SARRIS-LAB

Network Science

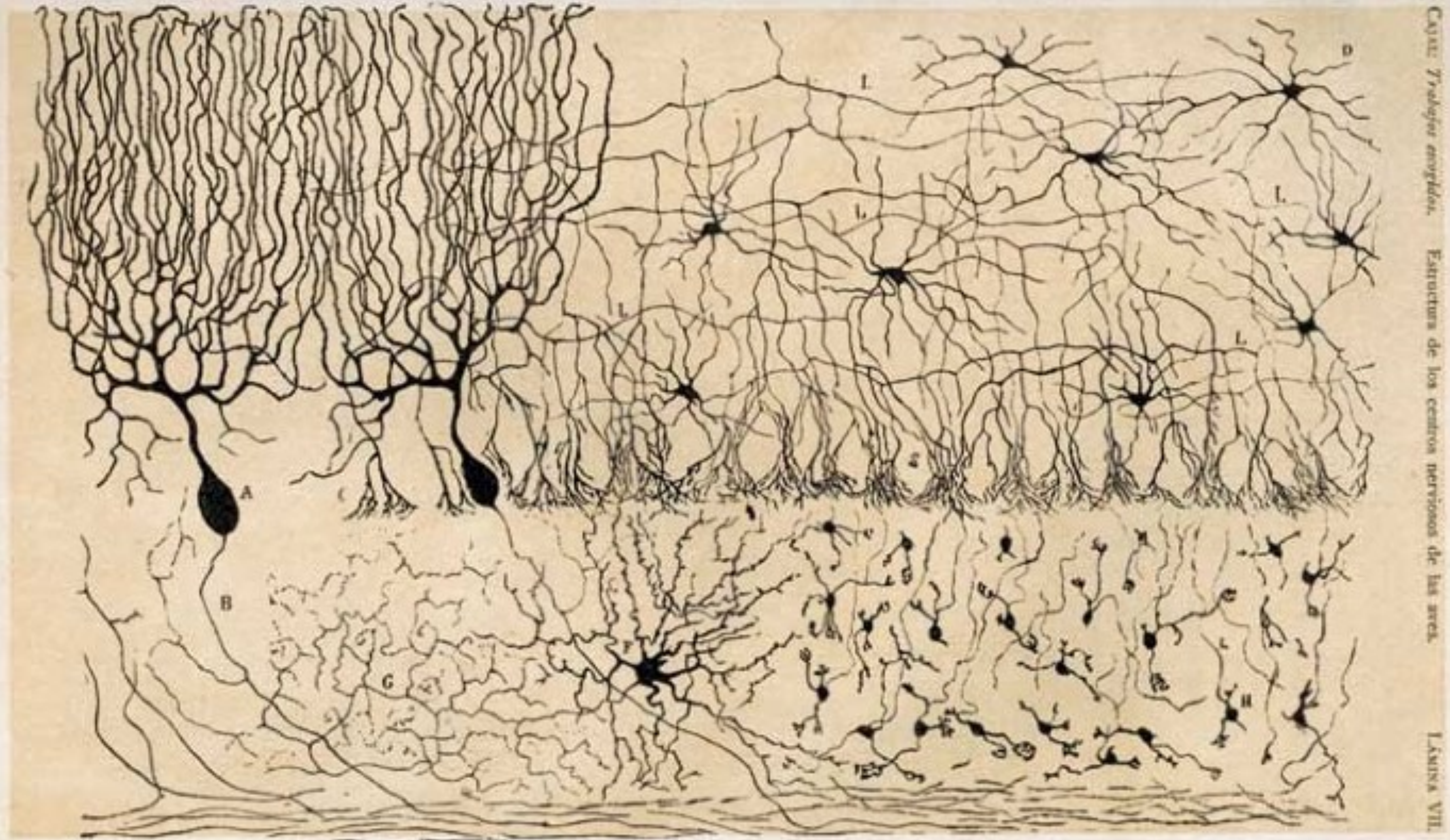
Basics

Savvas Paragkamian, post doc

What is a network?

From omics to networks?

