

A computational approach to biodiversity change

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DEPARTMENT *of* ENVIRONMENTAL
SCIENCE, POLICY, AND MANAGEMENT

Vertebrates on the brink as indicators of biological annihilation and the sixth mass extinction

Gerardo Ceballos^{a,1} , Paul R. Ehrlich^b , and Peter H. Raven^c

“Biodiversity Crisis”

Accelerated modern human-induced species losses: Entering the sixth mass extinction

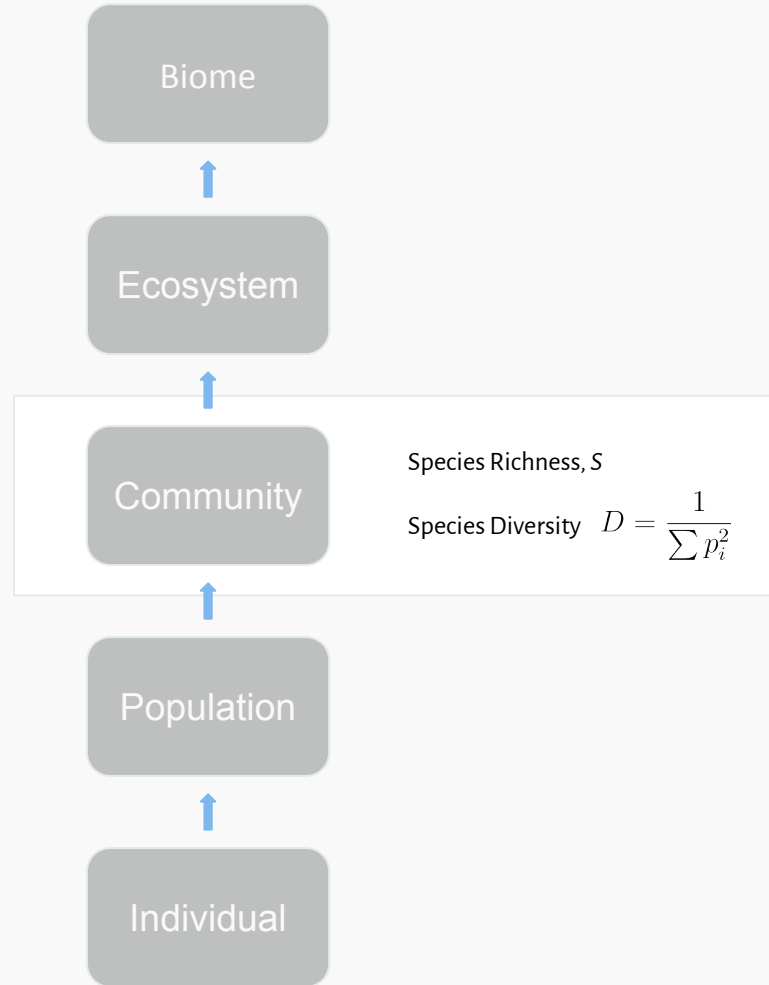
Gerardo Ceballos,^{1*} Paul R. Ehrlich,² Anthony D. Barnosky,³ Andrés García,⁴ Robert M. Pringle,⁵ Todd M. Palmer⁶

Biological annihilation via the ongoing sixth mass extinction signaled by vertebrate population losses and declines

