series corresponds to a rate of change in an Allochronic design in the RatesDB, so this ID is the same. Additionally, I checked (and modified as needed) all es\_ID in TimeSeriesDB for consistency with RatesDB.
- (TimeSeriesDB) The variables "Anthro/Nat(6Nat)" and "Anthro/Nat(6Anthro)" have exactly the same information. I removed "Anthro/Nat(6Nat)"
- (TimeSeriesDB) The variable "Pairwise group" is a counting variable of the number of time series (coming from allochronic pairwise comparisons). It is redundant with "es\_ID". I removed "Pairwise group".
- (TimeSeriesDB) Spaces, dashes, brackets and other symbols in column names can create issues in importing and processing data. Additionally, it is convenient that variables linking with RatesDB were spelt in the same way. I edited the column names as follows:

```
es_ID -> es_ID
Ref_ID -> ref_ID
Sys_ID -> sys_ID
Reference -> reference
Species -> species
System -> system
Taxa -> taxa
Disturbance -> old_disturbance
Out/in -> out_in
```

```

Anthro/Nat(6Anthro) -> anthro_nat
Sex -> sex
GenPhen -> genphen
Design -> design
Trait -> trait_description
Data type -> data.type
Data Scale -> data.scale
Population/Sample -> sample1
Population/Sample2 -> sample2
Years -> years
GTime -> gtime
Generations -> generations
Year -> date_year
N -> n
M -> mean
SD -> sd
obs -> obs

```

- (TimeSeriesDB) system s156, time series es4598, es4599, es4600, es4601, es4602, and es4603:

The species was replaced with the name used in RatesDB ("Rana esculenta complex").

- (TimeSeriesDB) in p139 the surname in "reference" was fixed (replacement of "Calvillo" with "Delgadillo Calvillo")
- (TimeSeriesDB) in p139 the journal volume number in "reference" was fixed (replacement of "38" with "39")
- (RatesDB) in p139 the surname in "reference" was fixed (replacement of "Calvillo" with "Delgadillo Calvillo")
- (RatesDB) in es4084 (p126; s126) I fixed "sample2" (replacement of "Blue tit Oosterhaut (1979)" with "Blue tit Oosterhaut (1998)")
- (RatesDB) in p126, s126 I added the "es9214" correspondig to Blue Tit in Vlieland
- (RatesDB) Gadus morhua, systems in Canadian shores. A system (s437) from Hutchings 2005 (NOFA 4Vs), was included within s409 from Beacham 1983 (NOFA 4Vs, 4Vn, 4W, 4X). I splited s409 into four systems:

```

NOFA 4Vs -> s437
NOFA 4Vn -> s409

```

NOFA 4W -> s1814

NOFA 4X -> s1815

- (RatesDB) *Gadus morhua*, systems in Canadian shores. A system (s065) from Olsen 2004 (NOFA 2J, 3K, 3L, 3N, 3O, 3Ps) overlapped with five systems (s1649, s1650, s1651, s1652, s1653) from Olsen 2005 (NOFA 2J, 3K, 3L, 3N+3O, 3Ps). Additionally, all these systems included two situations Harvesting and Moratorium period. I reordered these systems as followed:

NOFA 2J (fishing period) -> s1649

NOFA 3K (fishing period) -> s1650

NOFA 3L (fishing period) -> s1651

NOFA 3N+3O (fishing period) -> s1652

NOFA 3Ps (fishing period) -> s1653

NOFA 2J (moratorium period) -> s1816

NOFA 3K (moratorium period) -> s1817

NOFA 3L (moratorium period) -> s1818

NOFA 3N+3O (moratorium period) -> s1819

NOFA 3Ps (moratorium period) -> s1820

As a consequence es7427 to es7471 (all the es from p216) were modified by being computed only for the fishing period and es from es9215 to es9259 were added, recording the moratorium period.

Also, a system (s440) from Bratney et al. 2004 (NOFA 3Ps) was already included in s065 and it was the same than s1653. But here the system is "*Gadus morhua* (Atlantic cod) stock assessment in NAFO Subdiv. 3Ps, stock reopened after 1997 after closing for moratorium in 1993". So, I kept as a different system.

- (RatesDB) in p092 (Olsen 2004, Nature 428: 932-935) I updated the "system" for moratorium period (es4024, es4026, es4028, es4030, es4032, es4034, es4036, es4038, es4041, es4043, es4046, es4049, es4051, es4053, es4055, es4057, es4059, es4062, es4064). I replaced "*Gadus morhua* (Atlantic cod) subjected to fishing pressure in Newfoundland and Labrador" with "*Gadus morhua* (Atlantic cod) in moratorium period after fishing pressure in Newfoundland and Labrador".

- (RatesDB) in p092 (Olsen 2004, Nature 428: 932-935) I updated the "new\_disturbance" for moratorium period (es4024, es4026, es4028, es4030, es4032, es4034, es4036, es4038, es4041, es4043, es4046, es4049, es4051, es4053, es4055, es4057, es4059, es4062, es4064). I replaced "Hunt\_harv" with "Other". I let the variables "Introductions", "Other", "resp\_introduced", "Hunting\_Harvesting", "landscape\_change", "Pollution", "climate\_change" with the values 0, 5, 0, 0, 0, 0, 1, respectively
- (TimeSeriesDB) in p092 (Olsen 2004, Nature 428: 932-935) I updated the "system" for moratorium period (es4024, es4026, es4028, es4030, es4032, es4034, es4036, es4038, es4041, es4043, es4046, es4049, es4051, es4053, es4055, es4057, es4059, es4062, es4064). I replaced "Gadus morhua (Atlantic cod) subjected to fishing pressure in Newfoundland and Labrador" with "Gadus morhua (Atlantic cod) in moratorium period after fishing pressure in Newfoundland and Labrador".
- (TimeSeriesDB) Gadus morhua, systems in Canadian shores. A system (s065) from Olsen 2004 (NOFA 2J, 3K, 3L, 3N, 3O, 3Ps) was overlaped with five systems (s1649, s1650, s1651, s1652, s1653) from Olsen 2005 (NOFA 2J, 3K, 3L, 3N+3O, 3Ps). Additionally, all these systems included two situations Harvesting and Moratorium period. I reordered these systems as followed:
  - NOFA 2J (fishing period) -> s1649
  - NOFA 3K (fishing period) -> s1650
  - NOFA 3L (fishing period) -> s1651
  - NOFA 3N+3O (fishing period) -> s1652
  - NOFA 3Ps (fishing period) -> s1653
  - NOFA 2J (moratorium period) -> s1816
  - NOFA 3K (moratorium period) -> s1817
  - NOFA 3L (moratorium period) -> s1818
  - NOFA 3N+3O (moratorium period) -> s1819
  - NOFA 3Ps (moratorium period) -> s1820
- (RatesDB) Systems s064 and s1673 are the same system: Gadus morhua (Atlantic cod) in the southern Gulf of St Lawrence, response to fisheries/exploitation. I replaced sys\_ID=s1673 with sys\_ID=s064.
- (TimeSeriesDB) Systems s064 (p117) and s1673 (p218) are the same system: Gadus morhua (Atlantic cod) in the southern Gulf of St Lawrence, response to fisheries/exploitation. I replaced sys\_ID=s1673 with sys\_ID=s064.

- (RatesDB) System s126 (*Parus caeruleus*), from p130 and p126, merges five populations and rates were computed separately for each population. So, I split s126 into five systems. I kept s126 for Brunswick (52°16N; 10°32E) population (p130, Winkel 1997). I added s1821, s1822, s1823, and s1824 for Hoge Veluwe (52°05N 5°E), Liesbos (51°35N 4°40E), Oosterhaut (51°55N 5°50E), and Vieland (53°15N 5°E) populations (p126, Visser 2003).
- (TimeSeriesDB) System s126 (*Parus caeruleus*), from p130 and p126, merges five populations and rates were computed separately for each population. So, I split s126 into five systems. I kept s126 for Brunswick (52°16N; 10°32E) population (p130, Winkel 1997). I added s1821, s1822, s1823, and s1824 for Hoge Veluwe (52°05N 5°E), Liesbos (51°35N 4°40E), Oosterhaut (51°55N 5°50E), and Vieland (53°15N 5°E) populations (p126, Visser 2003).
- (RatesDB) System s414 (*Parus caeruleus*), from p181, merges three populations from two different places and rates were computed separately for each population. So, I split s414 into two systems. I kept s414 for French mainland (Rouviere) population. I added system s1825 for Piro and Muro populations in Corsica.
- (RatesDB) System s129 (*Parus caeruleus*), from p130 and p126, merges five populations and rates were computed separately for each population. So, I split s129 into five systems. I kept s129 for Brunswick (52°16N; 10°32E) population (p130, Winkel 1997). I added s1826, s1827, and s1828, for Hoge Veluwe (52°05N 5°E), Liesbos (51°35N 4°40E), and Oosterhaut (51°55N 5°50E) populations (p126, Visser 2003). Vieland (53°15N 5°E) population (p126, Visser 2003) was labelled as s128 (like in p099, Postma 2005).
- (TimeSeriesDB) System s129 (*Parus caeruleus*), from p130 and p126, merges five populations and rates were computed separately for each population. So, I split s129 into five systems. I kept s129 for Brunswick (52°16N; 10°32E) population (p130, Winkel 1997). I added s1826, s1827, and s1828, for Hoge Veluwe (52°05N 5°E), Liesbos (51°35N 4°40E), and Oosterhaut (51°55N 5°50E) populations (p126, Visser 2003). Vieland (53°15N 5°E) population (p126, Visser 2003) was labelled as s128 (like in p099, Postma 2005).
- (RatesDB) From p211 (Barot et al 2005), the systems s1642 (*Hippoglossoides platessoides* in NAFO 3L+3N+3O) and s1643 (*Hippoglossoides platessoides* in NAFO 3Ps) are the same as s435 (from p198, Dwyer et al. 2007) and s436 (from p199, Morgan et al. 2002) respectively. Additionally all these systems includes periods of fishing with



moratorium period. I reordered the systems as follows (and added new rates when necessary):

```
NAFO 2J+3K (fishing period) -> s1829
NAFO 3L+3N+30 (fishing period) -> s435
NAFO 3Ps (fishing period) -> s436

NAFO 2J+3K (moratorium period) -> s1641
NAFO 3L+3N+30 (moratorium period) -> s1642
NAFO 3Ps (moratorium period) -> s1643

Fishing period: up to 1993
Moratorium period: from 1994
```

The data extracted from figures from p198 and p199 was not in the workspace, I had to extract it again and I added it to the TimeSeriesDB.