Examples



CAJAL: *Trabajos escogidos.* Estructura de los centros nerviosos de las aves. LÁMINA VII.

600 πΧ Ομφαλος Δελφων

Δικτυο Ανθρωπινων Σχεσεων

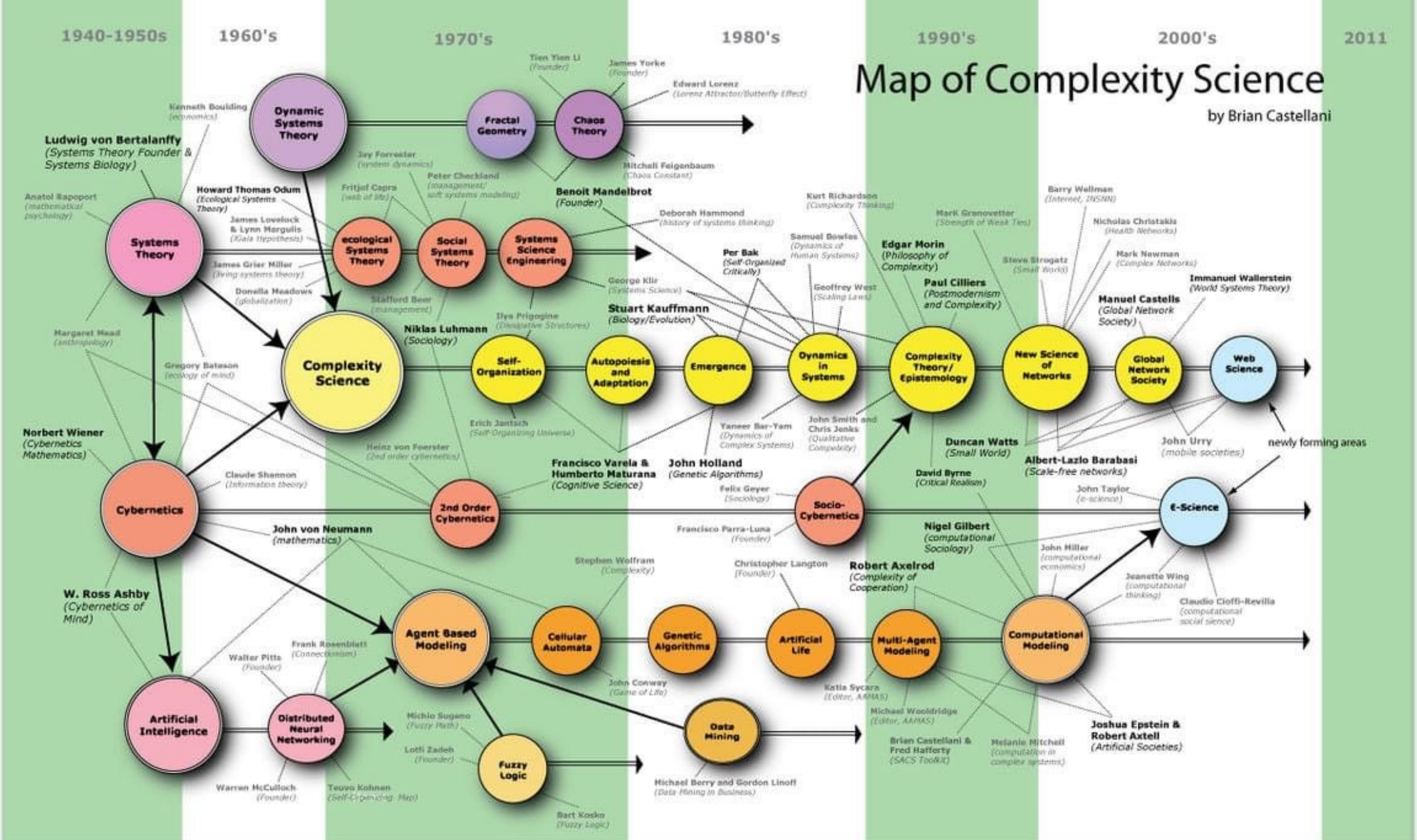
http://en.wikipedia.org/wiki/Oren_Patashnik

