



Ecological challenges and opportunities

Pablo A. Marquet

Tara workshop, Valparaíso, May 15-18, 2023

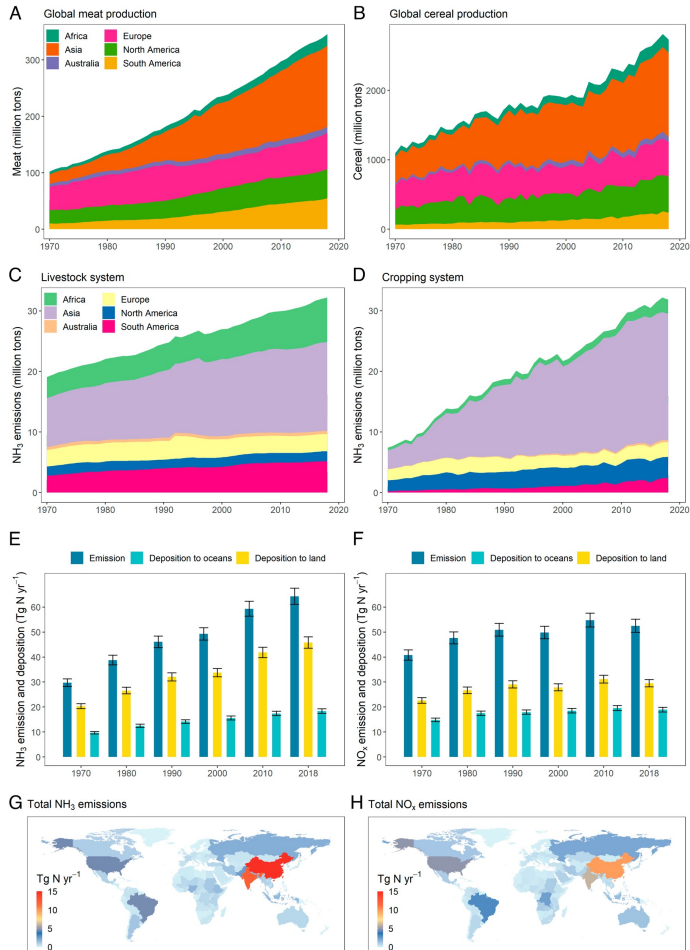
The most salient feature of life has been the stability of its bacterial mode from the beginning of the fossil record until today and, with little doubt, into all future time so long as the earth endures. This is truly the “age of bacteria”—as it was in the beginning is now and ever shall be.

Stephen Jay Gould (1994)

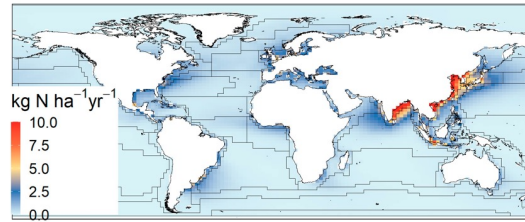
Border conditions.....

Nitrogen coming from the sky!!!

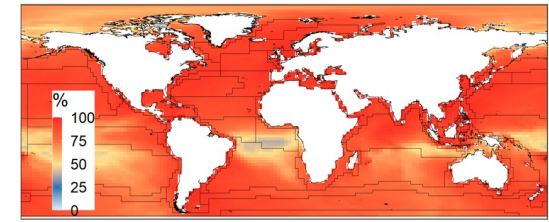
Ocean Nitrogen deposition



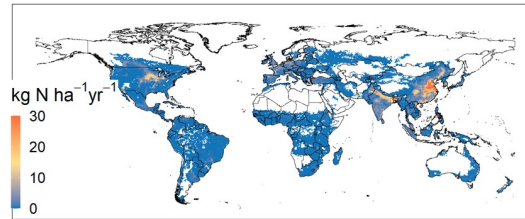
A Diff. in NH_x deposition by food production



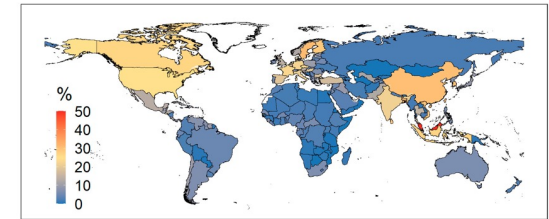
B Changes in NH_x deposition (%) by food production



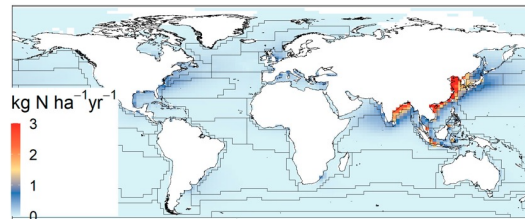
C NH_3 emissions by N fertilizer overuse



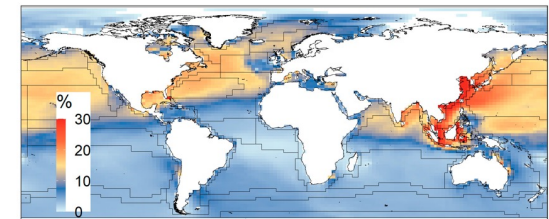
D Contribution of overused N fertilizer to NH_3 emission



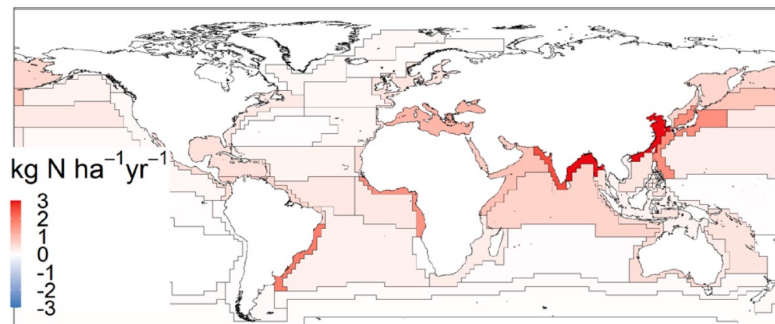
E Diff. in NH_x deposition by overused N fertilizer



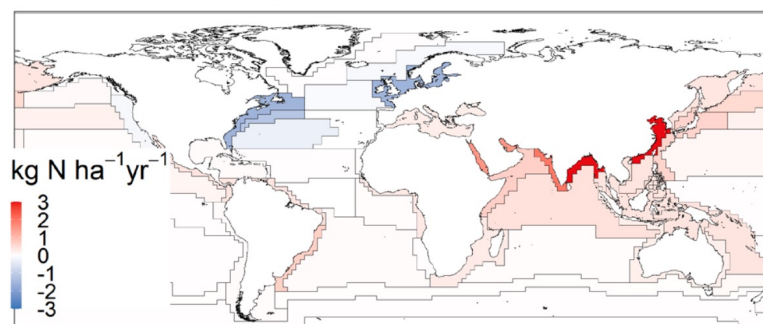
F Changes in NH_x deposition (%) by overused N fertilizer



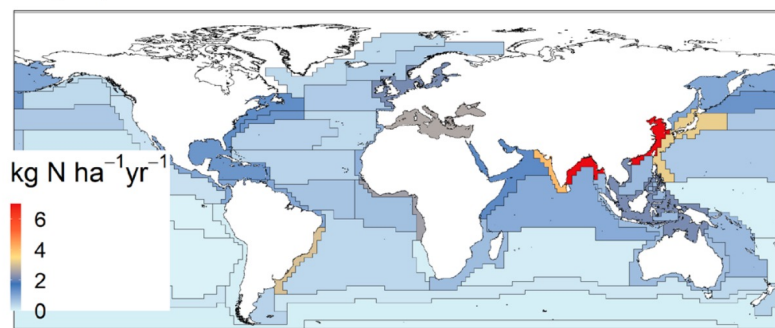
A Difference in total NH_x deposition between 1970-2018



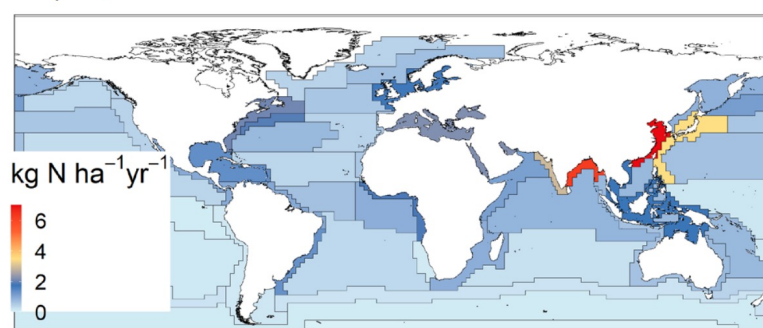
B Difference in total NO_y deposition between 1970-2018



C NH_x deposition in 2018



D NO_y deposition in 2018



PNAS

RESEARCH ARTICLE

SUSTAINABILITY SCIENCE



Modeling global oceanic nitrogen deposition from food systems and its mitigation potential by reducing overuse of fertilizers

Lei Liu^{a,1}, Wen Xu^b, Zhang Wen^c, Pu Liu^d, Hang Xu^e, Sheng Liu^f, Xiankai Lu^g, Buqing Zhong^h, Yixin Guoⁱ, Xiao Lu^g, Yuanhong Zhao^j, Xiuying Zhang^k, Songhan Wang^l, Peter M. Vitousek^m, and Xuejun Liu^{b,1}