- (RatesDB) I added coordinates for system s1829 and s1641 (NAFO divisions 2J+3K)
- (TimeSeriesDB) I added time series corresponding to es5918 to es5925, and es9260 to es9267 (from p198 and p199). Time series added: es5918, es5919, es5920, es5921, es5922, es5923, es5924, es5925, es9260, es9261, es9262, es9263, es9264, es9265, es9266, es9267.
- (RatesDB) From p133 (Yeh 2004), the systems s084 (Junco hyemalis) merge two populations (Coastal and Mountain populations) and rates were computed separately for each population. So, I split s084 into two systems. I kept s084 for the coastal population. I added s1830 for the mountain population. Also, I removed the "pending\_issues" comment (i.e. "Query for Daniel: Split in two systems; one for allochronic coastal and the other for allochronic mountain besides the next system (see below) which addresses synchronic coastal-mountain").
- (RatesDB) There were several systems for the same Ovis canadensis population (Ram Mountain, Alberta, Canada). s122 from Coltman 2003 (1977-1999), measuring mean weight and mean horn length of males; s420 from Pigeon 2017 (1975-2012), measuring mean age-adjusted female mass; s444 and s445 from Pigeon 2016 (Hunted 1976-1995 vs unhunted period 1996-2015), measuring body mass, horn base circumference, and horn length both in males and females. Even when it is the same population, the time

periods overlap and some traits are the same, the samples are different (different samples size, means and sd). I kept all the observations and time series, but I re-ordered the systems as:

s122 -> *Ovis canadensis* in Ram Mountain, Alberta, Canada. Hunted period (up to 1995)  
s445 -> *Ovis canadensis* in Ram Mountain, Alberta, Canada. Unhunted period (from 1996)

- (TimeSeriesDB) sex in es5869 time series was modified from female to mixed, in accordance with the RatesDB.
- (RatesDB) es7473, p217, s1655 RatesDB said "Area 2A", but area 2A does not exist. It is Area 2E. Fixed.
- (TimeSeriesDB) es7482, p217, s1664 TimeSeriesDB said "Area 1" and RatesDB said "Area 12". According to coordinates and figures in the papers, it is Area 12. Fixed.
- (RatesDB) p210, species name *Gadus morhua* had a bunch of spaces at the end. Removed
- (TimeSeriesDB) p210, species name *Gadus morhua* had a bunch of spaces at the end. Removed
- (RatesDB) p212, species name *Oncorhynchus keta* had a bunch of spaces at the end. Removed
- (TimeSeriesDB) p212, species name *Oncorhynchus keta* had a bunch of spaces at the end. Removed
- (RatesDB) p144, species name "*Mustela vison*" was replaced by "*Mustela vison*"
- (RatesDB) I removed authority from the species names *Plantago major* L., *Brassica rapa* L., *Anthoxanthum odoratum* L.
- (RatesDB) in p132 there were inconsistencies between species names and system description. es4309, es4310, and es4311 are *Lupinus bicolor*, these three were kept as s099. es4312, es4313, and es4314 are *Lotus purshianus*, these three were assigned to system s1787.
- (RatesDB) in p132 I added the following gtime.note:

*"Lupinus bicolor is an annual, seeds require to be scattered to germinate and flowering depends on day length (Dunn DB. 1956. The Breeding Systems of Lupinus, Group Micranthi. American Midland Naturalist, 55:443-472). A generation time of one year seems accurate."*

*"Lotus purshianus, a dicot, is an annual herb. It flowers in spring (to early summer) (<https://www.calflora.org/app/taxon?crn=10961>). Seeds do not have primary dormancy (Guerrant Jr EO & Raven A. 1995. Seed germination and storability studies of 69 plant taxa native to the Willamette Valley wet prairie. Portland, OR: The Berry Botanic Garden). So, generation time is one year."*

Also I added the papers Dunn 1956 and Guerrant 1995 to the folder of Wu 1985 in the workspace

- (RatesDB) in p131, s171 I added the following gtime.note:

*"Richards (1997) have estimated average generation time in natural populations of S. latifolia to be approximately 1.5 years by direct census of marked plants (Richards CM. 1997. The ecological genetics of population establishment in Silene alba. PhD Dissertation, Duke University, Durham, NC, USA.)"*

Also I added the paper Richards 1997 to the folder of wolfe 2004 in the workspace

- (RatesDB) in p129, the "gtime" of systems s028, s047, s051, and s167 were modified according to the following information (added to "gtime.notes"):

*"Generation time averaged from the estimation from different sources. First, it was computed with data from Woodburn TL & Sheppard AW. 1996. The demography of Carduus nutans as a native and an alien weed. Plant Protection Quarterly, 11:236-238. Second, with transitions matrix from COMPADRE database (Matrices 242153, 242147, 242151, 242152 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46679> [17 May 2021, Version 6.21.1.0])."*

*"Digitalis purpurea is a facultative biennial, a monocarpic species that can complete their life cycle within 2 years, but where a delay of reproduction until the third or later*

year is commonly observed because it must reach a threshold size to be able to be vernalized (Sletvold N. 2002. Effects of plant size on reproductive output and offspring performance in the facultative biennial *Digitalis purpurea*. *Journal of Ecology*, 90:958-966). While, 19% of seeds germinates in the same year their are release (in autum), 48% germinates in the following spring (Van Baalen J. 1982. Germination ecology and seed population dynamics of *Digitalis purpurea*. *Oecologia*, 53:61-67). Germination in autum allow a life cycle of one year, germination in springs allow a life cycle of two years (because vernalization is required). But also is posible that plants germinated in autum do not reach the size threshold required to be vernalized. Generation time computed from transitions matrices in COMPADRE database (Matrices 242803, 242806 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46874> [18 May 2021, Version 6.21.1.0]) vary from 3.47 to 7.84 years"

"The plant species *E. vulgare* (vipers's bugloss) is a self-compatible monocarpic perennial. Plants flowered at a mean age of 2.7 years on the sparse site and 3.4 years on the dense sites (Klemow KM & Raynal DJ. 1985. Demography of Two Facultative Biennial Plant Species in an Unproductive Habitat. *The Journal of Ecology*, 73:147-167). Levels of innate seed dormancy vary among populations, germination without cold stratification is low (less than 20%). Seed dispersal begins in mid Summer and continues through mid Autum. Most seedlings emerge in the spring (Klemow KM, Clements DR, Threadgill PF & Cavers PB. 2002. The biology of Canadian weeds. 116. *Echium vulgare* L. *Canadian journal of plant science*, 82:235-248). So, generation time is 3.5 years (3 for flowering plus 6 month for stratification). The generation time computed from transition matrix in COMPADRE database (Matrix 242943 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46613> [18 May 2021, Version 6.21.1.0]) is consistent, 3.67ys"

"*Jacobaea vulgaris* (synonym *Senecio jacobaea*) is a monocarpic perennial that spends its first year as a rosette. Flowering may take place in the second year, but is often delayed (vernalization depending on a size threshold). Its seeds do not possess innate dormancy. Most of the individuals flowered in the thirth (2 years old) or in fourth (3 years old) year (Van der Meijden E & van der Waals-Kooi RE. 1979. The Population Ecology of *Senecio Jacobaea* in a Sand Dune System: I. Reproductive Strategy and the Biennial Habit. *The Journal of Ecology*, 67:131-153). So, generation time is 2.5 years. Generation time computed from transition matrices from COMPADRE database (Matrices 245528, 245531,

245534, 245537, 245540 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46711> [18 May 2021, Version 6.21.1.0]) are quite variable (from 6.31 to 54.8 years). I kept the GT of 2.5 years, but the uncertainty is large."

Also, the papers Woodburn & Sheppard 1996, Sletvold 2002, Van Baalen 1982, Klemow & Raynal 1985, Klemow et al 2002, and the files with generation time analyses were added to the willis 2000 folder in the Workspace.

- (RatesDB) in p016, the "gtime" of systems s191, s192, s193, s194, s036, s037, s038, and s039 were modified according to the following information (added to "gtime.notes"):

*"Generation time computed from the COMPADRE database transition matrix (Matrix 246495 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46350> [18 May 2021, Version 6.21.1.0])) based on the work of Parker 1996 (Parker IM. 1996. Ecological factors affecting rates of spread in Cytisus scoparius, an invasive exotic shrub. Doctoral dissertation. University of Washintong)"*

*"Ulex europaeus starts to reproduce at 2 or 3 years old. It lives up to 30 years old. It follows the  $-3/2$  law of self-thinning (Rees M & Hill RL. 2001. Large-scale disturbances, biological control and the dynamics of gorse populations. J Appl Ecol 38:364–377). We assume that an increase in fecundity with age compensates for mortality, so the contribution of each age to the next generation is constant. This assumption probably underestimates the generation time, but less than just using the age at maturity."*

Also, the papers Parker 1996, Rees 2001 and the files with generation time analyses were added to the Buckley et al 2003 folder in the Workspace.

- (RatesDB) in p024 and p078, the "gtime" of system s007 was modified according to the following information (added to "gtime.notes"):

*"Generation time computed from COMPADRE database transition matrices (Matrices 241455, 241459, 241463, 241467, 241471, 241475, 241479, 241483, 241487, 241491, 241495, 241499, 241454, 241453, 241450, 241451, 241452 in COMPADRE Plant*

*Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46616> [20 May 2021, Version 6.21.1.0]). Plants live a year or less and flowered in their second year (Byers DL & Quinn JA. 1998. Demographic variation in *Alliaria petiolata* (Brassicaceae) in four contrasting habitats. *Journal of the Torrey Botanical Society*, 125:138-149). Seeds do not germinate in the same growing season because they need cold stratification (Anderson RC, Dhillon SS & Kelley TM. 1996. Aspects of the Ecology of an Invasive Plant, Garlic Mustard (*Alliaria petiolata*), in Central Illinois. *Restoration Ecology*, 4:181-191)."*

Also, the papers Byers & Quinn 1998, Anderson et al 1996 and the files with generation time analyses were added to the Cipollini et al 2005 folder in the Workspace.

- (RatesDB) in p132, I added the coordinates to systems s099 and s1787.
- (RatesDB) in p132, es4310, es4311, es4313 and es4314 are phenotypic (not genetic). Measures were made in a common garden but on tillers extracted from field. Fixed.
- (RatesDB) in p125 (system s081), es4375 and es4376 are measurements of growing so, they are Kingsolver\_Diamond="OtherLH". Even when growing at competence environment. Additionally, the two populations measured have 206 years of divergence (not only 54). The biological control was introduced 54 years ago, but here the comparison is not between populations in North America experiencing or not the biological control. Additionally, the "gtime" was modified according to the following information (added to "gtime.notes"):

*"According to Maron et al 2004, Ecological Monographs, 74(2):261-280"*

- (RatesDB) in p209, all cases where "design"="time series" were changed to "design"="Allochronic".
- (RatesDB) in p216, all cases where "taxa"="fish" were changed to "taxa"="Fish".
- (RatesDB) in p191, p192, p193, p195, p197, p198, p199, p201, p202, p203, p205, p206, p207, p208, p210, p211, p212, p213, p214 all cases where "sex"="Females" were changed to "sex"="female".
- (RatesDB) in p191, p195, p198, p199, p201, p203, p205, p210, p211 all cases where "sex"="Males" were changed to "sex"="male".

- (RatesDB) in p201, and p211 all cases where "coordinate.means"="Yes" were changed to "coordinate.means"="Y".
- (RatesDB) in p182 (es5802), "genphen"="genetic" was replaced with "genphen"="Genetic".
- (RatesDB) in p182, when "Roff\_Mousseau"="Life-history" was replaced with "Roff\_Mousseau"="Life-History".
- (RatesDB) in p182, when "Kingsolver\_Diamond"="Phenology" was replaced with "Kingsolver\_Diamond"="phenology".
- (RatesDB) in p190, all cases where "genphen"="phenotypic" were replaced with "genphen"="Phenotypic".
- (RatesDB) in p218, when "Roff\_Mousseau"="morphological" was replaced with "Roff\_Mousseau"="Morphological".
- (RatesDB) in p181, p210, p212, p213, and p214, when "Kingsolver\_Diamond"="Size" was replaced with "Kingsolver\_Diamond"="size".
- (RatesDB) in p177, p178, and p179, in all cases where trait is A50 (age at 50% maturity, years) "new.data.type"="time" was assigned. These were previously empty.
- (RatesDB) in p182, es5801 and es5803, traits are "residual clutch size" and "residual laying date". So, I assigned "new.data.type"="length residuals". These were previously empty.
- (RatesDB) in p190, when "new.data.type"="count " was replaced with "new.data.type"="count".
- (RatesDB) in p182 and p190, when "new.data.type"="date " was replaced with "new.data.type"="date".
- (RatesDB) in p197, when "new.data.type"="Index" was replaced with "new.data.type"="index".
- (RatesDB) in p215 and p218, when "new.data.type"="length" was replaced with "new.data.type"="linear".
- (RatesDB) in p197 p198 p199 p200 p201 p202 p203 p204, when "new.data.type"="Length" was replaced with "new.data.type"="linear".