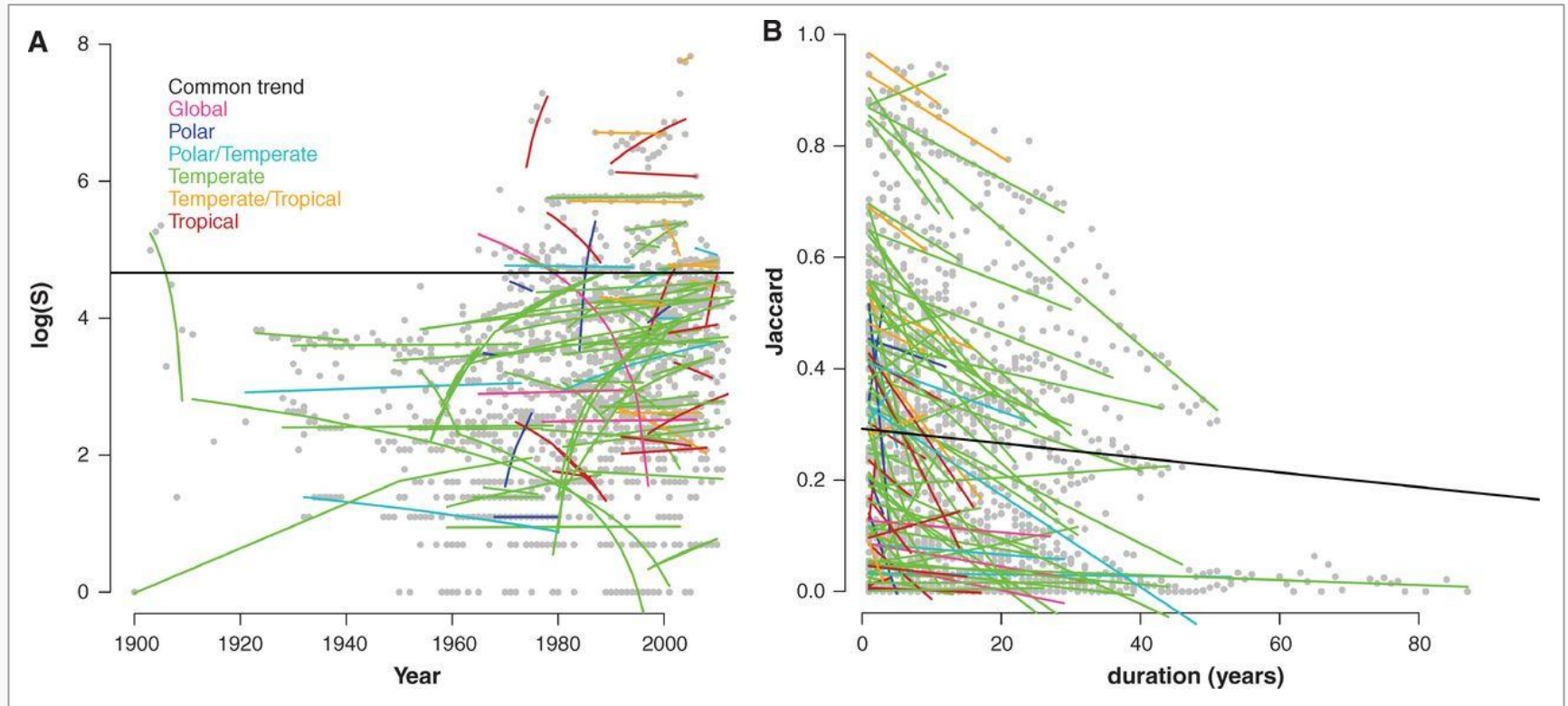
Gerardo Ceballos^{a,1}, Paul R. Ehrlich^{b,1}, and Rodolfo Dirzo^b







Do species-based metrics capture change?



Functional diversity as lens for biodiversity change

*“morpho-physio phenological traits which impact fitness indirectly via their effects on growth, reproduction and survival”
(Violle 2007)*



Does a functional approach
detect change beyond
species-based metrics?

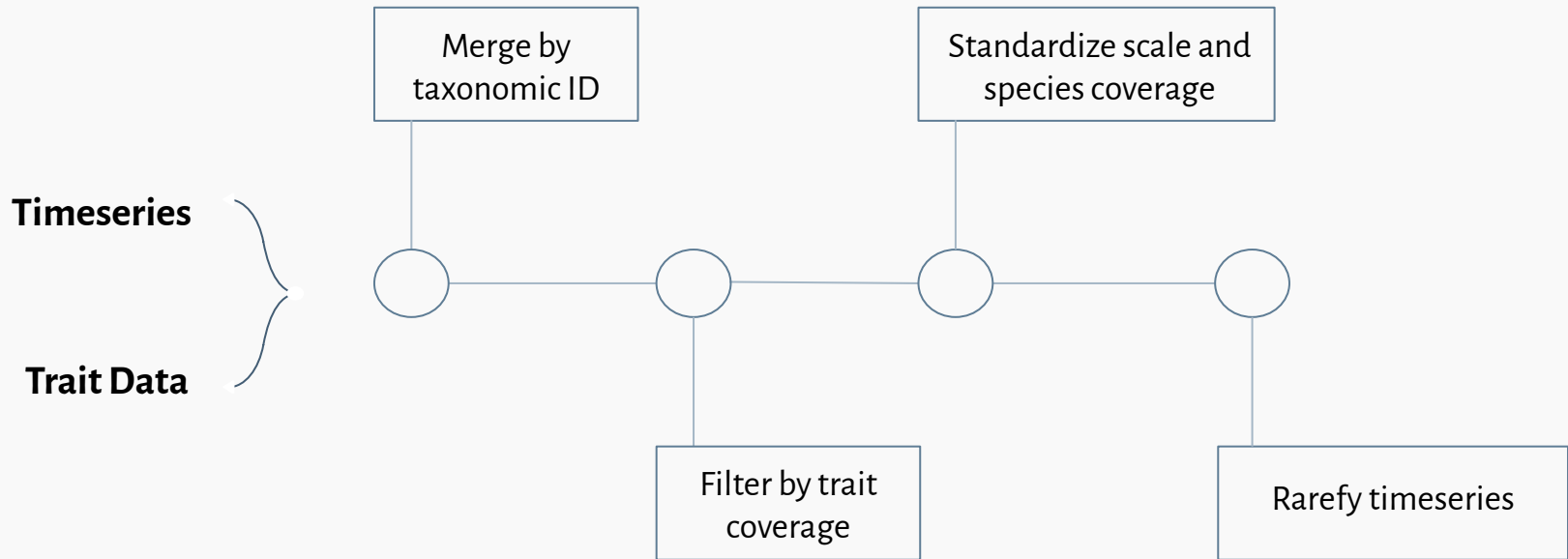
Bridging species and functional trait data