Edited by Stephen Carpenter, University of Wisconsin-Madison, Madison, WI; received January 9, 2023; accepted March 6, 2023

The Nitrogen cycle works different in polluted areas!!!

nature

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[Published: 24 January 2002](#)






Nitrogen loss from unpolluted South American forests mainly via dissolved organic compounds

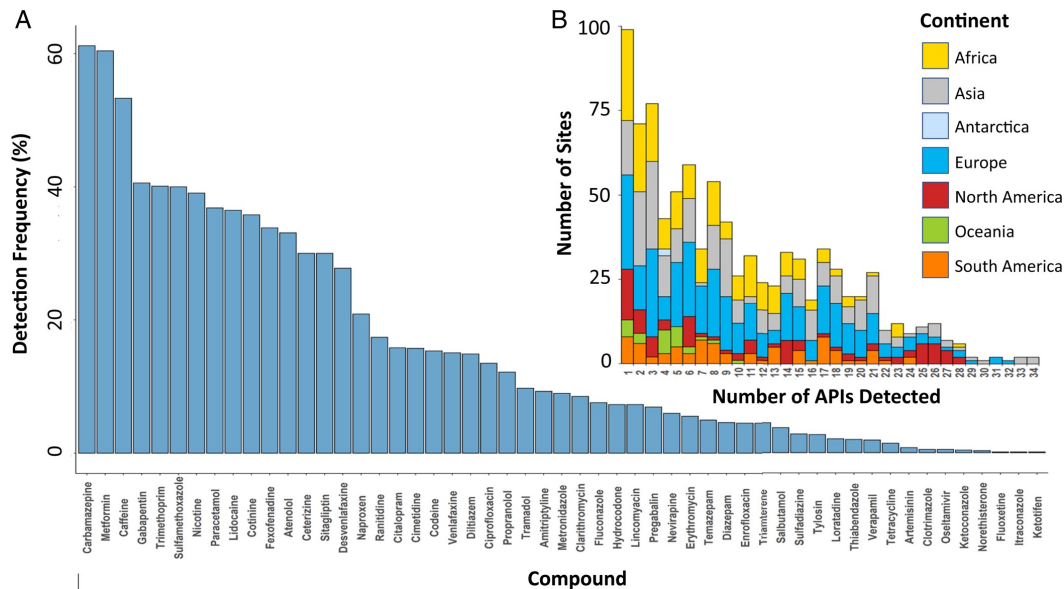
[Steven S. Perakis](#)  & [Lars O. Hedin](#)

S@\$%... coming from rivers



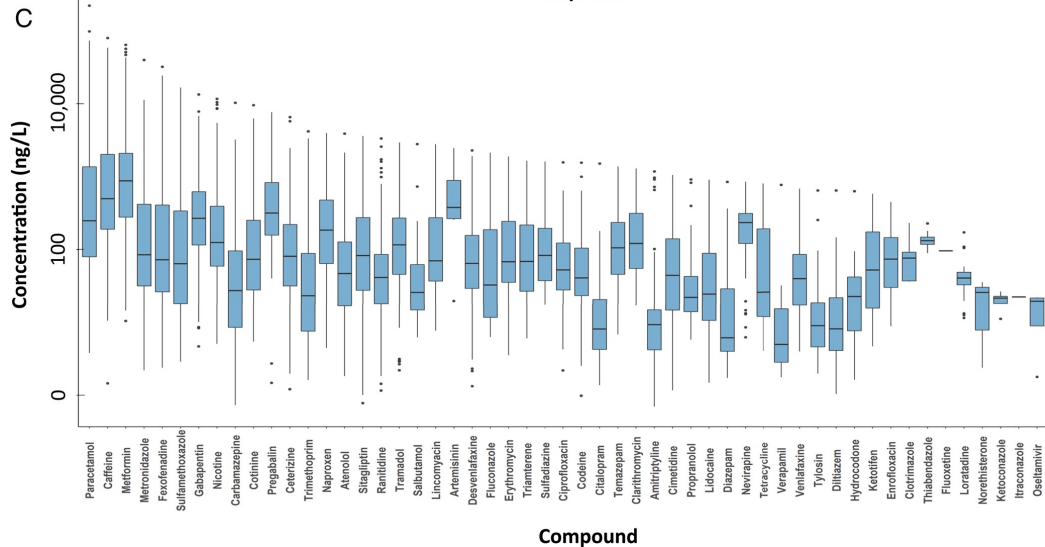
Pharmaceutical pollution of the world's rivers

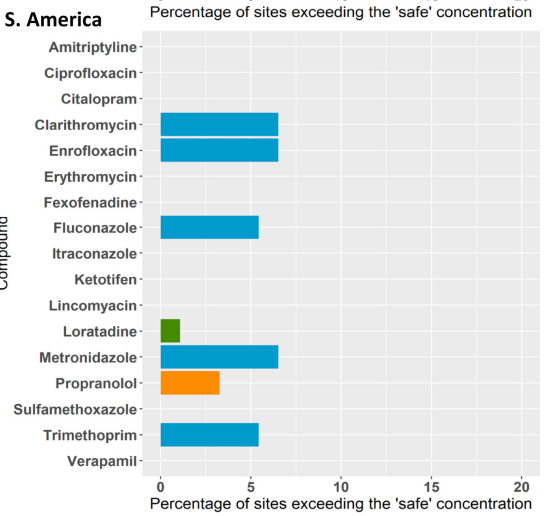
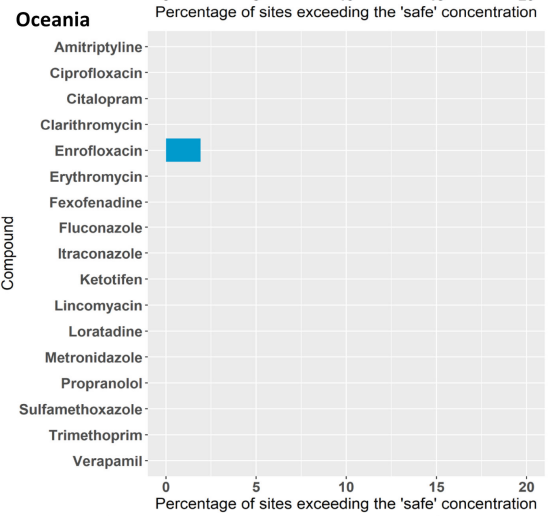
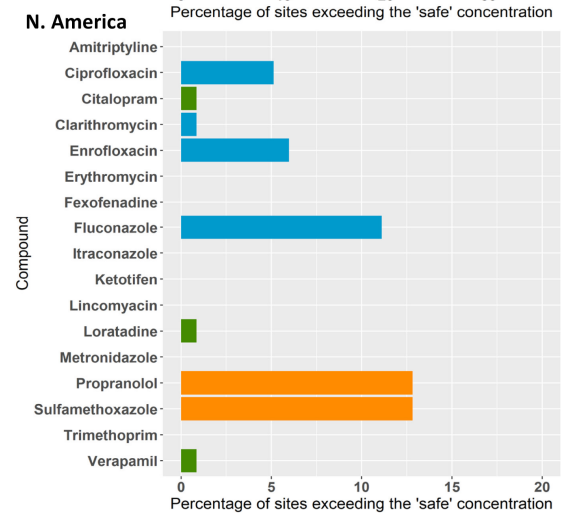
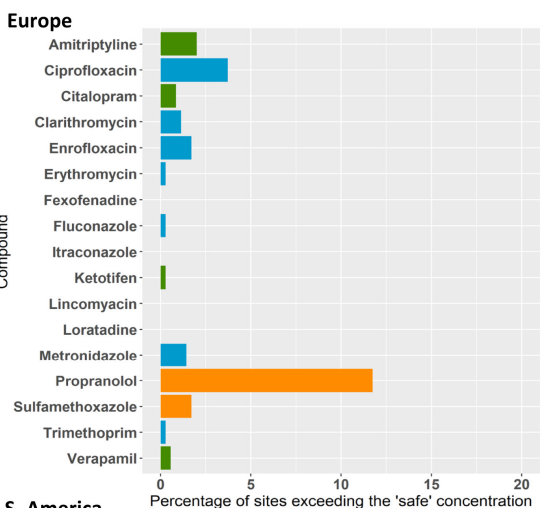
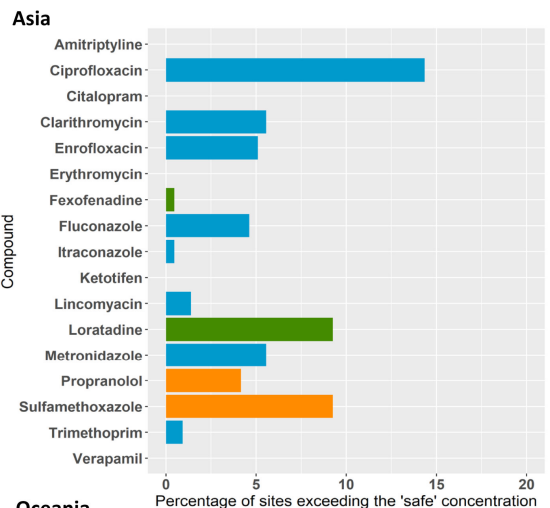
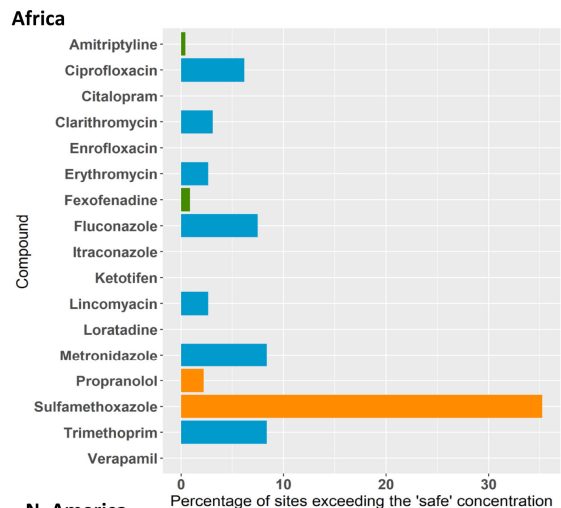
John L. Wilkinson^{a,1} , Alistair B. A. Boxall^a , Dana W. Kolpin^b , Kenneth M. Y. Leung^c , Racliffe W. S. Lai^c ,