- (RatesDB) in p204, when "new.data.type"="Mass" was replaced with "new.data.type"="cube (3D)".
- (RatesDB) in p182, when "new.data.type"="other " was replaced with "new.data.type"="other".
- (RatesDB) in p200 p201 p203 p204, when "new.data.type"="Other" was replaced with "new.data.type"="time". the trait is A50 (the average age -years- to maturity).
- (RatesDB) in p190, when "new.data.type"="proportion " was replaced with "new.data.type"="proportion".
- (RatesDB) in p217, when "new.data.type"="weight" was replaced with "new.data.type"="cube (3D)".
- (RatesDB) in p196, when "data.scale"="Interval" was replaced with "data.scale"="interval".
- (RatesDB) in p191 to p211, when "data.scale"="Ratio" was replaced with "data.scale"="ratio".
- (RatesDB) in p101, all traits are ratios of change (i.e.  $(X1-X2)/X1$ ). These amounts are not proportions because are not bounded between 0 and 1. But, the scale has a Zero. So, "new.data.type"="index" was replaced with "new.data.type"="other" and "data.scale"="unknown" was replaced with "data.scale"="ratio".
- (RatesDB) in p044, es4440, the trait is "Leaf survival (number of days until tagged leaves had fully senesced)", this amount has a trully zero (i.e. leaf survival  $< 1$  day). So, "data.scale"="unknown" was replaced with "data.scale"="ratio". Also, I removed the "pending\_issues" comment (i.e. "Data scale not resolved").
- (RatesDB) in p185, es5784 and es5785, the traits are "Clutch Size" and "Clutch Mass", but these are log-transformed. So, "data.scale"="unknown" was replaced with "data.scale"="ratio".
- (RatesDB) in the "out\_in" variable, the "in" values was replaced with "In" values.
- (RatesDB) in the "new\_disturbance" variable, the "Native response to invasive" values was replaced with "Response to introductions" values. This is in accordance with Sanderson et al 2021 paper. It can be a native or an introduced species responding to a newly introduced species. When it is native, "out\_in"="In". When it is introduced, "out\_in"="Out".



- (RatesDB) in p209, when "sex"="Males and Females" was replaced with "sex"="mixed".
- (RatesDB) in the "sex" variable, the "unknown" values were replaced with NAs
- (RatesDB) in general. I removed multiple empty spaces (i.e. " ", " ", " ", and so on) from references, systems, and other variables.
- (RatesDB) in the "coordinate.means" variable, an empty cell means "NO". I filled these with "N" to differentiate from a NA. If some coordinate value is missing, I let "coordinate.means" empty (i.e. NA).
- (RatesDB) in general. I unified the string for missing data. I choose the empty cell, so when uploading the database to R use `na.string=="`
- (RatesDB) in the p166, species name "Senecio Squalidus" was replaced with "Senecio squalidus".
- (RatesDB) in the p217, species name "Oncorhynchus tshawytscha" was replaced with "Oncorhynchus tshawytscha".
- (RatesDB) I added observations from es7500 to es9213.
- (RatesDB) I added the following variables related to the system (experimental and exp\_type):

experimental: states if the phenotypic change is driven by experimentally set conditions (N=no; Y=yes). It is not artificial selection (i.e. selection of specific attributes by choosing breeders and manipulating mating) but a process of natural selection in an experimental environment.

exp\_type:

01: A new environmental condition is imposed on a natural population, in the field, in situ

03: A new environmental condition is imposed on a natural population, in the field, ex situ (transplant)

05: A new environmental condition is imposed on a natural population, in a common garden/greenhouse experiment

07: A new environmental condition is imposed on an artificial population (it was an even set of genotypes from a natural population) in the field.

09: A new environmental condition is imposed on an artificial population (it was an even set of genotypes from a natural population) in a common garden experiment.

11: A new environmental condition is imposed on an artificial population (it was obtained by randomly crossing F2 individuals from a set of interbreeds between contrasting genotypes selected from a natural population) in a common garden experiment.

13: A selection pressure/agent is applied on an artificial population (F1 hybrid, it was obtained by crossing two contrasting genotypes of inbred strains) in an experimental field/common garden.

sp\_ncbi: The current name of the original taxon according to the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi>). Two species were not found in the NCBI database, *Stipa occidentalis* and *Diaptomus sanguineus*, these names were checked in The Plant List (<http://www.theplantlist.org/>) and WORMS (<https://www.marinespecies.org/index.php>) respectively.

- (RatesDB) in the p129, system s167, in the system description I added the current name of the species according to the NCBI (*Jacobaea vulgaris*).
- (RatesDB) in the p209, all coordinates stated as 0, are NAs according to the information in the workspace. I replaced "0" by empty cells (i.e. NAs)
- (RatesDB) in the p209, all gtimes stated as 0, are NAs according to the information in the workspace. I replaced "0" by empty cells (i.e. NAs). The same as for "generations"
- (RatesDB) in the p002, s004, I added the following gtime.note: "Generation Time is considered as the number of years required for a species to start producing seeds (this can underestimate the actual generation time) according to Engler R, Randin CF, Vittoz P, Czaka T, Beniston M, Zimmermann NE & Guisan A. 2009. Predicting future distributions of mountain plants under climate change: does dispersal capacity matter?. *Ecography*, 32:34-45."
- (RatesDB) in p038, the "gtime" of system s020 was modified according to the following information (added to "gtime.notes"):

"Authors guess that "one or two generations" have elapsed in the 70 years (Eränen 2009, *Journal of Evolutionary Biology* 22: 840-851). Transition matrix in COMPADRE database is one of shoots (ramets) transition matrix not one of individuals (genets) transition matrix. So, generation time can no be computed. We assume generation time equal to 70/1.5"

- (RatesDB) in p026, the "gtime" of system s088 was modified according to the following information (added to "gtime.notes"):

*"Lactuca muralis a herbaceous perennial hemicryptophyte. The plant is winter green dying completely back after flowering in the summer but then producing a small overwintering rosette(s) from a bud(s) on the rootstock. The plant is generally not monocarpic. Reproduction is entirely by seed. Most seeds germinate in the autumn and overwinter as a small rosette although some germinate in the following spring. Newly shed achenes germinate readily, giving rise in nature to seedling populations immediately after the flowering period. Seeds may also germinate after overwintering in the following spring. Flowering is possible after one season providing plants reach an appropriate size. After flowering the plant dies back completely, but in the autumn an overwintering rosette is produced from a bud or buds on the rootstock (Clabby G & Osborne BA. 1999. *Mycelis muralis* (L.) Dumort. (*Lactuca muralis* (L.) Gaertner). *Journal of ecology*, 87:156-172). There is no information about the lifespan of each individual through the new rootstock rosettes. So, the minimum generation time is one year (this can underestimate the actual generation time).*

- (RatesDB) in p076, the "gtime" of system s052 was modified from 1 to NA (empty cells). The information about generation time is not in the paper. Additionally, I was not able to find it in the literature and in "gtime.notes" or in the workspace, there is no information about the generation time of *Elymus multisetus*. Furthermore, this species is a long-lived perennial grass, so 1 year seems a severe underestimation of the actual generation time.

- (RatesDB) in p023 and p012, the "gtime" of system s101 was modified according to the following information (added to "gtime.notes"):

*"The species has been described as a facultative annual because it can set seed in one growing season (Shipley and Parent 1991, Johansson and Keddy 1991), however, this description is misleading because the species is not semelparous. *Lythrum salicaria* is a*

*perennial, with annual stems arising from a perennating rootstock. There are no reports in the literature concerning the longevity of single genets.*" (Mal TR, Lovett-Doust J, Lovett-Doust L & Mulligan GA. 1992. *The biology of Canadian weeds*. 100. *Lythrum salicaria*. *Canadian Journal of Plant Science*, 72:1305-1330.). Generation time was computed from COMPADRE database transition matrices (Matrices 244356, 244359 in COMPADRE Plant Matrix Database (2021). Available from: <https://www.compadre-db.org/Species/46816> [21 May 2021, Version 6.21.1.0])

- (RatesDB) in p060, the "gtime" of system s102 was modified according to the following information (added to "gtime.notes"):

*While individual trees can live over 100 years (Dray 2003), they can become reproductive within 1–2 years (Meskimen 1962, Vardaman 1994). So, a generation time of 2 years is a serious underestimation.*

- (RatesDB) in p026, the "gtime" of system s168 was modified according to the following information (added to "gtime.notes"):

*Senecio sylvaticus is an annual, mostly autogamous plant. Within the group of annual Senecio species, S. sylvaticus is not as strict summer annual as the co-occurring S. viscosus, but has also not such a variable seasonality as S. vulgaris. S. sylvaticus is rooting in the litter layer (A00) and fermentation layer (A0) and is very unproductive on mineral soils. Achenes of S. sylvaticus genninated in Autum or in Spring. From late Spring to mid Summer no germination was observed. In addition to the two different periods of gennination, there was a great difference in plant biomass of both life forms in spring. The biomass of the winter annual life forms was more than ten fold that of the summer annual life form in the last days of May. Under natural conditions, the summer annual populations did flower from summer to autum. (Ernst, W. H. O. (1989). Selection of winter and summer annual life forms in populations of Senecio sylvaticus L. Flora, 182(3-4), 221-231)*

- (RatesDB) in p056, p044, and p085 the "gtime" of system s173 was modified according to the following information (added to "gtime.notes"):

*Solidago gigantea is very simmlar to Solidago altissima (see Solidago altissima GTimeNotes). Solidago gigantea is a tall, erect perennial herb with annual aboveground shoots and persistent belowground rhizomes. Solidago gigantea produces long-creeping*

*plagiotropic, mostly purple or reddish rhizomes, mostly within the upper 10–20 cm of soil. In total, 3–50 rhizomes per ramet emerge close to the base of shoots from the previous year. Higher numbers have been observed after disturbances. Production of seeds, new shoots and new rhizomes occurs every year, and all aboveground shoots die back in autumn. Free carbohydrates are accumulated in the rhizome before the dormant period. Seedlings have never been observed within established patches of *S. gigantea*, suggesting that seeds are primarily important for long-distance dispersal and the colonization of new sites. However, seedlings may appear after a spring mowing, suggesting that successful establishment is dependent upon open conditions. In most cases, however, population increase is primarily the result of clonal growth. The relative significance of sexual reproduction increases with the age of the clone, whereas clonal growth is most essential during the first years after establishment. Individual clones are often easy to distinguish and frequently achieve 2–5 m diameter. Larger, older clones may contain thousands of ramets. Occasionally clones form ‘fairy circles’ around the initial centre of the genet. Under good conditions, almost all plants reproduce in their first year, and a single ramet produces up to 19,000 achenes. Under resource limited conditions, sexual reproduction is reduced to the benefit of vegetative growth (Weber E & Jakobs G. 2005. Biological flora of central Europe: *Solidago gigantea* Aiton. Flora - Morphology, Distribution, Functional Ecology of Plants, 200:109–118). Generation time should be long but I did not find any estimation. However, Meyer et al 2005 (Meyer G, Clare R, Weber E. 2005. An experimental test of the evolution of increased competitive ability hypothesis in goldenrod, *Solidago gigantea*. Oecologia, 144:299–307) observed that almost all plants grown from seeds flowered in the second year, more than a half flowered in the first year. So, in newly colonized areas a generation time of 2 years can be assumed. This would be a severe underestimation for established populations.*

- (RatesDB) in p034, es4235 to es4238, there were no information about the source for a generation time of 2 years for *Spartina alterniflora*. *Spartina alterniflora* have clonal growing, and clones can reach 100m diameter (Buhle ER, Feist BE & Hilborn R. 2012. Population dynamics and control of invasive *Spartina alterniflora*: inference and forecasting under uncertainty. Ecological Applications, 22:880–893). So, its generation time should be quite long. Transition matrix in COMPADRE, is not for genets but ramets, and is a simulation matrix. A generation time of 2 years is a severe underestimation. The "gtime" of system s174 was modified from 2 to NA (empty cell)

- (RatesDB) I added the variable "c\_value": c-value is the amount, in picograms, of DNA contained within a haploid nucleus (e.g. a gamete) or one half the amount in a diploid somatic cell.