Assemblage timeseries

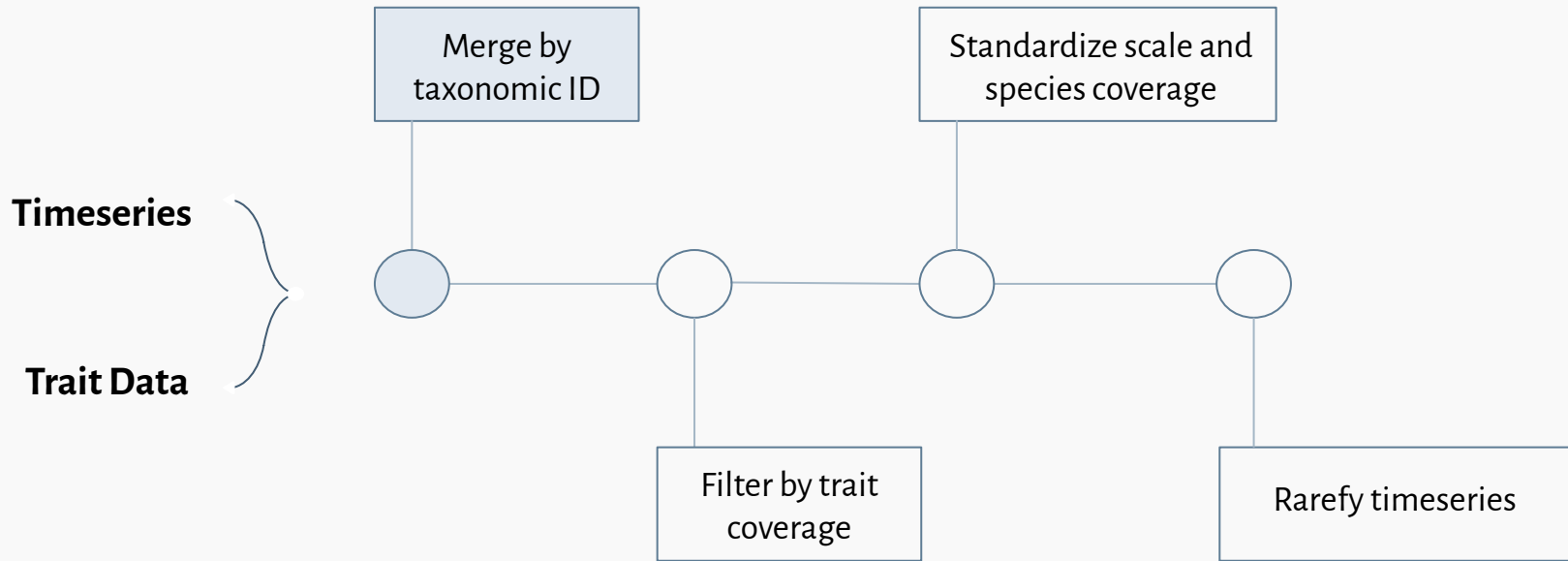


Functional trait databases

- Amphibio (amphibians)
- Elton Traits (mammals, birds)
- Bien (plants)
- Fishbase (fish)
- Fishtraits (fish)
- Marine Traits (fish)



Data
processing
pipeline



-
- Get taxonomic ID's for all species via taxadb
 - Resolve species with more than one accepted ID

**Data
processing
pipeline**

Taxadb: A high-performance local taxonomic database interface

- Taxonomic inconsistencies (synonyms, splits, etc) can lead to significant mismatches in synthesis work (some hidden, some obvious)
- Previous API approaches for interfacing with taxonomic data are not tractable for large datasets

IUCN Name	Category
<i>Pipile pipile</i>	CR
<i>Pipile cumanensis</i>	LC
<i>Pipile cujubi</i>	LC
<i>Pipile jacutinga</i>	EN
<i>Megapodius decollatus</i>	LC
<i>Scleroptila gutturalis</i>	LC
<i>Margaroperdix madagarensis</i>	LC
<i>Falciennis falciennis</i>	NT

Table 1: IUCN database example

Elton Name	Mass
<i>Aburria pipile</i>	1,816.59
<i>Aburria cumanensis</i>	1,239.22
<i>Aburria cujubi</i>	1,195.82
<i>Aburria jacutinga</i>	1,240.96
<i>Megapodius reinwardt</i>	666.34
<i>Francolinus levalliantoides</i>	376.69
<i>Margaroperdix madagascariensis</i>	245.00
<i>Catreus wallichii</i>	1,436.88
<i>Falciennis falciennis</i>	685.61
<i>Falciennis canadensis</i>	473.65

Table 2: Elton trait database example

IUCN Name	Category
<i>Pipile pipile</i>	CR
<i>Pipile cumanensis</i>	LC
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Table 2: Elton trait database example