Glossary:

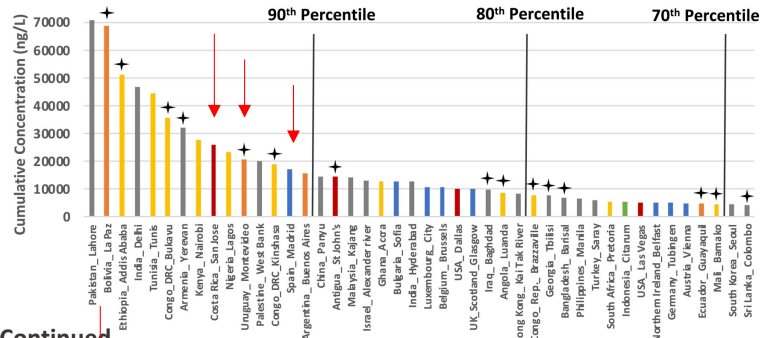
API = Active Pharmaceutical Ingredients



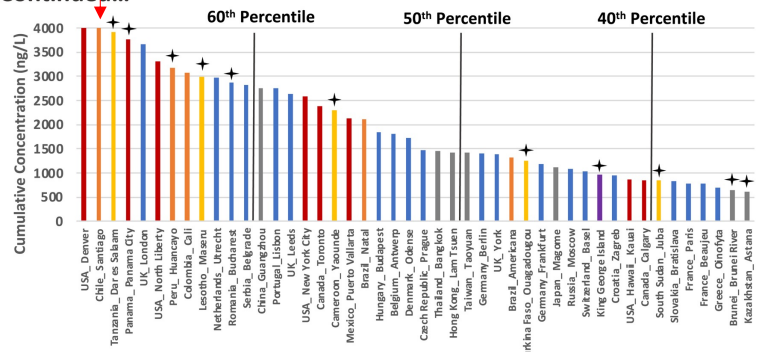


Endpoint Apical Resistance CEC

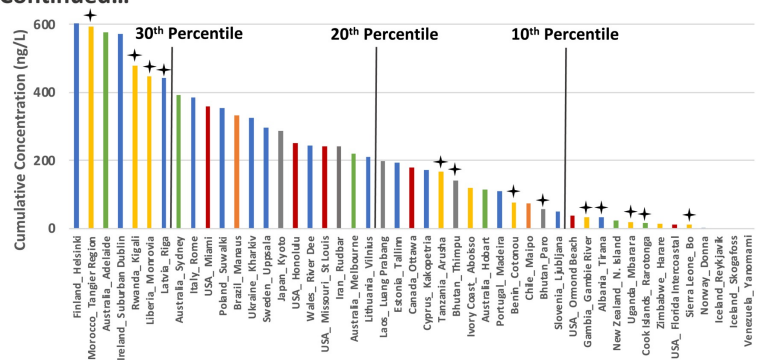
CEC= Critical Environmental Concentrations



Continued...



Continued...



- Africa
- Antarctica
- Asia
- Europe
- North America
- Oceania
- South America
- ✦ Country not previously monitored

Ecology, 69(2), 1988, pp. 508–515
© 1988 by the Ecological Society of America

THE INDETERMINACY OF ECOLOGICAL INTERACTIONS
AS PERCEIVED THROUGH PERTURBATION EXPERIMENTS¹

PETER YODZIS

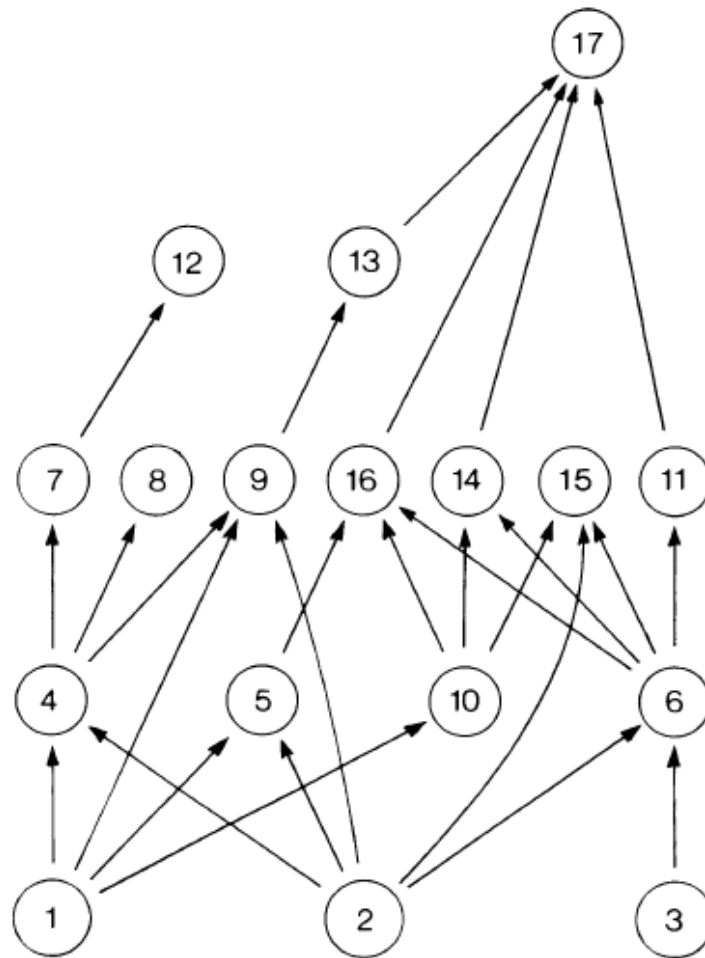


FIG. 1. Food web for Narragansett Bay, Rhode Island. Each vertex (circle) represents a species, and an arrow from vertex i to vertex j means that species j consumes species i .

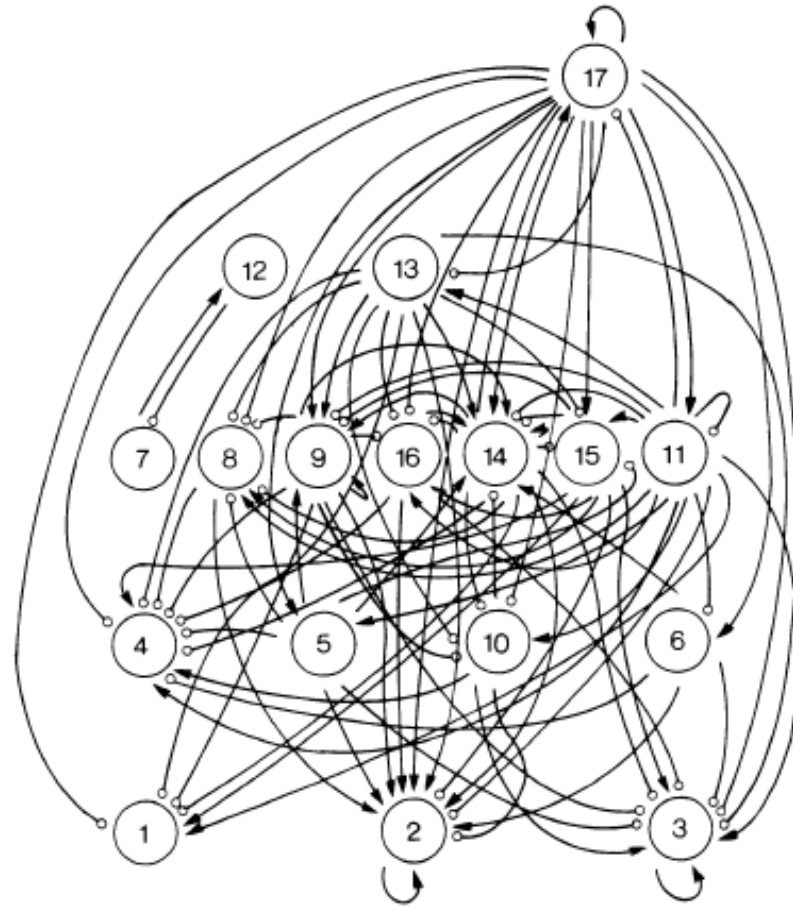
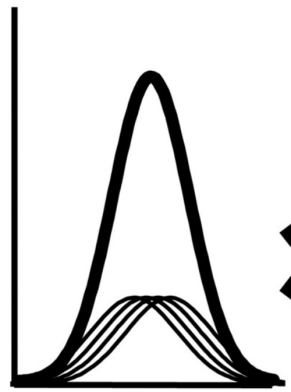


FIG. 4. Major effects on each species of the Narragansett Bay food web, obtained from another randomly generated plausible community matrix. Symbols here have the same meaning as in Fig. 2, except that here they are based on the inverse matrix A^{-1} rather than on the community matrix itself.