Detailed information of the variable in "species\_genome.csv" and "species\_genome\_README.txt"

#### WHEN MORE THAN ONE VALUE IS AVAILABLE FOR ONE SPECIES

- If there is no difference in ploidy level or chromosome number among records, c-values were averaged.
- Records using Feulgen densitometry (Fe), flow citometry (FC\_any type), DAPI microdensitometry (MDAPI), Gallocyanin chrom alum densitometry (GDC), or Fulgen image analysis densitometry (FIA) methods were preferred over other methods. So, when available, records using these methods were chosen for averaging.
- in birds, if the genome size was estimated from several congeners, the values of the multiple measurements of c-value (if more than one) for each congener were averaged previously, then the average among congeners was computed.
- in general, if the genome size was estimated from several subspecies, the value for each subspecies was averaged previously of averaging among them.
- in general, but specially in plants, when a species has more than one genome size due to differences in ploidy level or chromosome number, the system was revisited looking for information about particular ploidy levels of the involved populations for each case. If no information was found, the available c-values were averaged.
- (TimeSeriesDB) time series from Gorné & Díaz database were added. Situations where there is a replacement of space by time (i.e. several populations/plot of different age instead a single population along time) were not included. The added time series were:

es7811  
es7812  
es8033  
es8034  
es8035  
es8036  
es8037

es8291  
 es8294  
 es8892  
 es8893  
 es8894  
 es8895  
 es8896  
 es8921  
 es8923  
 es8924  
 es8925  
 es8926  
 es8927

- (TimeSeriesDB) missing data was set as empty cells instead of "NA".
- (TimeSeriesDB) in es3401, p047, s031 one date year was updated from 151 to 1951.
- (TimeSeriesDB) in es7322, p211, s1829 one date year was updated from 184 to 1984.
- (RatesDB) I added case es9280 in p143, s230. It was lacking from TimeSeriesDB
- (RatesDB) In papers p102, p133 and p134, systems where Junco hyemalis experienced a "Self induced range expansion", variable "out\_in" was modified from "Out" to "In", according to the metadata (Natural range expansions are considered "in").
- (RatesDB) In papers p102, and p134, Synchronic system (formerly s086) is exactly the same than s085. So, it was updated.
- (RatesDB) In paper p134, Allochronic system (formerly s086) is exactly the same than s084. So, it was updated.
- (TimeSeriesDB) time series es4612 was reload from the original paper Yeh 2004, Am.Nat, Table 2.
- (RatesDB) In paper p133, es4604, es4605, es4606, es4613, es4614 do not correspond with time series. So, "time.series" value was changes from "Yes" to "No".
- (RatesDB) I added the variable "env\_change":

env\_change:

ongoing (o): The environmental change has been progressing for a while and the phenotypic change was measured in a temporal window within this process (but not from the starting point)

novel (n): The environmental change has a defined starting point and phenotypic change was measured from this point.

This only affects Allochronic designs, synchronic are always "env\_change"="n" (because the proposed ancestral state is placed previous to the drivers happening).

When "new\_disturbance"="Other", if the driver it is unknown, "env\_change"="NA" (empty cell). But in some cases the driver of change is known, like "self induced range expansion", also experimental systems can represent "in situ natural variation" but from a known starting point. In these cases, the value of "env\_change" can be chosen.

- (RatesDB) I added the variable "transf\_data":

raw: mean and sd computed from raw data (non log transformed, or any other transformed-data).

ord: the trait is the score in the axis of an ordination analysis (i.e. PCA, CVA).

arcsin: arc sin ( $\sin^{-1}$ ) transformation.

arcsin.sqr: angular transformation, i.e.  $2 \cdot \sin^{-1}(\sqrt{x})$ .

resid: residuals of regression or other statistical model ( $y - \hat{y}$ ), centered variables ( $y - \bar{y}$ ), absolute ( $Y_t - Y_c$ ) or relative difference ( $[Y_t - Y_c] / Y_c = Y_t / Y_c - 1$ ) between a treatment and a control.

ln: mean and sd computed from natural log-transformed data. We also include data like  $\ln(x) / \ln(y)$  and  $\ln(x/y) / t$

log10: mean and sd computed from log10-transformed data. We also include data like  $\log_{10}(x) / \log_{10}(y)$  and  $\log_{10}(x/y)$

- (RatesDB) with the new variable "transf\_data" the six columns "n1\_ln", "n2\_ln", "mean1\_ln", "mean2\_ln", "sd1\_ln", and "sd2\_ln" are no need anymore. So I moved the information from these columns to the columns "n1\_r", "n2\_r", "mean1\_r", "mean2\_r", "sd1\_r", and "sd2\_r". Then I deleted the "\*\_ln" columns.



- (RatesDB) I replace the name of columns "n1\_r", "n2\_r", "mean1\_r", "mean2\_r", "sd1\_r", and "sd2\_r" with "n1", "n2", "mean1", "mean2", "sd1", and "sd2".
- (RatesDB) The original data from p055, system s124 (es1006 to es1009) is in log10. I added this information to the raw data column I added the variable "transf\_data".
- (RatesDB) es3937 (p046, s040). The original values for mean1 and mean2 are negative. I fixed this.
- (RatesDB) I recovered information of means for es5503 to es5661 (from paper p145, van Buskirk 2010). This information was in v4 of the database. Also I recovered 25 observations from the same paper but not recorded in v5 of the database. These cases spam from es9281 to es9305, and are additional systems s1831 to s1843.
- (RatesDB) in all cases from paper p145, van Buskirk 2010, (es5503 to es5661 plus es9281 to es9305) "years", "gtime", "generations" and "gtime.notes" are wrong. I recovered this information from v4 of the database (I also checked v3.5 and workspace). Labels for "sample1" and "sample2" are also wrong. "years" in v4 are also wrong, because there "years" are the number of datapoints to compute the regression model, it was took from "N.years" in workspace, but this is not the elapsed time. The elapsed time is (from v4 and workspace) "sample2" minus "sample1". Because "sample1" and "sample2" are the distance from the mean date of the dataset for each species (this is why sample 1 is negative amount and sample2 a positive amount). The whole period elapsed in this study is 1961-2007, but we do not know the specific period for each species. As a consequence, I set "sample1"="first year - approx 1961 (-XX)", and "sample2"="last year - approx 2007 (XX)". Where XX is the number for "sample1" and "sample2" in v4. I computed again the elapsed time ("years" and "generations") with this information and the "gtime" from v4.
- (RatesDB) paper p025 (Clegg 2002), system s197, this is a case of self-induced range expansion. So, new\_disturbance was changed from "introduction" to "other", and out\_in was changed from "Out" to "In". I also updated "Introductions", "Other", "resp\_introduced", "Hunting\_Harvesting", "landscape\_change", "Pollution", "climate\_change" accordingly.
- (RatesDB) paper p055 (Hill 1999), system s124, this is a case of self-induced range expansion. So, out\_in was changed from "Out" to "In".

- (RatesDB) paper p006 (Bell 2004), system s070, this is a case of self-induced range expansion. So, out\_in was changed from "Out" to "In".
- (RatesDB) in system s183, I added the aprox time of introduction according to Haugen 2000 Oikos.
- (RatesDB) in system s183, in es0973 to es0977 I changed "new.data.type" from "cube (3D)" to "other" because it is the ratio between gonad mass and somatic mass. It is dimensionless and it is not a proportion.
- (RatesDB) in system s117, paper p067. I updated Reference, it is Kinnison 1998a. Can. J. Zool. (not Kinnison 1999). The DOI was also wrong, I fixed it.
- (RatesDB) in system s092, paper p022. I added allochronic data for females (males sample size is too small) es9306 - es9308.
- (RatesDB) in system s196, the traits (critical photoperiod) is "new.trait.type"="time" but it is not "interval" "data.scale" because is not the hour of the day, is the amount of hours, it can be 0 (and it is a true 0). I changed to "data.scale"="ratio".
- (RatesDB) in system s019, paper p048, I added the "gtime.notes":

*"In the paper, authors assume two generations per year".*

- (RatesDB) in system s093, I fixed "gtime" (replaced 0.75 with 0.67) and add the following "gtime.notes":

*"The authors assumed that the elapsed time (9 years) correspond with 9 to 18 generations (mean value 13.5). So, generation time is between 0.5 and 1 (mean value  $9/13.5 = 0.67$ )."*

- (RatesDB) data from paper p002 (s004, s005, s012, s045, s058) was measured on tiller produced vegetatively from plants collected in the field, They are not testing the next generation, so the "genphen"="Phenotypic", not "Genetic". I changed that.
- (RatesDB) in data from paper p060, system s102, there was a mistake in the label of traits (and its attributes, i.e. "new.data.type", "Kingsolver.Diamond", etc). The right order of the traits is not:

Final Height (mm)  
Total Growth (mm/day)  
Biomass (mg)

Leaf Length (mm)

Leaf Width (mm)

but:

Final Height (mm)

Total Growth (mm/day)

Leaf Length (mm)

Leaf Width (mm)

Biomass (mg)

- (RatesDB) in data from paper p036, system s029, the trait for es4472 is "Stem mass ratio (stem mass / whole plant mass)" it is a "proportion" (it is addimentional and bounded between 0 and 1) is not "cube (3D)" because the trait is not the stem mass. Similar for es4470, es4486, es4488, and es4489. I changed these.
- (RatesDB) the system s202, paper p139, is not Hunting. Samples came from a herd located at the National Center for Disciplinary, Physiology and Animal Improvement Research (CENID-FyMA), of the National Institute for Forest, Agricultural and Animal Production Research (INIFAP-SAGARPA), Ajuchitlan, Queretaro, Mexico. It is a case of in situ natural variation ("new\_disturbance"="Other"). I changed this for "new\_disturbance" and "driver"
- (RatesDB) the system s203, paper p140, is not Hunting. Samples came from a farm dedicated to velvet production. It is a case of in situ natural variation ("new\_disturbance"="Other"). I changed this for "new\_disturbance" and "driver"
- (RatesDB) the system s150, paper p124, es4620, the trait is "Hind limb length (%SVL)" not "Hind limb length" so, it is a proportion trait.type not linear. I fixed that.
- (RatesDB) paper p162, the traits "Rel orange" and similar are the proportion of the total body area covered by a given color. So the trait type is a proportion not area(2D). I modified that and I made the trait descriptions more explicit.
- (RatesDB) paper p175, system s418, the sample size 2 (n2) was lacking for es5671 and es5672. I recovered these from the workspace.
- (RatesDB) Systems s410 (paper p185) and s070 (paper p006) are the same: "Gasterosteus aculeatus (threespine stickleback) Loberg Lake, AK longterm dataset" and "Gasterosteus aculeatus (Threespine stickleback) naturally colonizing Logberg Lake Alaska". I have unified under the ID s070 and the following description: "Gasterosteus

aculeatus (Threespine stickleback) naturally colonizing Logberg Lake Alaska (between 1983 and 1988)"