From Prof I. Antoniou

Complexity

Map of Complexity Science

by Brian Castellani



1940-1950s
1960's
1970's
1980's
1990's
2000's
2011

Dynamic Systems Theory
Fractal Geometry
Chaos Theory

Kenneth Boulding
(economics)

Tien Yien Li
(Founder)

James Yorke
(Founder)

Edward Lorenz
(Lorenz Attractor/Butterfly Effect)

Mitchell Feigenbaum
(Chaos Constant)

Benoit Mandelbrot
(Founder)

Systems Theory
ecological Systems Theory
Social Systems Theory
Systems Science Engineering

Ludwig von Bertalanffy
(Systems Theory Founder & Systems Biology)

Anatol Rapoport
(mathematical psychology)

Howard Thomas Odum
(Ecological Systems Theory)

James Lovelock & Lynn Margulis
(Gaia Hypothesis)

James Grier Miller
(living systems theory)

Donella Meadows
(globalization)

Jay Forrester
(system dynamics)

Fritjof Capra
(web of life)

Peter Checkland
(management/ soft systems modeling)

Stafford Beer
(management)

Deborah Hammond
(history of systems thinking)

George Klir
(Systems Science)

Complexity Science
Self-Organization
Autopoiesis and Adaptation
Emergence
Dynamics in Systems
Complexity Theory/ Epistemology
New Science of Networks
Global Network Society
Web Science

Margaret Mead
(anthropology)

Gregory Bateson
(ecology of mind)

Niklas Luhmann
(Sociology)

Ilya Prigogine
(Dissipative Structures)

Stuart Kauffmann
(Biology/Evolution)

Per Bak
(Self-Organized Critically)

Samuel Bowles
(Dynamics of Human Systems)

Kurt Richardson
(Complexity Thinking)

Geoffrey West
(Scaling Laws)

Edgar Morin
(Philosophy of Complexity)

Paul Cilliers
(Postmodernism and Complexity)

Mark Granovetter
(Strength of Weak Ties)

Steve Strogatz
(Small World)

Barry Wellman
(Internet, INSNN)

Nicholas Christakis
(Health Networks)

Mark Newman
(Complex Networks)

Manuel Castells
(Global Network Society)

Immanuel Wallerstein
(World Systems Theory)

Erich Jantsch
(Self-Organizing Universe)

Heinz von Foerster
(2nd order cybernetics)

Francisco Varela & Humberto Maturana
(Cognitive Science)

John Holland
(Genetic Algorithms)

Yaneer Bar-Yam
(Dynamics of Complex Systems)

John Smith and Chris Jenks
(Qualitative Complexity)

Duncan Watts
(Small World)

David Byrne
(Critical Realism)

Albert-Lazlo Barabasi
(Scale-free networks)

John Urry
(mobile societies)

newly forming areas

Cybernetics
2nd Order Cybernetics
Socio-Cybernetics
E-Science

Norbert Wiener
(Cybernetics Mathematics)

Claude Shannon
(Information theory)

Felix Geyer
(Sociology)

Francisco Parra-Luna
(Founder)

John Taylor
(e-science)

John von Neumann
(mathematics)

W. Ross Ashby
(Cybernetics of Mind)

Agent Based Modeling
Cellular Automata
Genetic Algorithms
Artificial Life
Multi-Agent Modeling
Computational Modeling

Stephen Wolfram
(Complexity)

Christopher Langton
(Founder)

Robert Axelrod
(Complexity of Cooperation)

Nigel Gilbert
(computational Sociology)

John Miller
(computational economics)

Jeanette Wing
(computational thinking)

Claudio Cioffi-Revilla
(computational social sience)

John Conway
(Game of Life)

Katia Sycara
(Editor, AAMAS)

Michael Wooldridge
(Editor, AAMAS)

Brian Castellani & Fred Hafferty
(SACS Toolkit)

Melanie Mitchell
(computation in complex systems)

Joshua Epstein & Robert Axtell
(Artificial Societies)