Elton Name	Mass	Category
<i>Aburria pipile</i>	1,816.59	—
<i>Aburria cumanensis</i>	1,239.22	—
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<i>Aburria jacutinga</i>	1,240.96	—
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<i>Francolinus levalliantoides</i>	376.69	—
<i>Margaroperdix madagascariensis</i>	245.00	—
<i>Catreus wallichii</i>	1,436.88	—
<i>Falciennis falciennis</i>	685.61	NT
<i>Falciennis canadensis</i>	473.65	—
<i>Pipile pipile</i>	—	CR
<i>Pipile cumanensis</i>	—	LC
<i>Pipile cujubi</i>	—	LC
<i>Pipile jacutinga</i>	—	EN
<i>Megapodius decollatus</i>	—	LC
<i>Scleroptila gutturalis</i>	—	LC
<i>Margaroperdix madagarensis</i>	—	LC

Table 3: Merge by species names

IUCN Name	Category
<i>Pipile pipile</i>	CR
<i>Pipile cumanensis</i>	LC
<i>Pipile cujubi</i>	LC
<i>Pipile jacutinga</i>	EN
<i>Megapodius decollatus</i>	LC
<i>Scleroptila gutturalis</i>	LC
<i>Margaroperdix madagarensis</i>	LC
<i>Falciennis falciennis</i>	NT

Table 1: IUCN database example

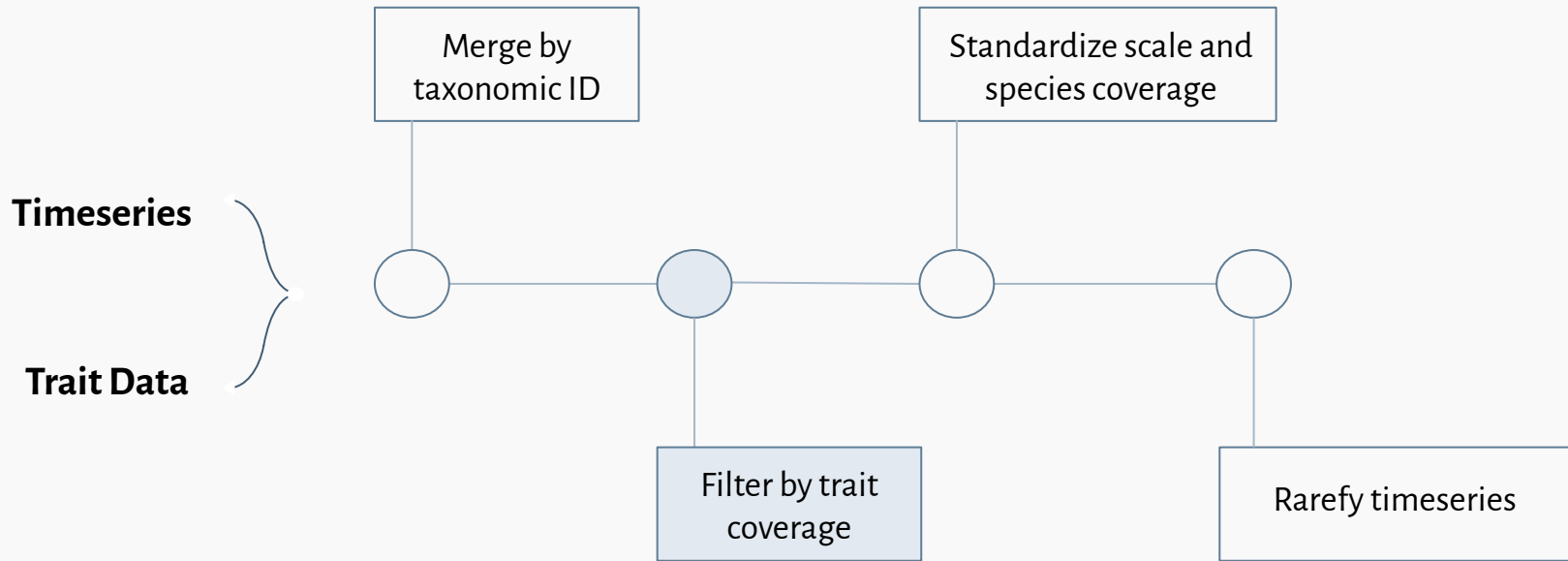
Elton Name	Mass
<i>Aburria pipile</i>	1,816.59
<i>Aburria cumanensis</i>	1,239.22
<i>Aburria cujubi</i>	1,195.82
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Table 2: Elton trait database example