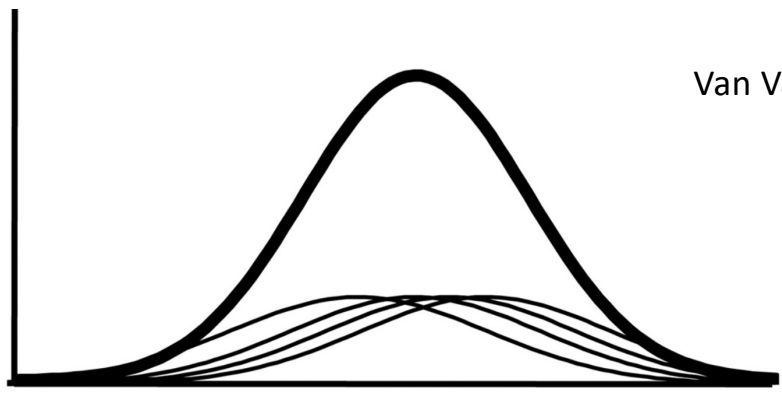
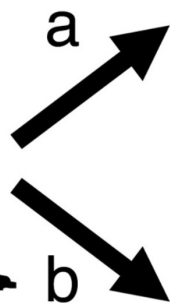
“For those doing practical work with environmental impacts, it is of crucial importance to understand that short-term observations of environmental impacts that can be viewed as press perturbations are close to useless for estimating probable long-term impacts. Moreover, as the present study makes clear, predicting those long-term effects not only requires data on the strengths of many interactions in the system, it requires very accurate data on many interaction strengths. This is a daunting prospect indeed.” (Yodzis 1988)

Niche complexity

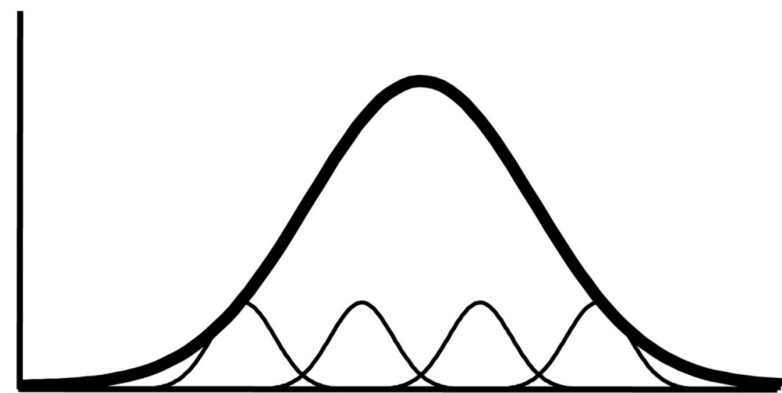
Frequency in diet



Prey size

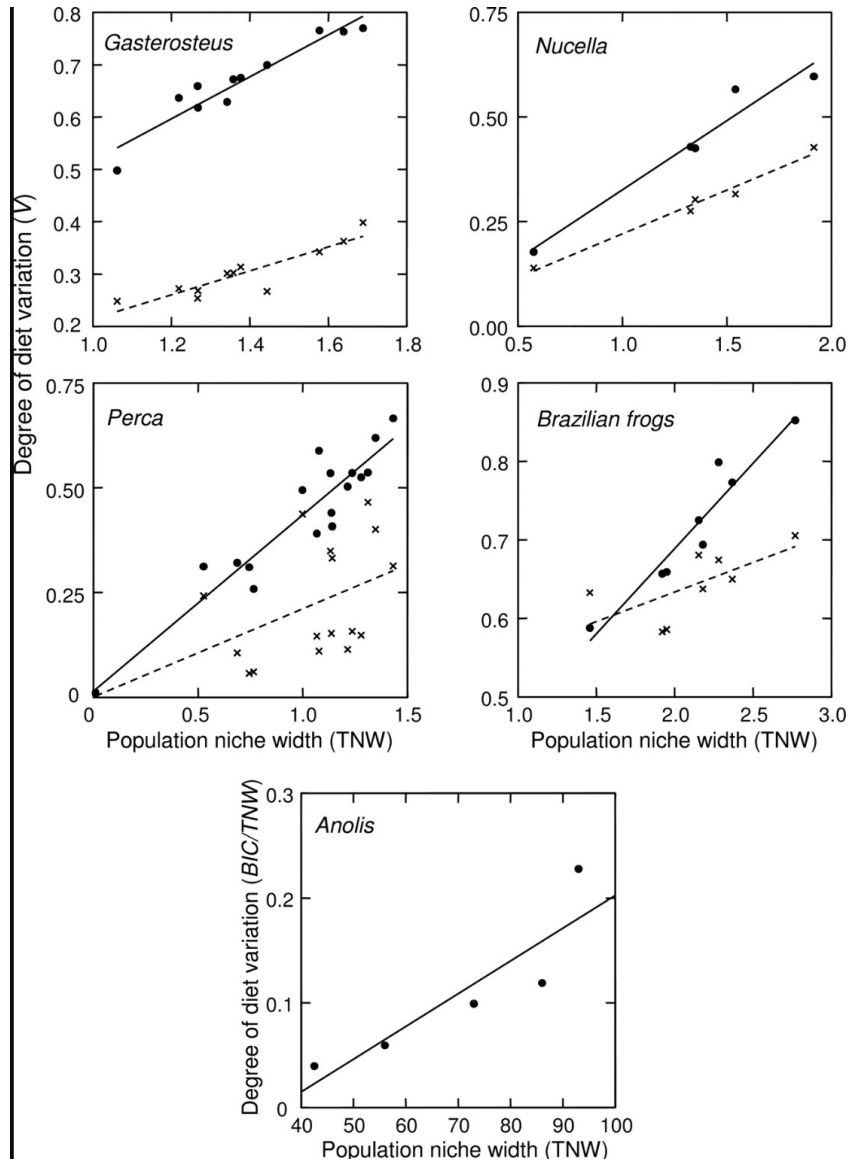


Roughgarden theory of niche width



Van Valen's Niche Variation Hypothesis

Niche axis



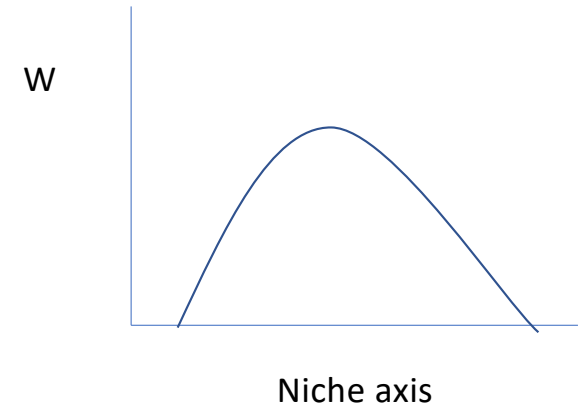
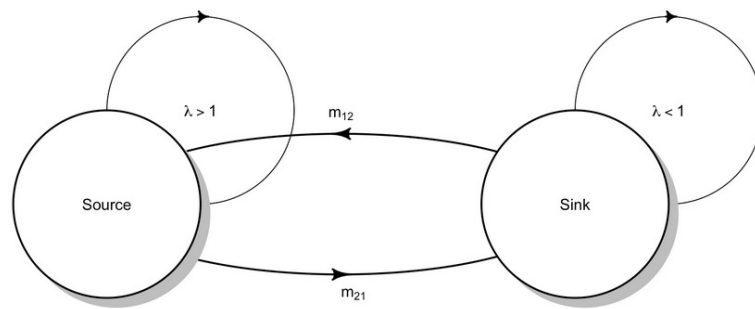


Figure 6.2: The simplest source-sink model, where $m_{21} > m_{12}$ so that net movement of individuals is from the source to the sink.