Artificial Intelligence
Distributed Neural Networking
Fuzzy Logic
Data Mining

Frank Rosenblatt
(Connectionism)

Walter Pitts
(Founder)

Warren McCulloch
(Founder)

Teuvo Kohnen
(Self-Organizing Map)

Michio Sugeno
(Fuzzy Math)

Lotfi Zadeh
(Founder)

Bart Kosko
(Fuzzy Logic)

Michael Berry and Gordon Linoff
(Data Mining in Business)

Less is more

More Is Different

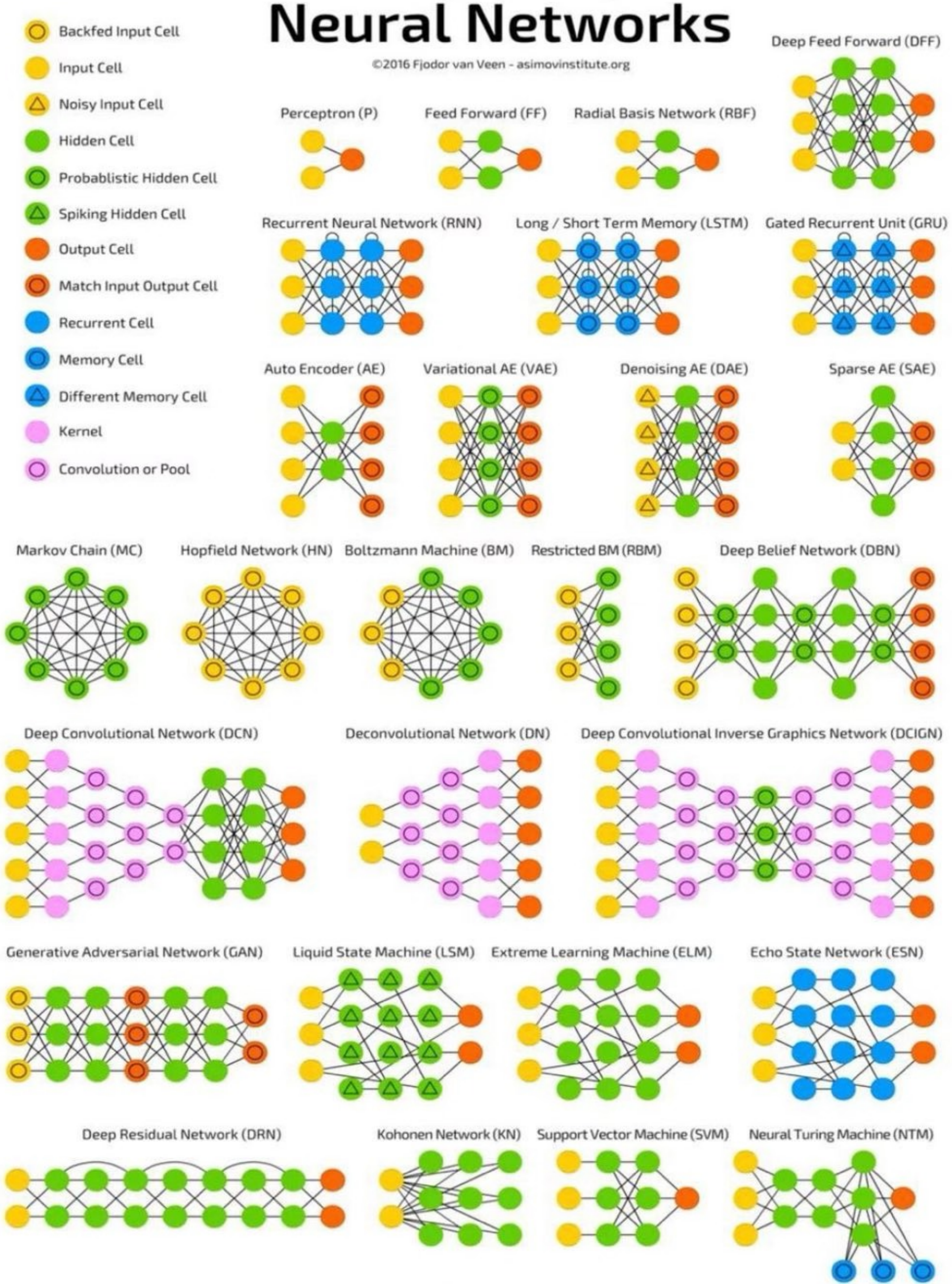
Large Language Models
Diffusion models
Deep Neural Networks