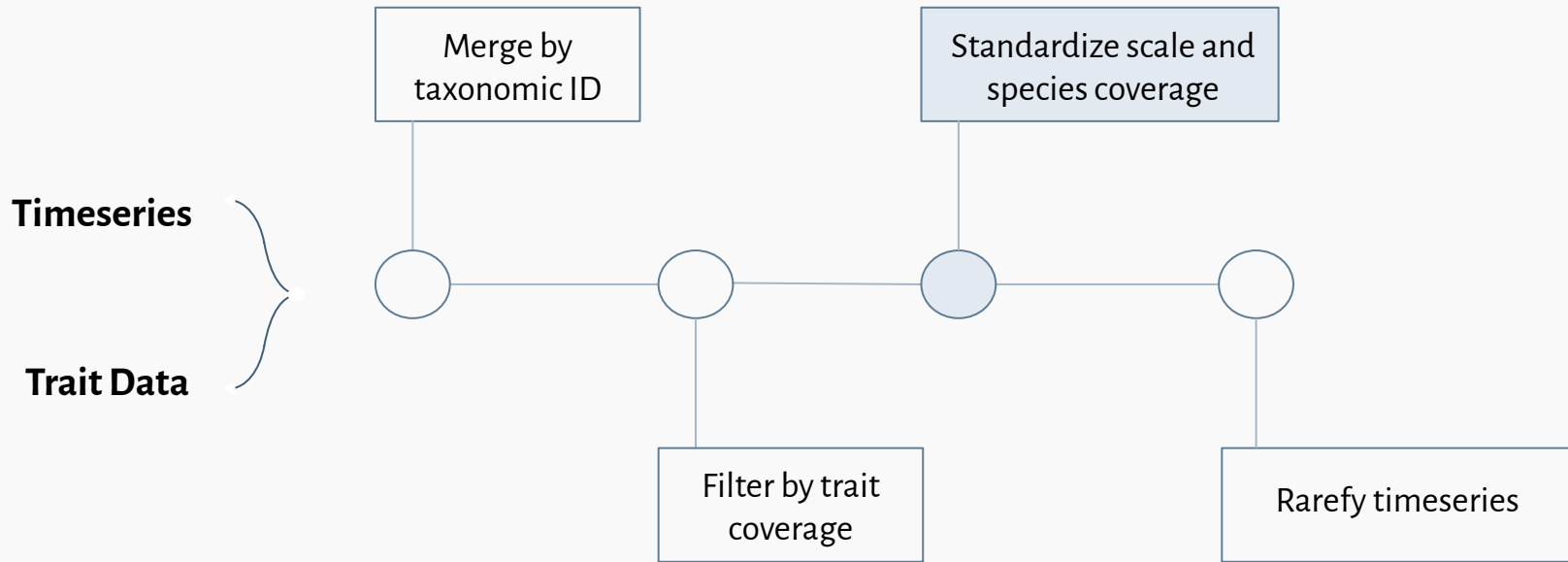
Elton Name	IUCN Name	Mass	Category	id
<i>Aburria pipile</i>	<i>Pipile pipile</i>	1,816.59	CR	COL:35517887
<i>Aburria cumanensis</i>	<i>Pipile cumanensis</i>	1,239.22	LC	COL:35537158
<i>Aburria cujubi</i>	<i>Pipile cujubi</i>	1,195.82	LC	COL:35537159
<i>Aburria jacutinga</i>	<i>Pipile jacutinga</i>	1,240.96	EN	COL:35517886
<i>Megapodius reinwardt</i>	–	666.34	–	COL:35521309
<i>Francolinus levalliantoides</i>	–	376.69	–	COL:35518087
<i>Margaroperdix madagascariensis</i>	<i>Margaroperdix madagarensis</i>	245.00	LC	COL:35521355
<i>Catreus wallichii</i>	–	1,436.88	–	COL:35518185
<i>Falciennis falciennis</i>	<i>Falciennis falciennis</i>	685.61	NT	COL:35521380
<i>Falciennis canadensis</i>	–	473.65	–	COL:35521381
–	<i>Megapodius decollatus</i>	–	LC	COL:35537166
–	<i>Scleroptila gutturalis</i>	–	LC	–

Table 3: Merge by species ID's



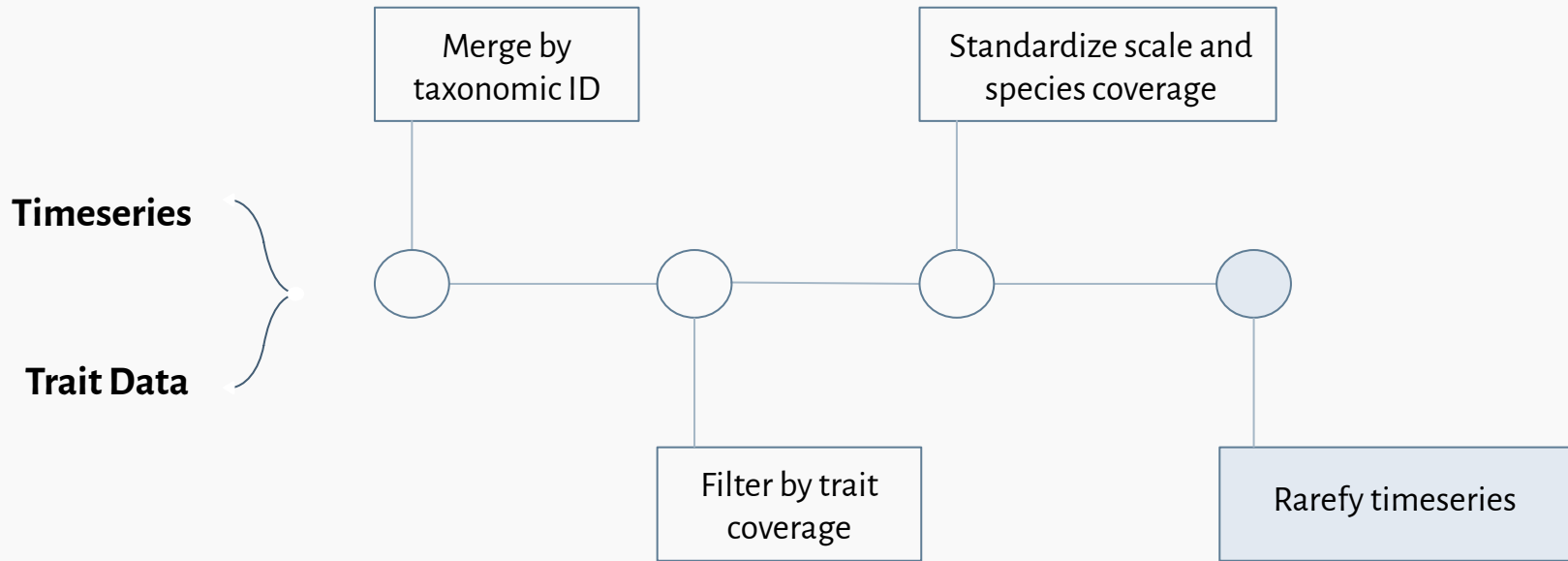
-
- Remove timeseries with < 85% trait coverage