- (RatesDB) paper p158, system s307. It is Synchronic, not Allochronic. I fixed it.
- (RatesDB) paper p101, system s155, all measurements are relative differences with a control level. So, the scale has no true zero. The zero is relative to the trait at the control level. So, "data.scale"="interval" (instead of "ratio").
- (RatesDB) paper p098, system s153, measurement is relative differences with a control level. So, the scale has no true zero. The zero is relative to the trait at the control level. So, "data.scale"="interval" (instead of "ratio").
- (RatesDB) paper p076, system s052, Cpi trait (es4409 - es4424) is a relative differences with a control level. So, the scale has no true zero. The zero is relative to the trait at the control level. So, "data.scale"="interval" (instead of "ratio").
- (RatesDB) paper p196, system s432, fruit size and seed mass are life history traits because are measurements of reproductive output, not size. I have replaced that. Sugar content is a physiological trait not morphological. I have replaced that. The data.scale of es5892 to es5894 is ratio while data.scale of es5895 to es5897 is interval (standardized variables). I fixed this.
- (RatesDB) paper p211, the trait "Annual growth increments (cm/yr)" is a rate not a linear, I have changed that in "new.data.type".
- (RatesDB) paper p214, system s1647, the trait "Weight at 50% maturation probability (g) at age ..." is a cube(3D) not a linear, I have changed that in "new.data.type".
- (RatesDB) paper p216, the trait "Survival rate of ... year-olds" is a proportion not a rate, I have changed that in "new.data.type". The trait "Annual growth increments (cm)" is a rate not a linear, I have changed that in "new.data.type".
- (RatesDB) paper p008, system s107, the number of generations does not fit the elapsed time (years) and the generation time. I find the generation time source in paper p095 (Pergams and Ashley 2001). I added the generation note: "generation time from Pergams and Ashley 2001, Genetica 112-113: 245-256. published demographic data was used to estimate generation time for each species (4.4 generations per year for *Mus musculus*)". I replace the number of generations 70 with 308 ( $70 \text{ years} * 4.4 = 70/0.227$ )

- (RatesDB) papers p020 and p021, system s083, I added the following "gtime.notes":

*"From the paper (Carrol 1997): Generation time is about 40 d (measured in captivity at 30 °C). There is a large difference between the host species in the annual pattern of seed availability. In the introduced host, a much larger seed crop is available for a much briefer annual period, while in the native host, smaller seed crops are available year-round. There is time for two or three generations of bugs to develop on the introduced host, while more generations may develop in the Keys on the native host depending on how individual bugs move among sequential seed crops on different host individuals. We take the generation time on the new host (gorne 2022)".*

I fit the "generations" according to this generation time (0.4).

- (RatesDB) paper p055, es1006 and es1007 correspond to *Pararge aegeria* subsp. *aegeria* but es1008 and es1009 are about *Pararge aegeria* subsp. *tircis*. Both subsp have different generation times. I kept system s124 for subsp *aegeria* and I assigned a new system (s1844) for subspecies *tircis*. The generation time was expressed as number of generations in a year. I replaced that with the fraction of the year spanning one generation (i.e. 0.22 instead of 4.5). I also add in "gtime.notes" the information from the paper:

*"P. aegeria develops continuously on Madeira (four to five generations per year) but only develops through 1.5 generations per year in Yorkshire (Blakeley 1996). This would result in approximately 100 generations since colonization for subspecies aegeria (and possibly more if P. aegeria arrived on Madeira before 1976), but only 30 generations for tircis."*

Also, I removed the "pending\_issues" note (i.e. "Split system in two; one for each sub-species? See e.g. deer mice split into different sub-species").

- (RatesDB) paper p043, systems s074 and s075. The number of generations was corrected according to years and generation time (gtime).
- (RatesDB) paper p084, system s068. The time (years) was updated from 0.00003 to 30 (1958 to 1988). Also, I removed the "pending\_issues" comment (i.e. "Year is 0").
- (RatesDB) paper p003 (Armbruster and Conn 2006), system s002. Generations different from years/gtime. I think that gtime was expressed as the number of generations per

- year instead of as the fraction of the year. because the species is a mosquito, the generation time should be less than a year, no longer tha one year. I have replaced it.
- (RatesDB) paper p063, system s148. Generations different from years/gtime. From the paper (Kingsolver 2007): "The WA population has three to four complete generations per year, whereas the NC population has five to six generations per year". So, gtime=0.222. I added the gtime.note and I fixed the information in generations.
  - (RatesDB) paper p157, system s306. From the paper (Leaver 2012): "The source population has a 2-year generation time although Mayer Pond fish may have transitioned to a 1-year generation time by the year 2000". So, gtime=1.5. I updated gtime and generations, according to this information. Also, I added gtime.notes.
  - (RatesDB) paper p073, system s072. "new.trait.type"="length residuals" was replaced with "linear". The new variable "transf\_data" informs that it is not raw data but a difference with the expected value from a regression.
  - (RatesDB) papers p096 and p097, system s023. "new.trait.type"="length residuals" was replaced with "linear". The new variable "transf\_data" informs that it is not raw data but a difference with the expected value from a regression.
  - (RatesDB) paper p182, system s408. "new.trait.type"="length residuals" was replaced with "count" and "date". The new variable "transf\_data" informs that it is not raw data but a difference with the expected value from a regression.
  - (RatesDB) paper p101, system s155. "new.trait.type"="other" was replaced with "prop" because the traits were measured as proportional change. The new variable "transf\_data"="resid" informs that it is not raw data but a difference with a control treatment. As a consequence, the "data.scale"="interval" because there is not a true zero, it depends on the value of the control. Also I removed the "pending\_issues" comment (i.e. "Data scale not resolved").
  - (RatesDB) paper p033, system s048, form es3987 to es3996, "new.trait.type"="other" was replaced with "rate" because the trait is the growth rate. From es3997 to es4010, "new.trait.type"="other" was replaced with "linear" because the trait is the maximum size (mm).
  - (RatesDB) paper p076, system s052, form es4393 to es4408, the trait is a measurement of growth but it is not a rate is a count. So, I replaced "new.trait.type"="rate" with "count".

- (RatesDB) paper p044, system s173, es4439, the trait is a measurement of growth but it is not a rate is a count. So, I replaced "new.trait.type"="rate" with "count".
- (RatesDB) paper p044, system s173, es4443, SLA is not an area, because depends on the allometric relationship. Its dimensionality is -1 (area/mass = 2D/3D). So, I replaced "new.trait.type"="area (2D)" with "other". es4444 is not a proportion because is fresh mass over dry mass. It is the reciprocal of a proportion. I replaced "new.trait.type"="proportion" with "other".
- (RatesDB) paper p085, system s173, es4455, Rhizome mass over length is not a cube, because depends on the allometric relationship. Its dimensionality is 2 (mass/linear= 3D/1D). So, I replaced "new.trait.type"="cube (3D)" with "other".
- (RatesDB) paper p036, system s029, Stem length area ( $\text{cm}^2 \text{ g}^{-1}$ ) and Leaf area ratio (total leaf area / whole plant mass) are not areas, because depends on the allometric relationship. Their dimensionality is -1 (area/mass = 2D/3D). So, I replaced "new.trait.type"="area (2D)" with "other".
- (RatesDB) paper p078, system s007, the trait "First year herbivory rank" comes from an ordinal scale of 0–4, 4 being the greatest amount of herbivory. So, I replaced "new.trait.type"="other" with "index".
- (RatesDB) paper p146, system s283, "stomatal conductance" is a rate. I replaced "new.data.type"="other" with "rate".
- (RatesDB) paper p175, system s418, "standardized gonad mass [SGM = ( $10^3 \times \text{ovary mass [g]} / (\text{caudal length})^3$ )]" is a ratio, its dimensionality is 0. I replaced "new.data.type"="cube (3D)" with other.
- (RatesDB) paper p182, system s408, "average breeding values clutch size" is a genetic property but it is expressed as the number of eggs. I replaced "new.data.type"="other" with "count".
- (RatesDB) paper p193, system s428, "Fulton's Coefficient (body condition) (weight over length<sup>3</sup>)" is a ratio, dimensionality 0. I replaced "new.data.type"="index" with "other".
- (RatesDB) paper p195, system s431, "Fulton's Coefficient (body condition) (weight over length<sup>3</sup>)" is a ratio, dimensionality 0. I replaced "new.data.type"="linear" with "other".

- (RatesDB) paper p017, system s166, "Aborted spikes" is a trait related to fecundity, so it is a life history trait. I replaced "Kingsolver\_Diamond"="othermorphology" with "otherLH".
- (RatesDB) paper p017, system s166, "1000-grain weight" is a trait related to parental investment, so it is a life history trait. I replaced "Kingsolver\_Diamond"="size" with "otherLH".
- (RatesDB) paper p026, system s168, "Pappus volume" is a morphological trait. I replaced "Kingsolver\_Diamond"="otherLH" with "othermorphology".
- (RatesDB) paper p076, system s052, the measurements were performed on plants from the field, transplanted to a common garden for measurement purposes but it is still a case of "genphen"="Phenotypic" because the environment of development of the plants was different. I replaced "Genetic" with "Phenotypic" in the "genphen" variable.
- (RatesDB) paper p166, system s315, the traits: "Total number of seed heads", "Total weight of seed heads (buds)", "Total number of flower heads (buds)", "Total weight of flower heads", "Number of all capitula", "Weight of all capitula", "Proportion of biomass which is reproductive", "Proportion of reproductive biomass which is seed heads" are proxies of fecundity and reproductive allocation. So, these traits are "Kingsolver\_Diamond"="otherLH" not "othermorphology" or "phenology". I made the replacement.
- (RatesDB) paper p195, system s431, the trait "Condition Factor (Fulton's Index: mass over length<sup>3.2</sup>)" is not related to size because is the ratio between size (mass) and length<sup>3.2</sup>, so it is an allometric relationship. An individual can be very small with a high Fulton's index (a sphere) or big but with a small Fulton's index (very elongated shape). So I replaced "size" with "othermorphology".
- (RatesDB) System s151, papers p104, p105, p106, p037, p080, and p081. I unified the generation time as 0.575. This is from Reznick 1997. Also, I added the gtime.note: from Reznick 1997:

*"Guppies breed throughout the year and have overlapping generations. We estimated generation time  $T$  using the life table method, which is based on estimates of birth and death schedules in natural populations. We estimated mortality rates from mark-recapture experiments on guppies from seven low-predation localities, including the Aripo and El Cedro experimental sites. Because the life table method requires age-specific survival, we*



*estimated the ages of individuals in different size classes using growth rate equations derived for the same fish in the mark-recapture experiments based on their sizes at the beginning and end of the recapture interval. We estimated size-specific fecundity with dissections and embryo counts from females collected from these same localities, plus from additional collections. We estimated the frequency of reproduction from laboratory studies, conducted at temperatures and food availabilities similar to those in the field. With this information, we estimated the mean generation time of fish in low-predation localities to be 210 days, or 1.74 generations per year".*

So, gtime=0.575.