Niche

Colwell and Fuentes (1975)

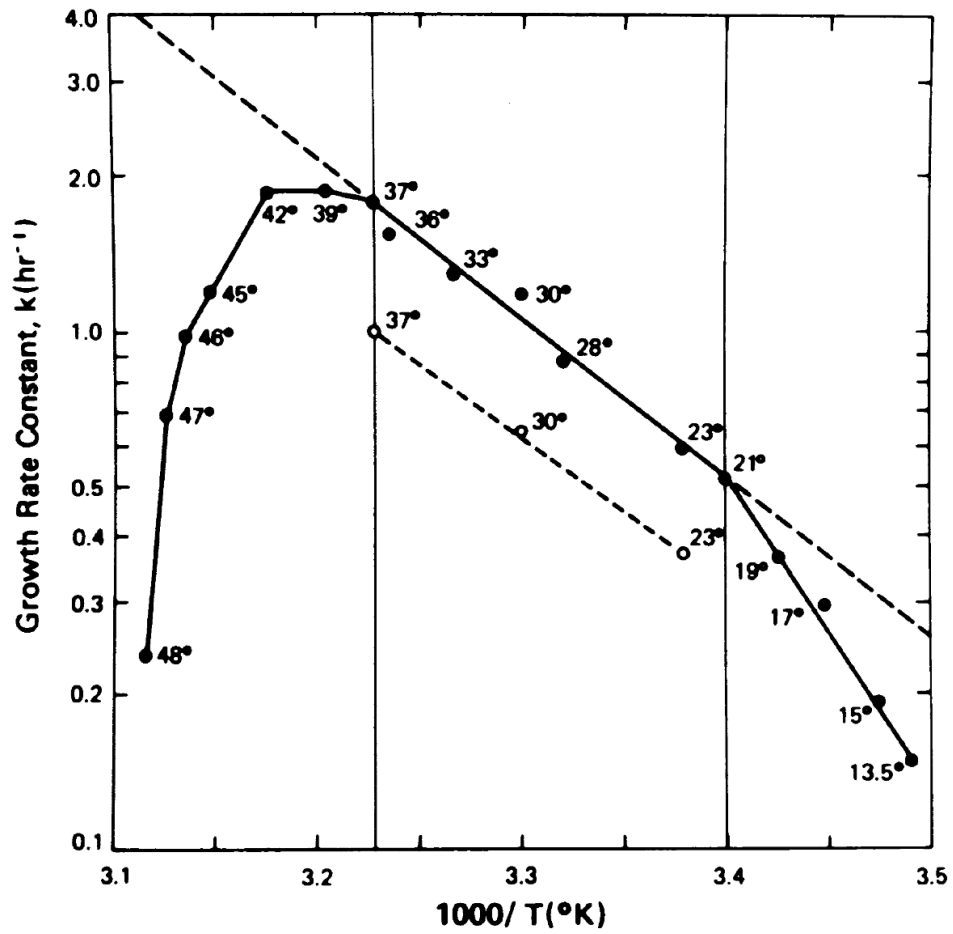


Columbarium

Colwell and Fuentes (1975)



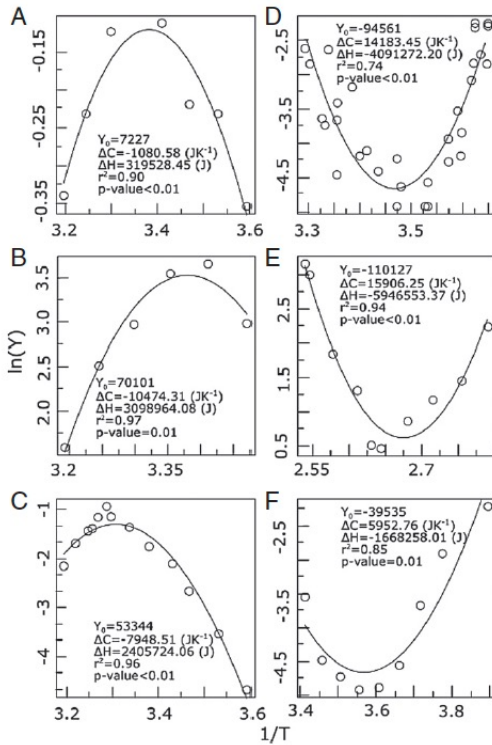
Temperature



Growth rate of E. coli

Herendeen et al

$$K = ae^{-e/KT}$$



The Eyring–Evans–Polanyi (EEP) transition state theory (TST)

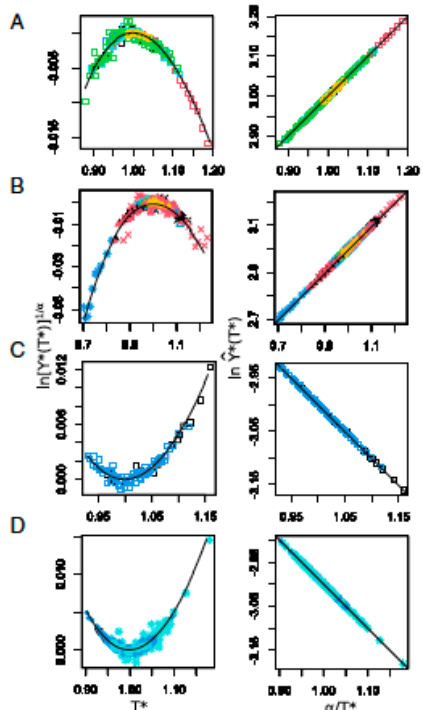
$$k = \frac{k_B}{h} T e^{\Delta S/R} e^{-\Delta H/RT}.$$

PNAS

RESEARCH ARTICLE | ECOLOGY

A general theory for temperature dependence in biology

José Ignacio Arroyo^{ab,1,2}, Beatriz Díez^{cd,e}, Christopher P. Kempes^b, Geoffrey B. West^b, and Pablo A. Marquet^{ab,fg,h,1,2}



- Enzyme activity parameters
- Body size
- △ Carbon stock
- + Developmental rate
- × Ecosystem flux
- ◇ Functional response (Handling time, feeding rate)
- ▽ Generation time
- ▣ Maximum germination
- * Metabolic rate
- ⊕ Mutation rate
- ◆ Performance
- ⊠ Population density
- ⊞ Population flux
- ✕ Population growth rate
- ⊞ Energy use
- Species richness
- Latency period
- ▲ Community abundance
- ◆ Mortality rate
- Fecundity
- Mass-specific metabolic rate
- Archaea
- Bacteria
- Unicellular eukaryotes
- Ectotherm
- Endotherm
- Virus
- Multicellular eukaryotes

$$Y(T) \approx Y_0 \left(\frac{1}{T} \right)^{\frac{-\overline{\Delta C}}{R} - \alpha} e^{\frac{-\overline{\Delta H}}{RT}}$$

$$Y^{*1/a} = T^* e^{1/T^* - 1}$$

$$\hat{Y}^*(T^*) \equiv (e/T^*)^a Y^*(T^*) = e^{a/T^*}$$

General patterns

Diffusion processes



Sewall Wright



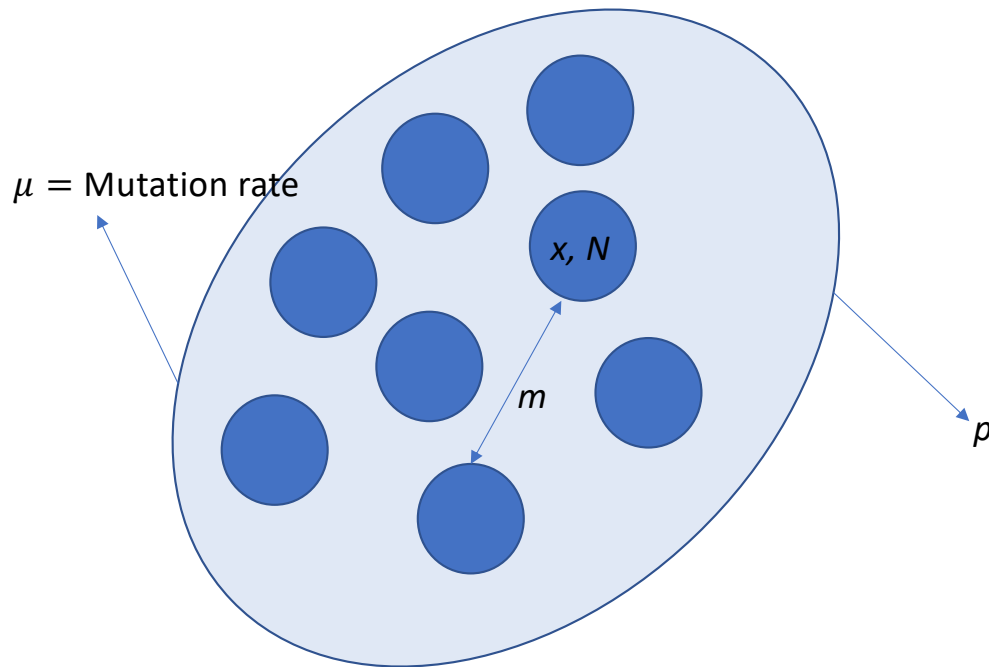
Andrey Kolmogorov



Ronald Fisher

- The frequency of genes in a structured population

$$\rho_{\infty}(x) = \frac{\Gamma(4Nm)}{\Gamma(4Nmp)\Gamma(4Nmq)} x^{4Nm q-1} (1-x)^{4Nmp-1}.$$



x = Frequency of a given allele in a local population

N = Effective population size

m = Proportion of migrating individuals among population each generation.

p = Frequency of a given allele in the total population

Kolmogorov (1935) Dokl. Akad. Nauk SSSR 3 (1935), 129-132.

Large population of N individuals consisting of s partial populations with n individuals each ($N=sn$)

Each generation k individuals disperse randomly across the partial populations.