**Data
processing
pipeline**



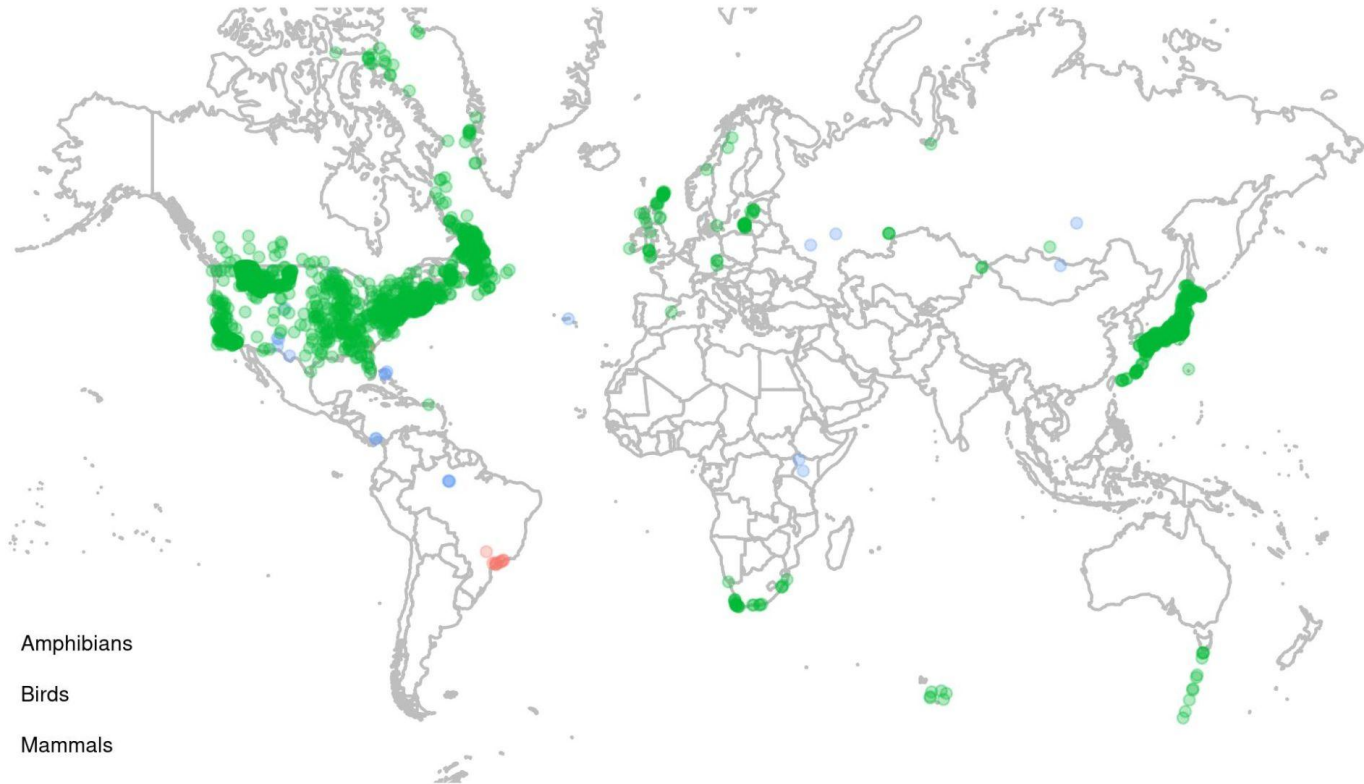
-
- Define an individual timeseries based on grid cell
 - Cell size defined by (mean + sd) of the extent of single location studies, ~74 sq km

Data processing pipeline



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- Account for inconsistent sampling within years by bootstrap resampling the minimum number of samples in a year for each timeseries.