ChatGPT
AlphaFold
EVO


INPUT LAYER
HIDDEN LAYERS
OUTPUT LAYER

A mostly complete chart of

Neural Networks



Types of Networks

Unipartite

Bipartite

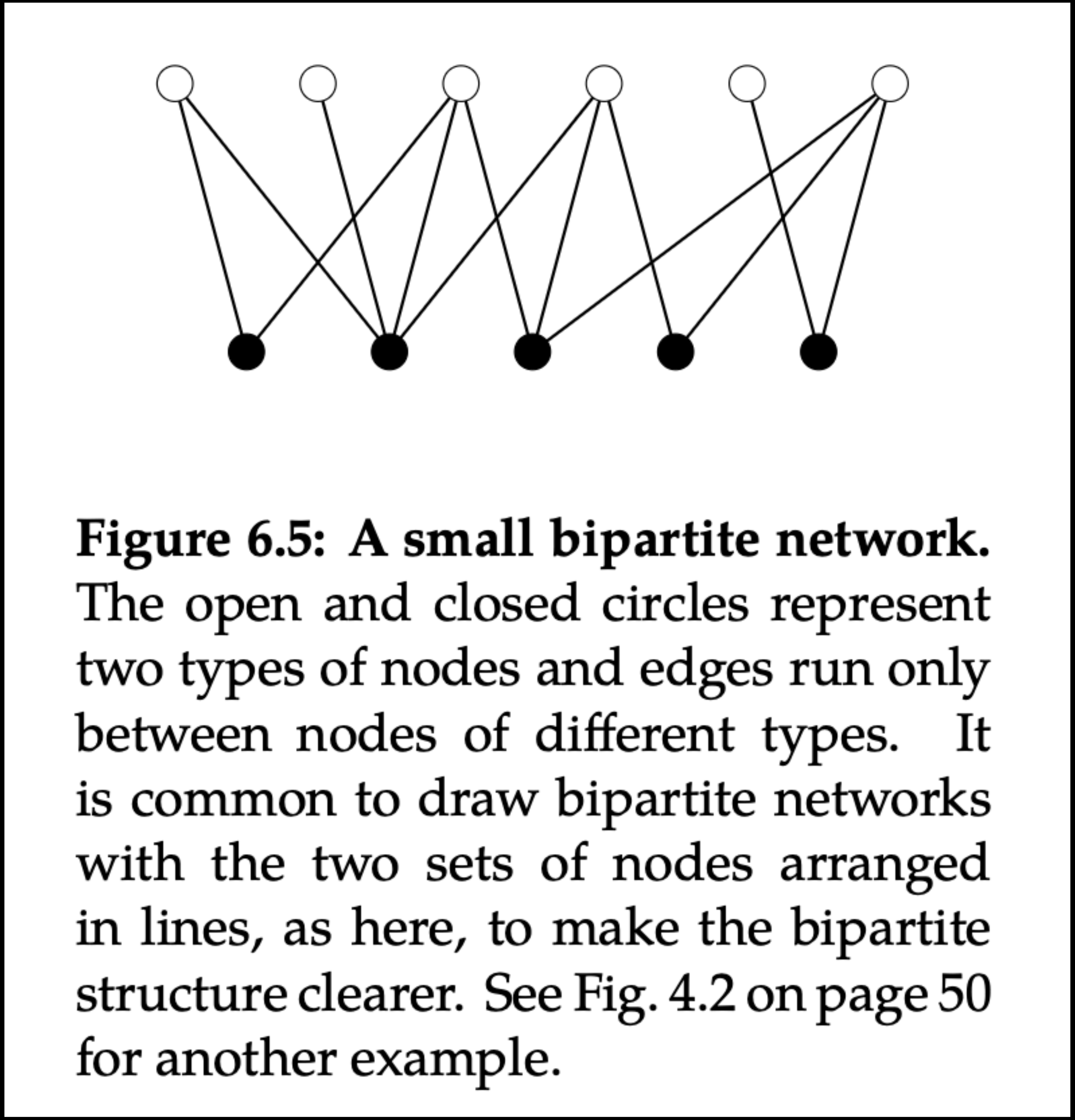
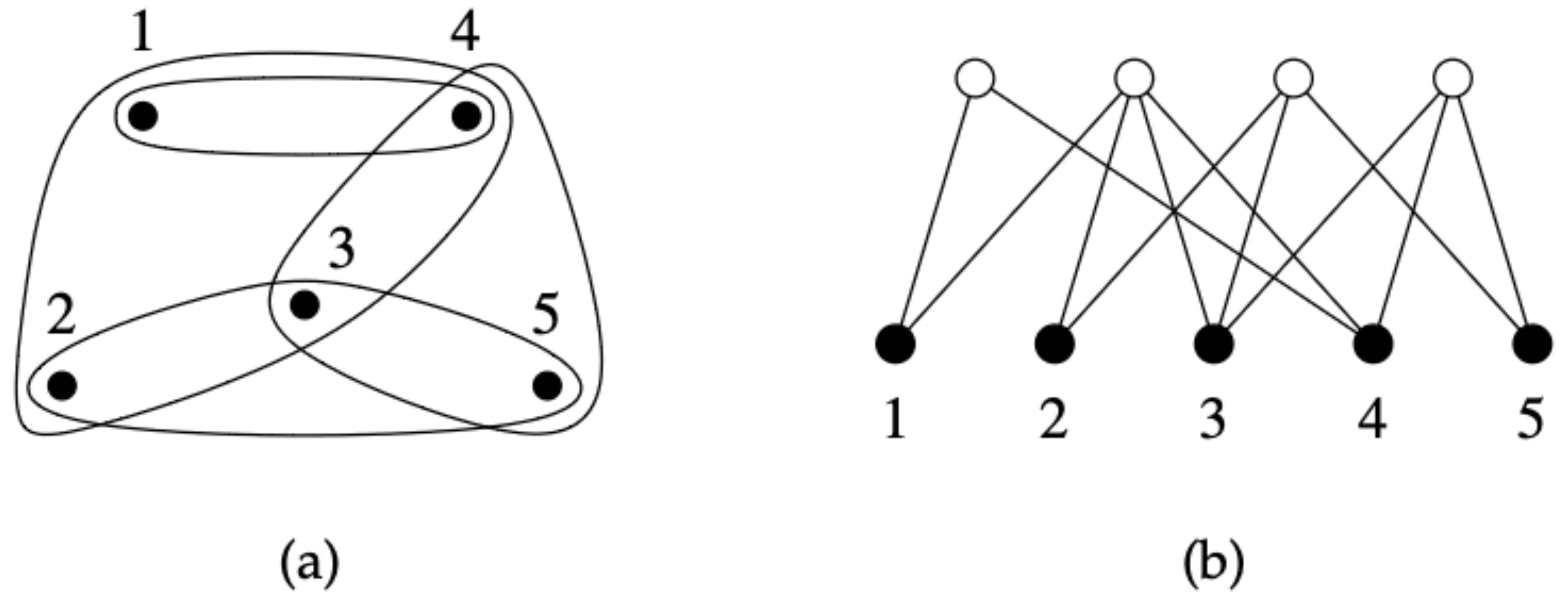


Figure 6.5: A small bipartite network. The open and closed circles represent two types of nodes and edges run only between nodes of different types. It is common to draw bipartite networks with the two sets of nodes arranged in lines, as here, to make the bipartite structure clearer. See Fig. 4.2 on page 50 for another example.