- (RatesDB) System s109, I updated the "gtime", "generations", and "gtime.notes" according:

*"Gtime according to The Marine Life Information Network  
(<https://www.marlin.ac.uk/species/detail/1501>): 2-5 years."*

- (RatesDB) System s135, paper p111, the species is "Passer montanus" not "Passer domesticus". I fixed this mistake.
- (RatesDB) Paper p173, system s322, the generation time assigned for males and females was different. I unified both according to the gtime in other similar systems, i.e. introduction of Passer domesticus from Europe to America (gtime=1).
- (RatesDB) Paper p027 (system s035) and paper p028 (system s034): the traits "centroid size=sqrt(sum((distances of each landmark to centroid)^2)))" is a "new.data.type"="linear". The dimensionality of the variable is 1, even when complex it is a sum of linear dimensions. I replaced "other" with "linear".
- (RatesDB) paper p003, system s002, the generation times are wrong, 4 to 5.5 years for a mosquito. I updated the "gtime" and "generations" according to the following information (added to "gtime.notes"):

*"According to Nur Aida et al 2008 (Trop Biomed 25(2): 117-125), the generation time is 20.14 days (0.055 years), but this is in the lab. It does not take into account the winter in USA. According to Waldock et al 2013 (Pathogens and Global Health 107(5): 224-241) in North America, a photoperiod of 13:11 (L:D) induces diapause in Ae. albopictus. I (gorne) computed the number generations in one year according to the*

number of days longer than 13 hours in one year. Then computed the generation time as the average of the gtime (reciprocal of the number of generations in one year) in both locations. i.e. Florida 5.38 G/y (113 days), Texas 5.81 G/y (122 days), New York 6.95 G/y (146 days)".

- (RatesDB) papers p087 and p088, system s119, the generation times are wrong, 2.5 years for a beetle. I updated the "gtime" and "generations" according to the following information (added to "gtime.notes"):

*"Under good conditions Onthophagus taurus display 2 generations each year (<https://www.ukbeetles.co.uk/onthophagus-taurus>). The adults are active from early spring to late autumn, they pair up in the spring. The development is rapid and under optimum conditions of nutrition and temperature the cycle from egg to adult takes eight to ten weeks, there are often two generations each year and in warmer climates this is the norm. Well fed and later instar larvae will overwinter in the brood chamber, continuing to feed in mild spells and producing very early spring adults. Those that eclose and emerge in the autumn will return to the burrow to overwinter."*

- (RatesDB) paper p051, system s183, es0978 to es0984 is a time series. I took the first time point (1923) and the last (1997) to compute the rate of change under the ID es0978. The time series (1923, 1930, 1951, 1964, 1967, 1981, 1991, 1997) was moved to TimeSeriesDB. The same situation with es0985 to es0987.
- (RatesDB) papers p087 and p088, system s119, traits "range of horn lengths within a sample (parameter a,  $\text{horn\_length} = y_0 + (a * \text{body\_size} / (c^b + \text{body\_size}^b))$ )" and "slope coefficient for the relationship between horn length and body size (parameter b,  $\text{horn\_length} = y_0 + (a * \text{body\_size} / (c^b + \text{body\_size}^b))$ )", have true Zeros (range=0; slope=0) so I consider as "data.scale"="ratio". Also, I removed the "pending\_issues" comment (i.e. "Data scale not resolved").
- (RatesDB) paper p061, system s043, trait "slope...", have true Zero (slope=0) so I consider as "data.scale"="ratio". Also, I removed the "pending\_issues" comment (i.e. "Data scale not resolved").
- (RatesDB) paper p160, system s309, the trait RW is "Relative Warps" is a measurement of the change in the morphometric matrix. It is linear but is a change relative to a reference, so, it has non true zero, so, it is a resid, "data.scale"="interval". I removed the "pending\_issues" comment.

- (RatesDB), in the variable "new.data.type" I added a new category. "ad\_ratio": a dimensionless ratio, that is not a proportion because the numerator is not a component or fraction of the denominator. Most of cases fitting this new category were previously classified as "other". Now I have added definitions of all the categories in the "new.data.type" variable, providing inclusion/exclusion criteria and examples. Also, I generated a definition for "index": ordinal variables and their derivations. So, all the traits previously classified as "index" but not fitting this definition were recategorized as "other" or the appropriate category.

- (RatesDB), in the variable "new.data.type" I added the following category (and reclassified the cases):

ad\_ratio: The ratio between two independent amounts with the same dimensionality is a dimensionless ratio. It is not a proportion because the numerator is not a component or fraction of the denominator. e.g. shoot:root ratio, C:N ratio, reproductive over vegetative biomass.

- (RatesDB), in the variable "new.data.type" I defined "index" and reclassified the cases accordingly:

index: ordinal variables and their derivations. So, even when a trait is called "index" in the primary source of information is not necessarily an index according to the current classification. For example, "index of ear size" ( $[EL \times EW]^{0.5}$ ) is a called index but it is quantitative variable proportional to the ear size, its dimensionality is 1. We classified this trait as "other". Another example is "Gonadosomatic index (ova mass over body mass)" this is a "proportion" even when called index.

- (RatesDB), all the definitions of the categories in "new.data.type" were updated, and some cases were recategorized accordingly. See metadata of the version #6 of the PROCEED database.
- (RatesDB), a new variable "trait\_type", derivated from "Kingsolver\_Diamond" was added. This new variable includes two categories not included in the original one ("growth" and "response"). All the categories (the new and the preexisting) were defined and some cases were recategorized according to the new definitions. See the metadata of the version #6 for more details.
- (RatesDB) In some cases "taxa\_fine" resolution is equal or broader than "taxa". So, I replaced the definition and categories in "taxa" with: "taxa" is a coarse classification,

not necessarily a clade (monophyletic group). Current categories are: Annelid, Mollusc, Arthropod, Fish, Amphibian, Mammal, Bird, Reptile, Plant.

I replaced taxa\_fine with the two following classifications:

class: taxonomic clade of rank "class" including the studied species, according to the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Root>) in May 2022.

order: taxonomic clade of rank "order" including the studied species, according to the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Root>) in May 2022.

- (RatesDB) in es4006 (p033, s048), the name of sample 2 was wrong. I replaced "Patnowskie (1973)" with "Patnowskie (1999)".
- (RatesDB) sample 1 must be, when possible, the ancestral population or the population from the ancestral place/source/condition. This condition was not always met in previous versions of the database. I checked all systems and I inverted the order of samples (names, coordinates, sample size, mean, and sd) for the following cases:

es_ID	ref_ID	sys_ID
es0649	p008	s107
es0650	p008	s107
es0651	p008	s107
es0886	p052	s183
es0887	p052	s183
es0889	p052	s183
es0890	p052	s183
es0892	p052	s183
es0893	p052	s183
es0895	p052	s183
es0896	p052	s183
es0898	p052	s183
es0899	p052	s183
es0901	p052	s183
es0902	p052	s183
es0904	p052	s183
es0905	p052	s183
es0907	p052	s183

es0908	p052	s183
es0910	p052	s183
es0911	p052	s183
es0913	p052	s183
es0914	p052	s183
es0916	p052	s183
es0917	p052	s183
es0919	p052	s183
es0920	p052	s183
es0922	p052	s183
es0923	p052	s183
es0925	p052	s183
es0926	p052	s183
es0928	p052	s183
es0929	p052	s183
es0931	p052	s183
es0932	p052	s183
es0934	p052	s183
es0935	p052	s183
es0937	p052	s183
es0938	p052	s183
es1136	p065	s117
es1137	p065	s117
es1138	p065	s117
es1139	p065	s117
es1140	p066	s117
es1141	p066	s117
es1142	p066	s117
es1143	p066	s117
es1144	p066	s117
es1145	p067	s117
es1146	p067	s117
es1147	p067	s117
es1148	p100	s117
es1149	p068	s117
es1150	p068	s117
es1151	p068	s117
es1153	p067	s117
es1154	p069	s117
es1155	p069	s117
es1156	p100	s117
es2531	p114	s066
es2532	p114	s066

es2537	p114	s066
es2538	p114	s066
es2543	p114	s066
es2544	p114	s066
es3417	p064	s117
es3418	p064	s117
es3489	p095	s107
es3490	p095	s107
es3491	p095	s107
es3492	p095	s107
es3493	p095	s158
es3494	p095	s158
es3495	p095	s158
es3496	p095	s158
es3497	p095	s158
es3498	p095	s158
es3499	p095	s158
es3500	p095	s158
es3501	p095	s158
es3502	p095	s158
es3507	p101	s155
es3508	p101	s155
es3509	p101	s155
es3510	p101	s155
es3511	p101	s155
es3512	p101	s155
es3513	p101	s155
es3514	p101	s155
es3515	p101	s155
es3516	p101	s155
es3517	p101	s155
es3518	p101	s155
es3519	p102	s085
es3520	p102	s085
es3521	p102	s085
es3522	p102	s085
es3523	p102	s085
es3524	p102	s085
es3575	p003	s002
es3576	p003	s002
es3577	p003	s002
es3581	p003	s002
es3582	p003	s002

es3583	p003	s002
es3587	p003	s002
es3588	p003	s002
es3589	p003	s002
es3602	p003	s002
es3603	p003	s002
es3604	p003	s002
es3608	p003	s002
es3609	p003	s002
es3610	p003	s002
es3614	p003	s002
es3615	p003	s002
es3616	p003	s002
es3629	p003	s002
es3630	p003	s002
es3631	p003	s002
es3635	p003	s002
es3636	p003	s002
es3637	p003	s002
es3641	p003	s002
es3642	p003	s002
es3643	p003	s002
es3656	p003	s002
es3657	p003	s002
es3658	p003	s002
es3662	p003	s002
es3663	p003	s002
es3664	p003	s002
es3668	p003	s002
es3669	p003	s002
es3670	p003	s002
es3683	p003	s002
es3684	p003	s002
es3685	p003	s002
es3689	p003	s002
es3690	p003	s002
es3691	p003	s002
es3695	p003	s002
es3696	p003	s002
es3697	p003	s002
es3710	p003	s002
es3711	p003	s002
es3712	p003	s002

es3716	p003	s002
es3717	p003	s002
es3718	p003	s002
es3722	p003	s002
es3723	p003	s002
es3724	p003	s002
es3737	p003	s002
es3738	p003	s002
es3739	p003	s002
es3743	p003	s002
es3744	p003	s002
es3745	p003	s002
es3749	p003	s002
es3750	p003	s002
es3751	p003	s002
es3764	p003	s002
es3765	p003	s002
es3766	p003	s002
es3770	p003	s002
es3771	p003	s002
es3772	p003	s002
es3776	p003	s002
es3777	p003	s002
es3778	p003	s002
es3791	p003	s002
es3792	p003	s002
es3793	p003	s002
es3797	p003	s002
es3798	p003	s002
es3799	p003	s002
es3803	p003	s002
es3804	p003	s002
es3805	p003	s002
es3818	p003	s002
es3819	p003	s002
es3820	p003	s002
es3824	p003	s002
es3825	p003	s002
es3826	p003	s002
es3830	p003	s002
es3831	p003	s002
es3832	p003	s002
es3845	p003	s002