\bar{p} = gene frequency in the large population

p = gen frequency in a local population

Δp = change in the frequency of p over one generation

$q = 1 - p$

Following Wright and Fisher:

$$M(p) = E(\Delta p) = \frac{k}{n}(\bar{p} - p) \quad \text{Var}(p) = E(\Delta p)^2 = \frac{pq}{2n}$$

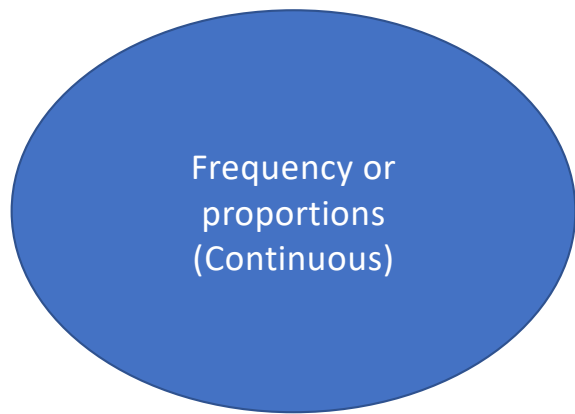
“Since s is large, the variation of the total concentration \bar{p} will proceed much more slowly than those of the partial concentrations p . Therefore, \bar{p} can temporarily be taken constant. The concentrations p in partial populations deviate from \bar{p} in either direction. After sufficiently long time the fluctuations of p around \bar{p} result in a certain stationary probability distribution for the concentrations p .” (Kolmogorov 1935)

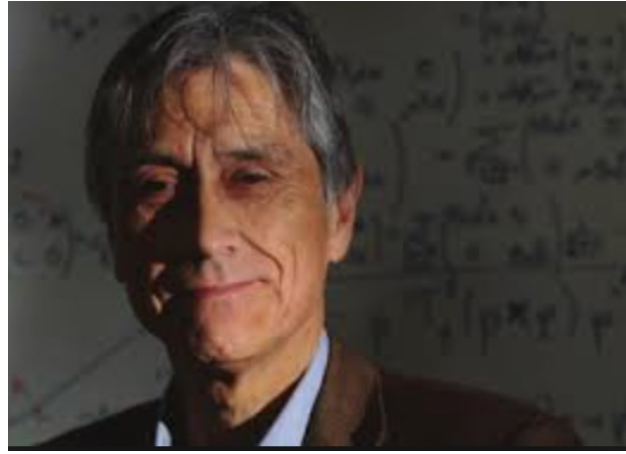
This stationary distribution satisfies the Kolmogorov forward or Fokker-Planck equation:

$$\frac{1}{2} \frac{\partial^2}{\partial p^2} (\text{Var}(p)\mu) - \frac{\partial}{\partial x} (M(p)\mu) = 0$$

Whose solution $\mu(p)$ is:

$$\mu(p) = \frac{1}{\text{B}(4k\bar{p}, 4k\bar{q})} p^{4k\bar{p}-1} q^{4k\bar{q}-1}$$



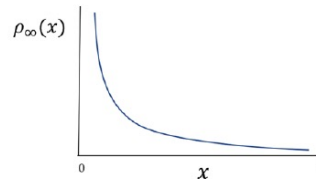
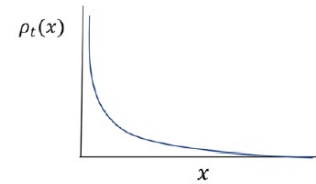
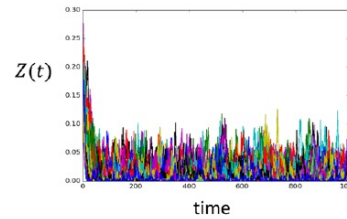
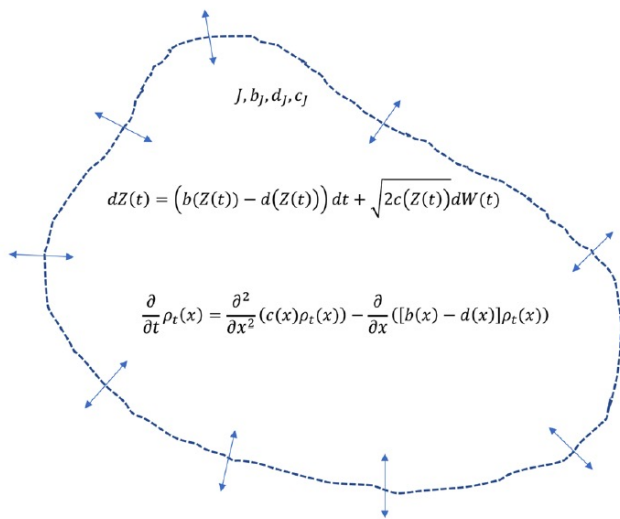


Prof. Rolando Rebolledo

**La méthode des martingales appliquée à l'étude de
la convergence en loi de processus**

Mémoires de la S. M. F., tome 62 (1979), p. I-V+1-125.

http://www.numdam.org/item?id=MSMF_1979__62__R1_0



$$B_J(n) = b_J(n) + c_J(n)$$

$$D_J(n) = d_J(n) + c_J(n).$$

$$b(x) = b_0 + b_1 x$$

$$d(x) = d_0 + d_1 x$$

$$c(x) = \gamma x(1 - x),$$

$$\rho_\infty(x) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha) + \Gamma(\beta)} x^{\alpha-1} (1 - x)^{\beta-1}$$

SCIENTIFIC REPORTS

OPEN On the proportional abundance of species: Integrating population genetics and community ecology

24 March 2017
21 November 2017

Pablo A. Marquet^{1,2,3,4,5}, Guillermo Espinoza¹, Sebastian R. Abades⁵, Angela Ganz⁷ & Rolando Rebolledo^{7,8}

$$\rho_{\infty}(x) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha) + \Gamma(\beta)} x^{\alpha-1} (1 - x)^{\beta-1}$$

The Proportional Species Abundance Distribution (PSAD)

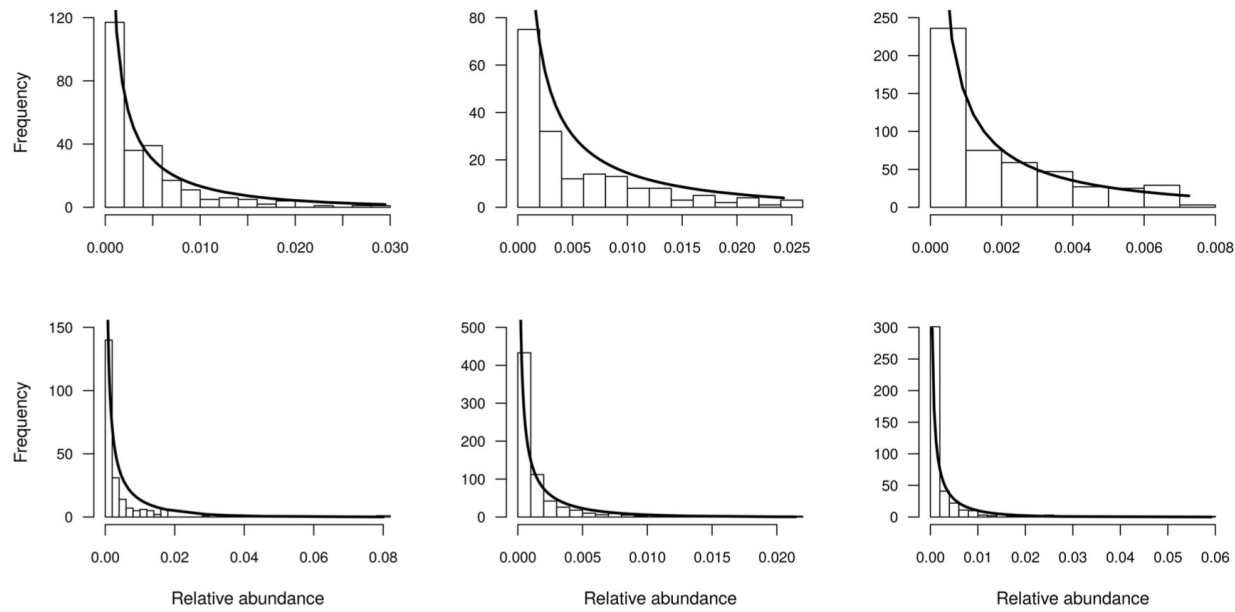
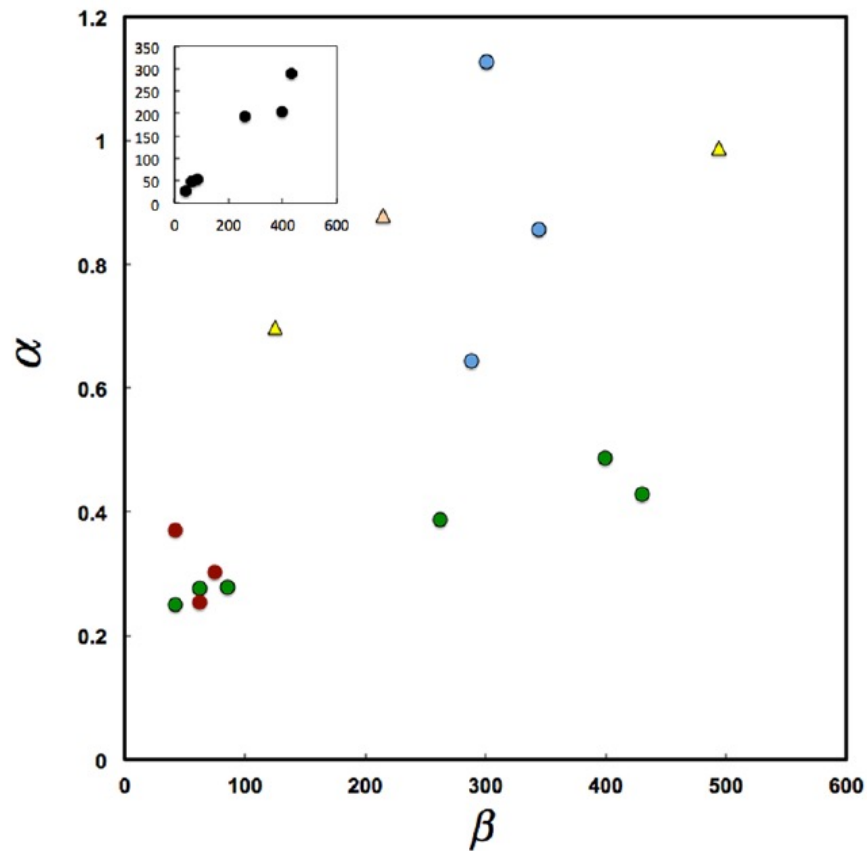