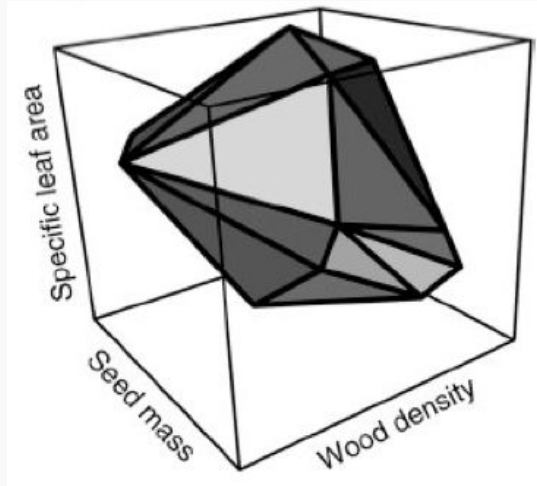
**Data
processing
pipeline**



53 studies and 2443 individual timeseries.

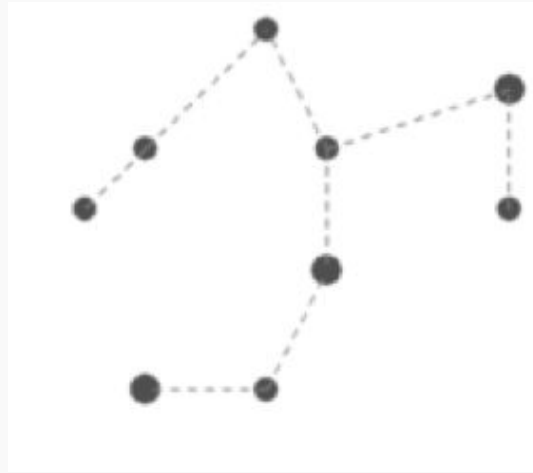
Functional Diversity Metrics

Richness



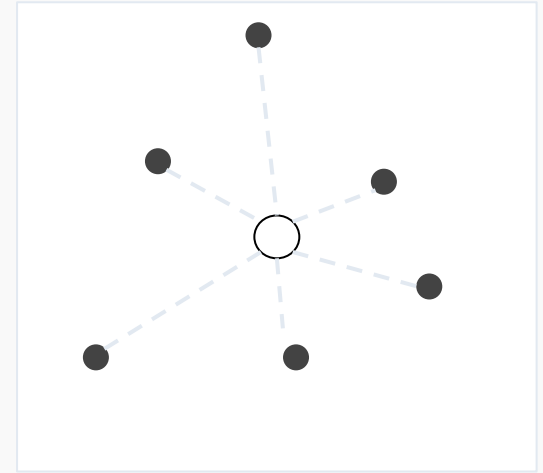
FRic

Evenness

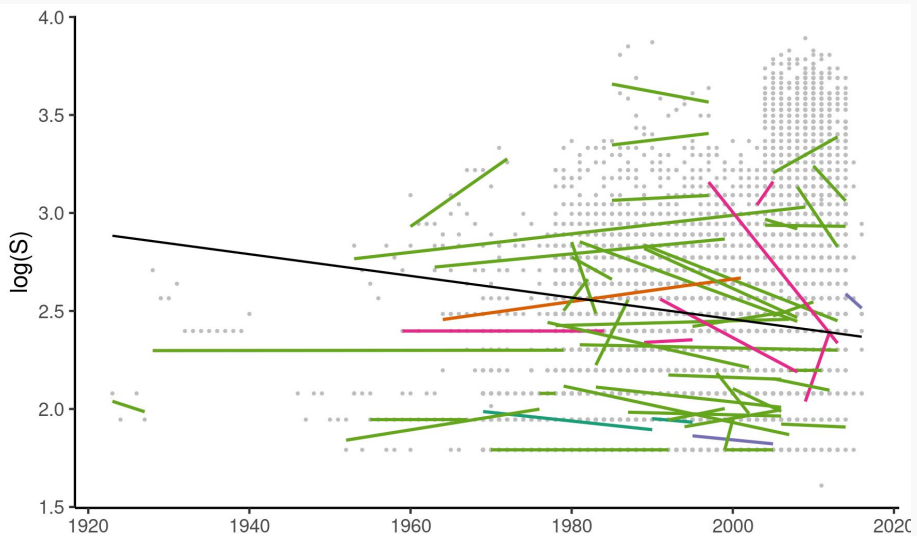


FEve

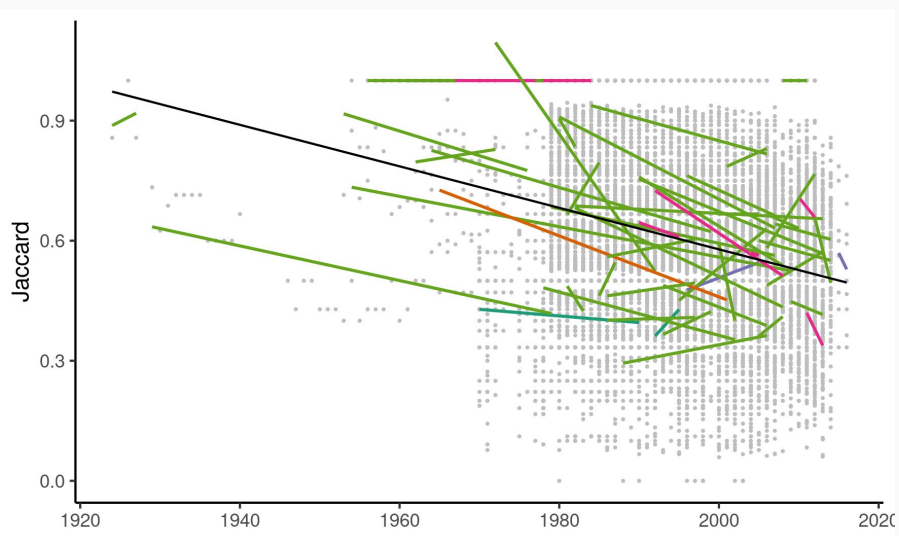
Divergence



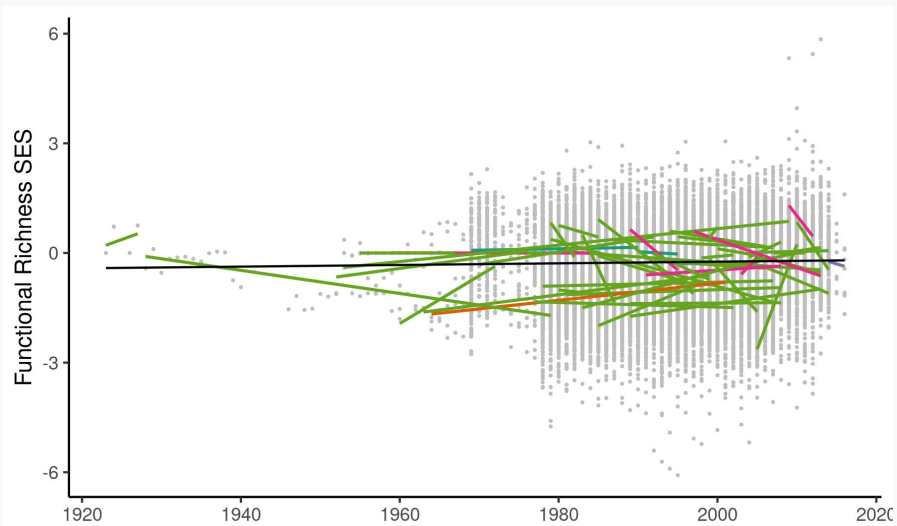
FDiv



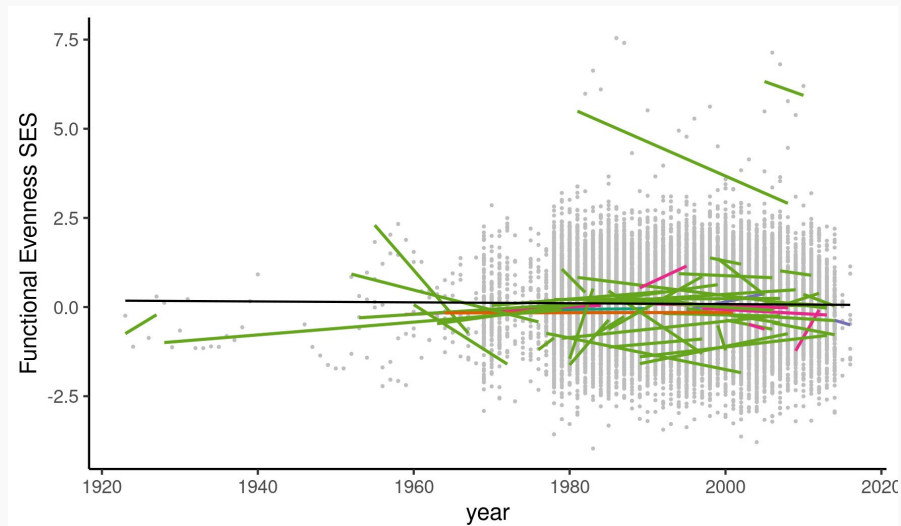
Non significant
(slope: -0.06, p-value = 0.16)



Significantly decreasing
(slope: -0.05, p-value = ~0)



Non significant
(slope: 0.02, p-value = 0.54)



Non significant
(slope: -0.01, p-value = 0.65)

Conclusions

While some communities are experiencing significant functional losses, others are experiencing significant gains.

Is the lack of trend due data limitations, or a true reflection of the ecology?

Are there general rules that predict scenarios in which functional loss accompanies particular species level shifts?

Acknowledgements



Advisor: Dr Carl Boettiger



Dr Perry de Valpine



Dr Benjamin Blonder



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