es3846	p003	s002
es3847	p003	s002
es3851	p003	s002
es3852	p003	s002
es3853	p003	s002
es3857	p003	s002
es3858	p003	s002
es3859	p003	s002
es3872	p003	s002
es3873	p003	s002
es3874	p003	s002
es3878	p003	s002
es3879	p003	s002
es3880	p003	s002
es3884	p003	s002
es3885	p003	s002
es3886	p003	s002
es3977	p028	s034
es3978	p028	s034
es3979	p028	s034
es3980	p028	s034
es3981	p028	s034
es3982	p028	s034
es3983	p028	s034
es3984	p028	s034
es4192	p002	s004
es4193	p002	s005
es4194	p002	s012
es4195	p002	s045
es4196	p002	s058
es4206	p012	s101
es4207	p012	s101
es4208	p012	s101
es4209	p012	s101
es4235	p034	s174
es4236	p034	s174
es4237	p034	s174
es4238	p034	s174
es4309	p132	s099
es4310	p132	s099
es4311	p132	s099
es4312	p132	s1787
es4313	p132	s1787

es4314	p132	s1787
es4315	p060	s102
es4316	p060	s102
es4317	p060	s102
es4318	p060	s102
es4319	p060	s102
es4320	p060	s102
es4321	p060	s102
es4322	p060	s102
es4323	p060	s102
es4324	p060	s102
es4325	p060	s102
es4326	p060	s102
es4327	p060	s102
es4328	p060	s102
es4329	p060	s102
es4330	p060	s102
es4331	p060	s102
es4332	p060	s102
es4333	p060	s102
es4334	p060	s102
es4335	p060	s102
es4336	p060	s102
es4337	p060	s102
es4338	p060	s102
es4339	p060	s102
es4340	p060	s102
es4341	p060	s102
es4342	p060	s102
es4343	p060	s102
es4344	p060	s102
es4345	p060	s102
es4346	p060	s102
es4347	p060	s102
es4348	p060	s102
es4349	p060	s102
es4350	p060	s102
es4351	p060	s102
es4352	p060	s102
es4353	p060	s102
es4354	p060	s102
es4355	p060	s102
es4356	p060	s102

es4357	p060	s102
es4358	p060	s102
es4359	p060	s102
es4360	p060	s102
es4361	p060	s102
es4362	p060	s102
es4363	p060	s102
es4364	p060	s102
es4365	p060	s102
es4366	p060	s102
es4367	p060	s102
es4368	p060	s102
es4369	p060	s102
es4370	p060	s102
es4371	p060	s102
es4372	p060	s102
es4373	p060	s102
es4374	p060	s102
es4377	p076	s052
es4378	p076	s052
es4379	p076	s052
es4380	p076	s052
es4381	p076	s052
es4382	p076	s052
es4383	p076	s052
es4384	p076	s052
es4385	p076	s052
es4386	p076	s052
es4387	p076	s052
es4388	p076	s052
es4389	p076	s052
es4390	p076	s052
es4391	p076	s052
es4392	p076	s052
es4393	p076	s052
es4394	p076	s052
es4395	p076	s052
es4396	p076	s052
es4397	p076	s052
es4398	p076	s052
es4399	p076	s052
es4400	p076	s052
es4401	p076	s052

es4402	p076	s052
es4403	p076	s052
es4404	p076	s052
es4405	p076	s052
es4406	p076	s052
es4407	p076	s052
es4408	p076	s052
es4409	p076	s052
es4410	p076	s052
es4411	p076	s052
es4412	p076	s052
es4413	p076	s052
es4414	p076	s052
es4415	p076	s052
es4416	p076	s052
es4417	p076	s052
es4418	p076	s052
es4419	p076	s052
es4420	p076	s052
es4421	p076	s052
es4422	p076	s052
es4423	p076	s052
es4424	p076	s052
es4435	p044	s173
es4436	p044	s173
es4437	p044	s173
es4438	p044	s173
es4439	p044	s173
es4440	p044	s173
es4441	p044	s173
es4442	p044	s173
es4443	p044	s173
es4444	p044	s173
es4445	p044	s173
es4446	p044	s173
es4447	p044	s173
es4448	p044	s173
es4449	p044	s173
es4450	p044	s173
es4451	p044	s173
es4452	p044	s173
es4453	p044	s173
es4454	p085	s173

es4455	p085	s173
es4456	p085	s173
es4457	p085	s173
es4458	p085	s173
es4459	p085	s173
es4462	p075	s163
es4463	p036	s029
es4464	p036	s029
es4465	p036	s029
es4466	p036	s029
es4467	p036	s029
es4468	p036	s029
es4469	p036	s029
es4470	p036	s029
es4471	p036	s029
es4472	p036	s029
es4473	p036	s029
es4474	p036	s029
es4475	p036	s029
es4476	p036	s029
es4477	p036	s029
es4478	p036	s029
es4479	p036	s029
es4480	p036	s029
es4481	p036	s029
es4482	p036	s029
es4483	p036	s029
es4484	p036	s029
es4485	p036	s029
es4486	p036	s029
es4487	p036	s029
es4488	p036	s029
es4489	p036	s029
es4490	p036	s029
es4491	p036	s029
es4492	p036	s029
es4493	p036	s029
es4494	p036	s029
es4495	p036	s029
es4496	p131	s171
es4497	p131	s171
es4498	p131	s171
es4499	p131	s171

es4500	p131	s171
es4501	p131	s171
es4502	p131	s171
es4503	p131	s171
es4504	p131	s171
es4505	p131	s171
es4506	p131	s171
es4507	p131	s171
es4508	p131	s171
es4509	p131	s171
es4510	p131	s171
es4511	p131	s171
es4512	p131	s171
es4513	p131	s171
es4514	p078	s007
es4515	p078	s007
es4516	p078	s007
es4517	p078	s007
es4518	p078	s007
es4519	p078	s007
es4520	p078	s007
es4521	p078	s007
es4522	p078	s007
es4523	p078	s007
es4524	p078	s007
es4525	p078	s007
es4526	p078	s007
es4527	p078	s007
es4528	p078	s007
es4529	p078	s007
es4530	p078	s007
es4531	p078	s007
es4532	p078	s007
es4533	p078	s007
es4534	p078	s007
es4535	p078	s007
es4536	p078	s007
es4537	p078	s007
es4538	p078	s007
es4539	p078	s007
es4540	p078	s007
es4541	p078	s007
es4542	p078	s007

es4543	p078	s007
es4544	p078	s007
es4545	p078	s007
es4546	p078	s007
es4547	p078	s007
es4548	p078	s007
es4549	p078	s007
es4550	p078	s007
es4551	p078	s007
es4552	p078	s007
es4553	p078	s007
es4554	p078	s007
es4555	p078	s007
es4556	p078	s007
es4557	p078	s007
es4558	p078	s007
es4559	p078	s007
es4560	p078	s007
es4561	p078	s007
es4562	p078	s007
es4563	p078	s007
es4564	p078	s007
es4565	p078	s007
es4566	p078	s007
es4567	p078	s007
es4568	p078	s007
es4569	p078	s007
es4570	p078	s007
es4571	p078	s007
es4572	p078	s007
es4573	p078	s007
es4574	p078	s007
es4575	p078	s007
es4576	p078	s007
es5278	p161	s310
es5279	p161	s310
es5280	p161	s310
es5281	p161	s310
es5282	p161	s310
es5283	p161	s310
es5284	p161	s310
es5285	p161	s310
es5286	p161	s310

es5287	p161	s310
es5288	p161	s310
es5289	p161	s310
es5290	p161	s310
es5291	p161	s310
es5292	p161	s310
es5293	p161	s310
es5393	p170	s318
es5394	p170	s318
es5395	p170	s318
es5396	p170	s318
es5397	p170	s318
es5398	p170	s318

- (RatesDB) sample 1 must be, when possible, the ancestral population or the population from the ancestral place/source/condition. However, in some systems there is not ancestry relationship among populations. These are synchronic studies where the populations being compared are derived from a common ancestral population, but this ancestral population is not one of the population being compared. As a consequence I added a new variable "samp1\_anc" (yes/no) pointing out if sample 1 is (somehow) the ancestral population.
- (RatesDB) in paper p163, system s313, the traits "Carapace length" and "Principal Component 1 of Length and Width" were considered measurements of "size" (instead of "othermorphology").
- (RatesDB) the variable "outlier" was removed from the database.
- (RatesDB) data from paper p114, system s066 was wrong, all traits have the same values and none of these values meet the values in the paper. Additionally, there are more possible comparisons because there are two data sets for each population (two date). I replaced es2531 to es2548 with es9309 to es9368. This includes five trait, four populations, and the two datasets. Additionally, I fixed the elapsed time between comparisons, because it is not always 55 years.
- (RatesDB) due to the situation from the paper p114 (system s066) I check for similar situations throughout the whole database (i.e. means repeated for different traits, that may be due to an error in the data entry):

```
datos <- read.csv("RatesDB6.csv", na.string="")
```



```

#means repeated within a system
m1_s <- paste(datos$sys_ID, datos$mean1, sep=".")
m2_s <- paste(datos$sys_ID, datos$mean2, sep=".")

d1_m1_s <- duplicated(m1_s)
d2_m1_s <- duplicated(m1_s, fromLast=T)

dup_m1s <- (d1_m1_s+d2_m1_s)>0

d1_m2_s <- duplicated(m2_s)
d2_m2_s <- duplicated(m2_s, fromLast=T)

dup_m2s <- (d1_m2_s+d2_m2_s)>0

#means repeated within each system for the same trait
m1_t_sy <- paste(datos$trait_description, datos$mean1, datos$sys_ID, sep=".")
m2_t_sy <- paste(datos$trait_description, datos$mean2, datos$sys_ID, sep=".")

d1_m1ts <- duplicated(m1_t_sy)
d2_m1ts <- duplicated(m1_t_sy, fromLast=T)

dup_m1ts <- (d1_m1ts+d2_m1ts)>0

d1_m2ts <- duplicated(m2_t_sy)
d2_m2ts <- duplicated(m2_t_sy, fromLast=T)

dup_m2ts <- (d1_m2ts+d2_m2ts)>0

#difference between both
datos[dup_m1s!=dup_m1ts, c(1:3)]
datos[dup_m2s!=dup_m2ts, c(1:3)]

```

Several cases were found, but only two were due to mistakes. These were the paper p114 (system s066), previously mentioned, and the paper p033 (system s048). In this new case, the values for one trait had been duplicated in a second trait. I replaced the wrong values with the correct ones.

- (RatesDB) in paper p124, system s150, the trait “Predator escape speed ( $\text{cm s}^{-1}$ )” was recategorized as "Kingsolver\_Diamond"="behaviour" and "trait\_type"="behaviour".