Figure 1. Fit of the Beta distribution to different animal and plant communities. First row, from left to right Amazon birds (community 10 in Table 1), Lepidoptera (12 in Table 1), butterflies (11 in Table 1), second row from left to right Tropical trees (6 in Table 1), Tropical trees (2 in Table 1) and Coral reefs (14 in Table 1)

$$\rho_{\infty}(x) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha) + \Gamma(\beta)} x^{\alpha-1} (1-x)^{\beta-1}$$



● Marine communities

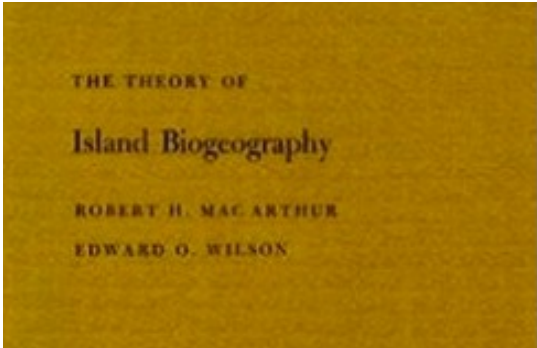
● Shrublands

● Tropical Forest

▲ Bird communities

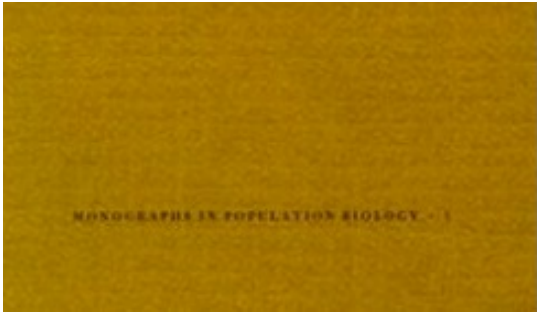
$\alpha \sim$ Dispersal

$\beta \sim$ Speciation



$$(3-4) \quad \frac{dP_s(t)}{dt} = -(\lambda_s + \mu_s)P_s(t) + \lambda_{s-1}P_{s-1}(t) + \mu_{s+1}P_{s+1}(t).$$

$$Z(t) = Z(0) + \int_0^t \theta(Z(s))ds + \int_0^t \sigma(Z(s))dW_s, \quad (t \geq 0).$$



$$\rho_\infty(x) = \frac{\Gamma(\alpha + \beta)}{\Gamma(\alpha) + \Gamma(\beta)} x^{\alpha-1} (1-x)^{\beta-1}$$

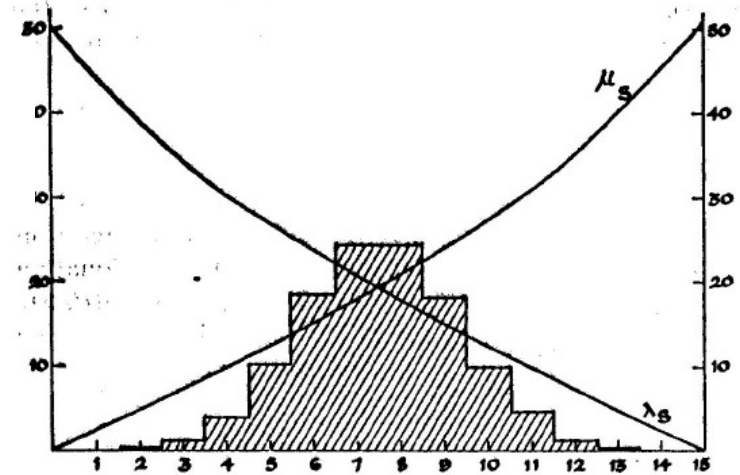
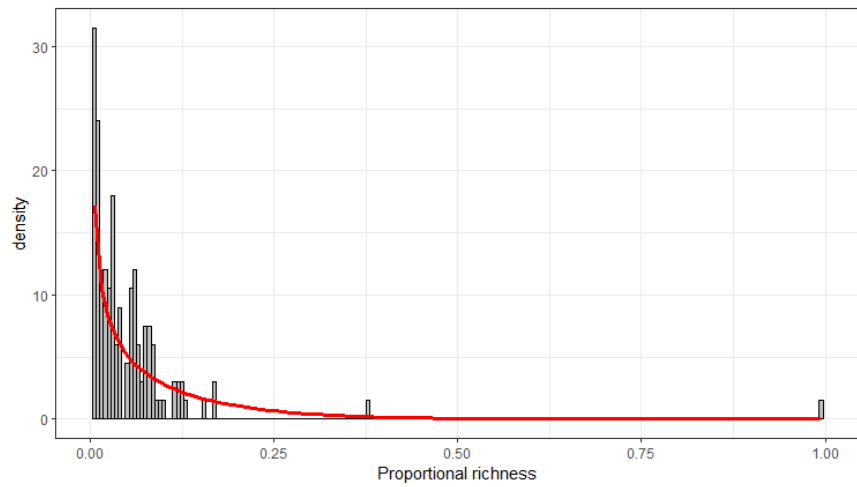


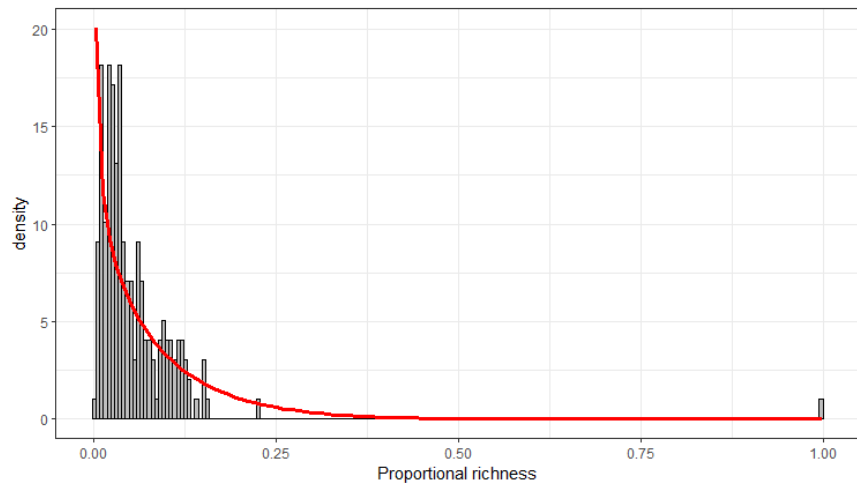
FIGURE 19. A particular case of a predicted distribution of numbers of species on a family of island biotas all with identical extinction and immigration curves and all having had time to reach equilibrium. The histogram represents the number of islands with each number of resident species in an equilibrium situation. The species pool from which the biotas were assembled contained 15 species. If the immigration and extinction curves were straighter, the variance of equilibrium species numbers would be even greater; yet this large variance is still consistent with the equilibrium condition.