- (RatesDB) the information in "landmark" was included into "coordinate.notes".
- (RatesDB) Because I have already checked and fixed all the problems due to duplicated systems (i.e. same system reported by more than one paper with more than one sys\_ID). I re check that flags and then, I removed "repeated\_systems".
- (RatesDB) in paper p028, system s034, the name of the samples was wrong, it was SC SC when it should be SC MO. I fixed that.
- (RatesDB) In system s035 there are three comparisons, one of them is exactly the same as in system s034. The other two include one of the populations compared in s034 plus a new one. So, I identified all as s035, and eliminated s034.
- (RatesDB) In system s059 there are several sampled pop along time, one of them is exactly the same as in system s060. The other are different populations in Europe. So, I identified all as s059, and eliminated s060.
- (TimeSeriesDB) For a given variable and case, there were some differences between TimeSeriesDB and RatesDB. So, I updated TimeSeriesDB with the information in the RatesDB for the following variables:

```

v      ref_ID
v      sys_ID
v      released_sys
v      released_es
v      reference
v      species
v      system
v      taxa
v      out_in
v      sex
v      genphen
v      trait_description
v      data.scale
v      gtime
v      date_year

```

- (TimeSeriesDB) I removed the following variables from the TimeSeriesDB:

```

X      old_disturbance
X      anthro_nat
X      design

```

```
X    data.type
X    sample1
X    sample2
X    years
X    generations
```

- (TimeSeriesDB) I added the following variables from the TimeSeriesDB:

```
o    uts_ID (unic time series identifier: i.e. an ID for each entry in
the TimeSeriesDB. format: from "uts_0000" to "uts_zzzz")
o    sp_ncbi
o    class
o    order
o    c_value
o    experimental
o    exp_type
o    new_disturbance
o    env_change
o    trait_type
o    new.data.type
o    transf_data
o    time_years (elapsed time in years form the beginning of the time
serie)
o    time_generations (elapsed time in generations form the beginning
of the time serie)
```

- (TimeSeriesDB) I produce a new version of the time series data base called  
"PROCEEDv6\_TimeSeriesDB.csv"

```
#####
#CODE FOR THE PREVIOUS ITEMS

setwd("/home/gorne/LUCAS/trabajo/ciencia/mis_proyectos/evol_rates_DB/
PROCEEDv6")
ratesDB <- read.csv("PROCEEDv6_RatesDB.csv", na.string="")

tser <- read.csv("PROCEEDv6_TimeSeriesDB.csv", na.string="")

#updating TimeSeriesDB with current information in RatesDB
tser$sp_ncbi <- NA
tser$c_value <- NA
tser$experimental <- NA
```

```

tser$exp_type <- NA
tser$new_disturbance <- NA
tser$env_change <- NA
tser$Kingsolver_Diamond <- NA
tser$new.data.type <- NA

i=1
for (i in 1:nrow(tser)){
  tser$ref_ID[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"ref_ID"]
  tser$sys_ID[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"sys_ID"]
  tser$released_sys[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"released_sys"]
  tser$released_es[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"released_es"]
  tser$reference[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"reference"]
  tser$species[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"species"]
  tser$system[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"system"]
  tser$taxa[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"taxa"]
  tser$out_in[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"out_in"]
  tser$sex[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"sex"]
  tser$genphen[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"genphen"]
  tser$trait_description[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"trait_description"]
  tser$data.scale[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"data.scale"]
  tser$gtime[i] <- ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"gtime"]
  tser$sp_ncbi[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"sp_ncbi"]
  tser$c_value[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"c_value"]
  tser$experimental[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"experimental"]
  tser$exp_type[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"exp_type"]
  tser$new_disturbance[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"new_disturbance"]
  tser$env_change[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"env_change"]
  tser$Kingsolver_Diamond[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"Kingsolver_Diamond"]

```

```

      tser$new.data.type[i] <-
ratesDB[which(tser$es_ID[i]==ratesDB$es_ID),"new.data.type"]
}

#Adding "time_years" and "time_generations" variables

starts <- which(!duplicated(tser$es_ID))

time_years <- vector(mode="numeric", length=nrow(tser))

i=1
for(i in 1:length(starts)){
  if(i<length(starts)){
    for(j in starts[i]:(starts[i+1]-1)){
      if(!is.na(tser$time_years[j])){
        time_years[j] <- tser$time_years[j]
        next}
      time_years[j] <- tser$date_year[j]-
tser$date_year[starts[i]]
    }
  }
  if(i==length(starts)){
    for(j in starts[i]:nrow(tser)){
      if(!is.na(tser$time_years[j])){
        time_years[j] <- tser$time_years[j]
        next}
      time_years[j] <- tser$date_year[j]-
tser$date_year[starts[i]]
    }
  }
}

time_generations <- time_years / tser$gtime
time_generations[which(!is.na(tser$time_generations))] <-
tser$time_generations[which(!is.na(tser$time_generations))]

#Adding "uts_ID"
digits <- c("0","1","2","3","4","5","6","7","8","9",
            "a","b","c","d","e","f","g","h","i","j","k","l",
            "m","n","o","p","q","r","s","t","u","v","w","x","y","z")
c1 <- 0

```

```

c2 <- 0
c3 <- 0
c4 <- 0

uts_ID_end <- "uts_zzzz"
uts_ID <- vector(mode="character", length=length(digits)^4)

i=1
repeat{
  i1 <- (as.integer((i-1)/length(digits)^3)+1)
  i2 <- (as.integer((i-1)/length(digits)^2)+1) -
length(digits)*as.integer((i-1)/length(digits)^3)
  i3 <- (as.integer((i-1)/length(digits)^1)+1) -
length(digits)*as.integer((i-1)/length(digits)^2)
  i4 <- (as.integer((i-1)/length(digits)^0)+1) -
length(digits)*as.integer((i-1)/length(digits)^1)

  c1 <- digits[i1]
  c2 <- digits[i2]
  c3 <- digits[i3]
  c4 <- digits[i4]

  uts_ID[i] <- paste("uts_",c1,c2,c3,c4, sep="")
if(uts_ID[i]==uts_ID_end) {break}
if(i==nrow(tser)) {break}
i=i+1
}

#choosing and sorting variables in the new TimeSeriesDB

new_tser <- data.frame(uts_ID=uts_ID[1:nrow(tser)],
  es_ID=tser$es_ID,
  ref_ID=tser$ref_ID,
  sys_ID=tser$sys_ID,
  released_sys=tser$released_sys,
  released_es=tser$released_es,
  reference=tser$reference,
  taxa=tser$taxa,
  species=tser$species,
  sp_ncbi=tser$sp_ncbi,
  sex=tser$sex,
  c_value=tser$c_value,

```

```

        system=tser$system,
        genphen=tser$genphen,
        out_in=tser$out_in,
        new_disturbance=tser$new_disturbance,
        env_change=tser$env_change,
        experimental=tser$experimental,
        exp_type=tser$exp_type,
        trait_description=tser$trait_description,
        new.data.type=tser$new.data.type,
        data.scale=tser$data.scale,
        Kingsolver_Diamond=tser$Kingsolver_Diamond,
        gtime=tser$gtime,
        date_year=tser$date_year,
        time_years=time_years,
        time_generations=time_generations,
        n=tser$n,
        mean=tser$mean,
        sd=tser$sd,
        obs=tser$obs
    )

write.csv(new_tser, "PROCEED TimeSeriesDB v01.csv", na="")
#####

```

- (RatesDB) in systems s311, s312, and s317 (from papers p162 and p169) I added gtime.notes with the source of information for the gtime, i.e.: from Reznick 1997:

*"Guppies breed throughout the year and have overlapping generations. We estimated generation time  $T$  using the life table method, which is based on estimates of birth and death schedules in natural populations. We estimated mortality rates from mark-recapture experiments on guppies from seven low-predation localities, including the Aripo and El Cedro experimental sites. Because the life table method requires age-specific survival, we estimated the ages of individuals in different size classes using growth rate equations derived for the same fish in the mark-recapture experiments based on their sizes at the beginning and end of the recapture interval. We estimated size-specific fecundity with dissections and embryo counts from females collected from these same localities, plus from additional collections. We estimated the frequency of reproduction from laboratory studies, conducted at temperatures and food availabilities similar to those in the field. With this*

*information, we estimated the mean generation time of fish in low-predation localities to be 210 days, or 1.74 generations per year".*

- (RatesDB) in the system s308 (from paper p159) I added gtime.notes with the source of information for the gtime, i.e.:

*"in the paper, authors assume three generations per year".*

- (RatesDB) in paper p185, system s070, the elapsed time ("years") was wrong (24), it is 23 (2015-1992), I fixed this. I modified the gtime according the information in the correspondence and I added mor information to gtime.notes:

*"According correspondence with Baker (2019) gtime is variable. file: "Jbaker correspondence5d.pdf" shows a table of gtimes for this lake during this period. The gtime average for whole period (1986-2015) is 1.3976. The average for the specific timeframe (1992-2015) is 1.296. The correspondence with Aguirre (2012) agrees that the gtime is between 1 and 2 years (0.5 to 1 generations a year)".*

- (RatesDB) in paper p167, system s070, the gtime was wrong. I fixed it and I added the information in gtime.notes:

*"According correspondence with Baker (2019) gtime is variable. file: "Jbaker correspondence5d.pdf" shows a table of gtimes for this lake during this period. The gtime average for whole period (1986-2015) is 1.3976. The average for the specific timeframe (1990-2009) is 1.333. The correspondence with Aguirre (2012) agrees that the gtime is between 1 and 2 years (0.5 to 1 generations a year)".*

- (RatesDB) in paper p006, system s070, the gtime was wrong. I fixed it and I added the information in gtime.notes:

*"According correspondence with Baker (2019) gtime is variable. file: "Jbaker correspondence5d.pdf" shows a table of gtimes for this lake during this period. The gtime average for whole period (1986-2015) is 1.3976. The average for the specific timeframe (1992-2001 or 1990-2001) is 1.5 or 1.57. The correspondence with Aguirre (2012) agrees that the gtime is between 1 and 2 years (0.5 to 1 generations a year)".*

- (RatesDB) in paper p001, system s070, the gtime was wrong. I fixed it and I added the information in gtime.notes:



*"According correspondence with Baker (2019) gtime is variable. file: "Jbaker correspondence5d.pdf" shows a table of gtimes for this lake during this period. The gtime average for whole period (1986-2015) is 1.3976. The average for the specific timeframe (1991-2006 or 1990-2006) is 1.304 or 1.333. The correspondence with Aguirre (2012) agrees that the gtime is between 1 and 2 years (0.5 to 1 generations a year)"*

- (RatesDB) in paper p151, system s289, the number of generations (and gtime) was provided by the authors. I added this to the gtime.notes.
- (RatesDB) in paper p073, system s072, The authors assumed that the elapsed time (12 years) correspond with 12 generations. So, generation time is 1 year. I added this to the gtime.notes.
- (RatesDB) in paper p072, system s071, The authors assumed that the generation time is 1 year. I added this to the gtime.notes.
- (RatesDB) in paper p158, system s307, years and number of generations provided by in the paper. I added this to the gtime.notes.
- (RatesDB) in paper p160, system s309, years and number of generations provided by in the paper. I added this to the gtime.notes.
- (RatesDB) in paper p164, systems s307 and s309, generation time for the same system estimated as 1 year by previous papers (Divino 2016 and Wund 2016). I added this to the gtime.notes.
- (RatesDB) The exp\_type=13 is artificial selection or too close. So, I removed the paper p222, system s1679 from the database. Also, I removed this category from exp\_type factor.
- (RatesDB) (TimeSeriesDB) I added Phylum taxonomic information according to NCBI database (<https://www.ncbi.nlm.nih.gov/taxonomy>).
- (RatesDB) paper p144 (formerly Meiri 2008). The year of the citation was wrong, it is 2009. So, I replaced Meiri 2008 with Meiri 2009. Additionally, the author (Shai Meiri) granted us permission to make the data freely available. So, I removed the comment about not making it publicly available and I added the correspondence to the workspace folder in Dropbox.