"In principle one could solve eq. 3-4...for our purpose is more useful to find the mean $M(t)$ and the variance, $var(t)$, of the number of species at time t . These can be estimated in nature by measuring the mean and variance in number of species of a series of islands of about the same distance and are and hence of the same λ and μ ." pp.33-34

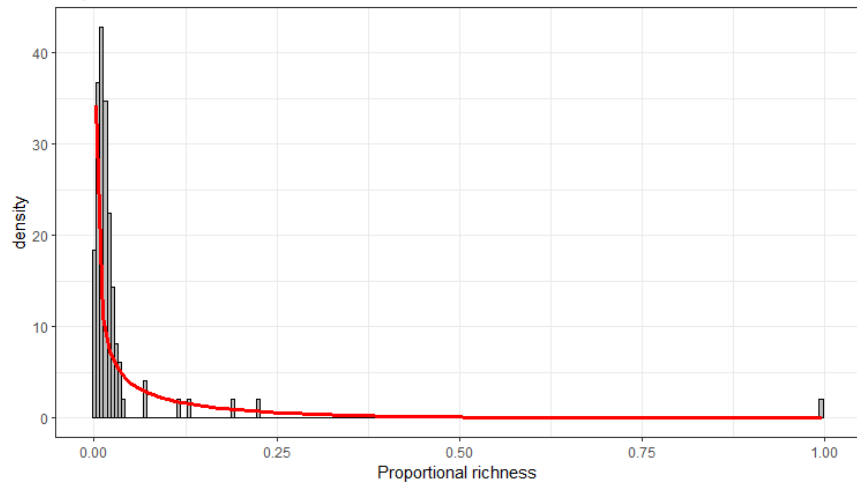
Mammals



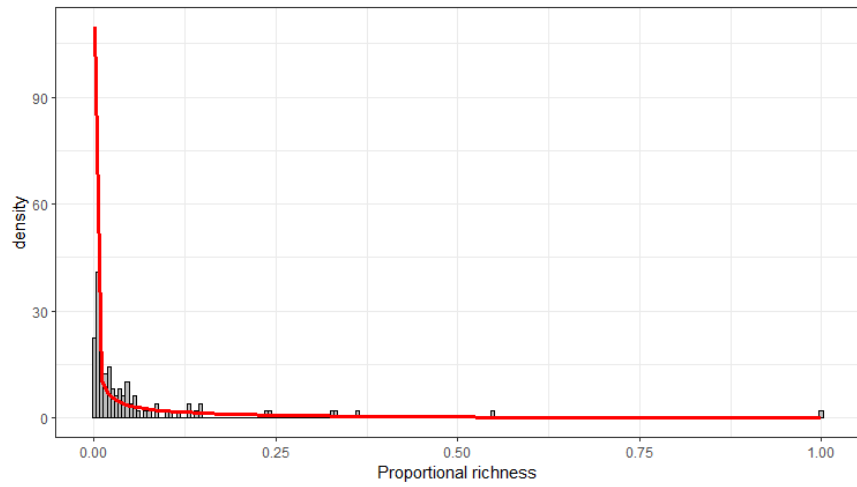
Birds



Reptiles



Plantas



Some Sources of Stochasticity at Different Levels of Organization

Frequency of Gene families
within Genomes

- Mutation
- Lateral gene transfer
- Gene duplication

Frequency of genes within
and among population

- Mutation
- Drift
- Migration
- Loss

Frequency of individuals
among species

- Birth
- Death
- Migration

Frequency of species
Among communities

- Speciation
- Extinction
- Migration

Abundance of gene families within genomes

- Birth-death processes are applicable to understand genome evolution
- Driving processes are similar

Duplication

Mutation

Lateral gene transfer and retroviral infection

Plasmids

Gene extinction

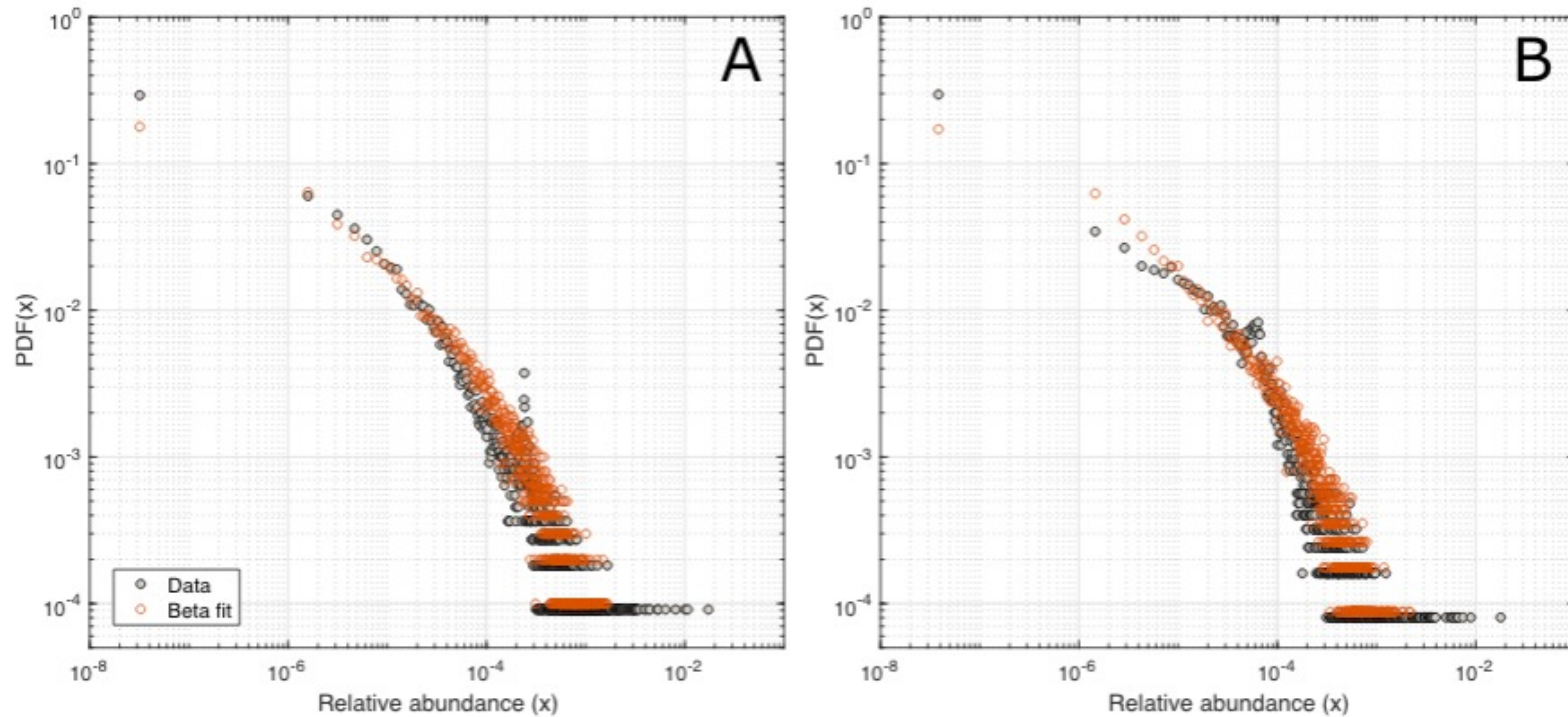


Figure 1. The relative abundance of protein families follows a Beta distribution. The relative abundance of protein families in bacteria and eukarya according to the Pfam classification. **A.** Data from 7,694 bacterial proteomes; 11,106 families; and 30,743,438 genes. Best fit beta distribution parameters: $\alpha=0.273$ (0.264, 0.283), $\beta=3,031.9$ (2823.4, 3240.4). **B.** Data from 1,496 eukaryotic proteomes; 12,579 families; and 25,625,956 genes. Best fit beta distribution parameters: $\alpha=0.291$ (0.281, 0.300), $\beta=3,655.2$ (3424.3, 3886.2).

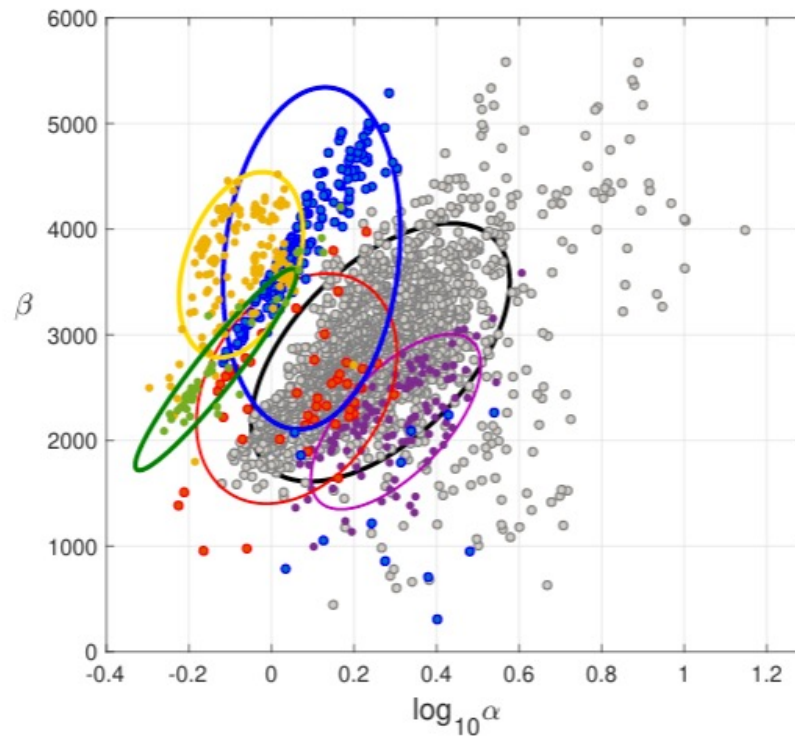


Figure 2. Shape parameters of Beta distributions arising from the relative abundance of gene families in genomes. Annotations of protein families (Pfam v32) in Uniprot reference proteomes (n=17,543). Reference proteomes include Archea (n=285, magenta), Bacteria (n=6,554, grey); unicellular eukarya (n=1,202, red); plants (n=, green); metazoa (n=, yellow); fungi (n=, blue). The total number of protein families classified by Pfam is 15,964.

Gracias