Newman 2018

Hypergraph



(a) (b)

Figure 6.4: A hypergraph and corresponding bipartite graph. These two networks convey the same information—the membership of five nodes in four different groups. (a) The hypergraph representation in which the groups are represented as hyperedges, denoted by the loops circling sets of nodes. (b) The bipartite representation in which we introduce four new nodes (open circles at the top) representing the four groups, with edges connecting each of the original five nodes (bottom) to the groups to which it belongs.

Newman 2018

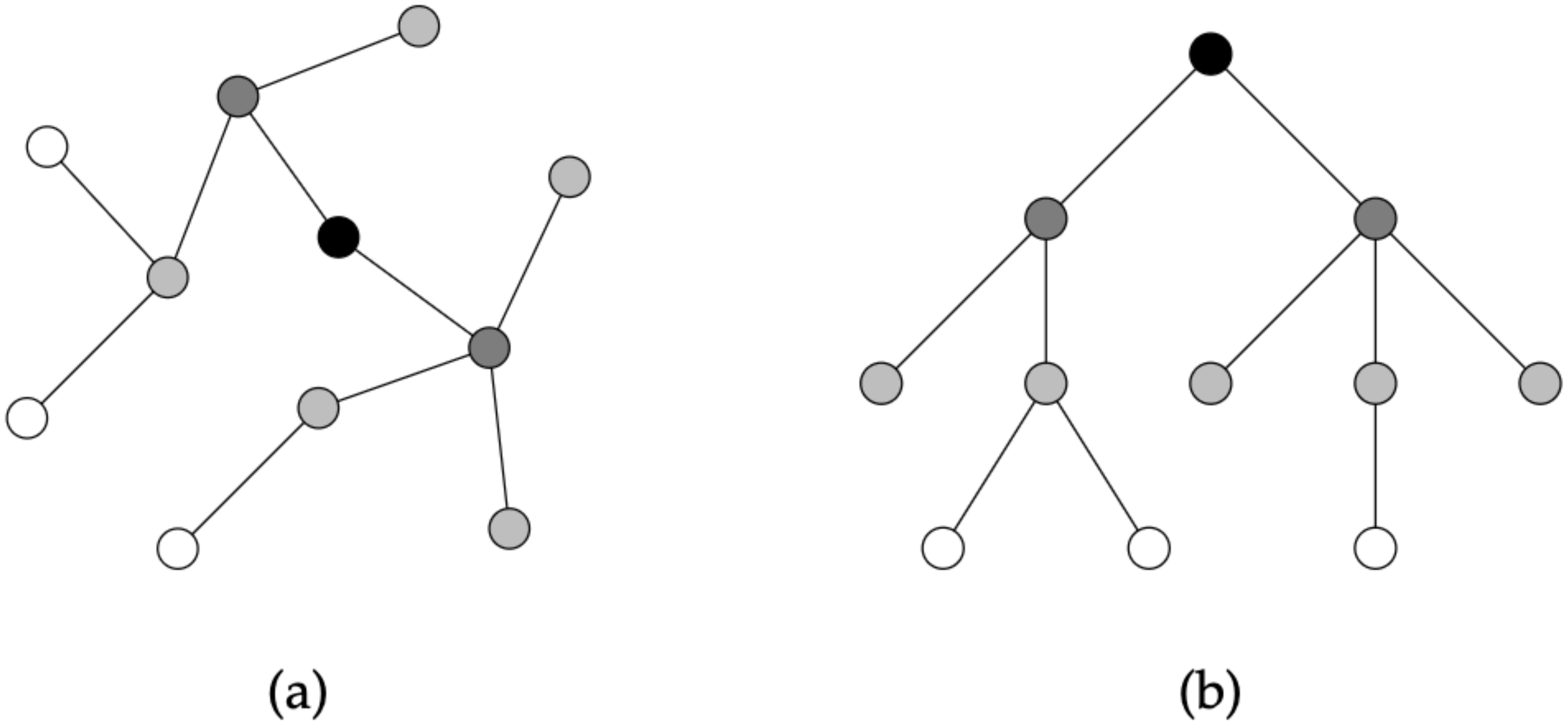
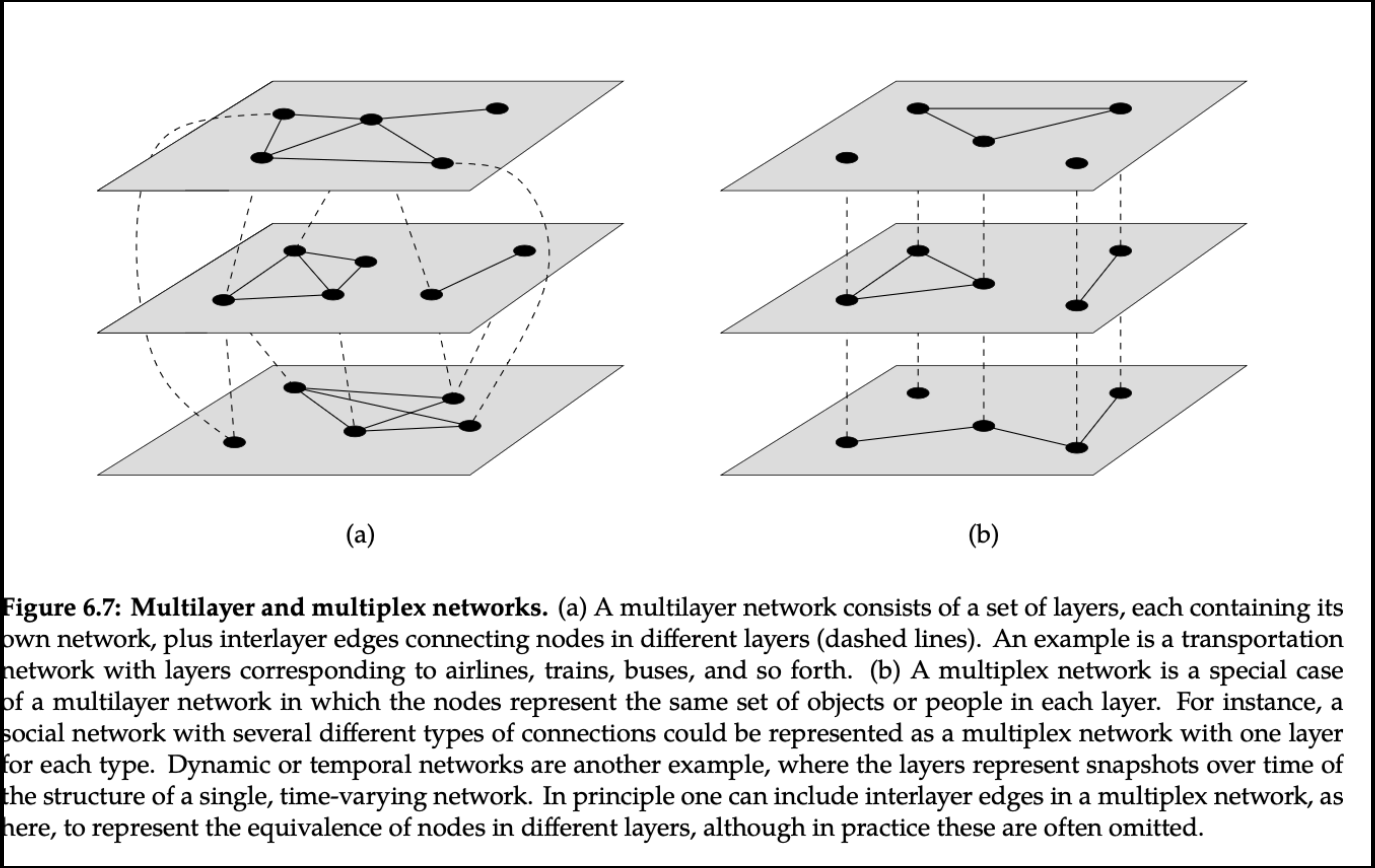


Figure 6.8: Two sketches of the same tree. The two panels here show two different depictions of a tree, a network with no closed loops. In (a) the nodes are positioned on the page in any convenient position. In (b) the tree is a laid out in a "rooted" fashion, with a root node at the top and branches leading down to "leaves" at the bottom.

Newman 2018

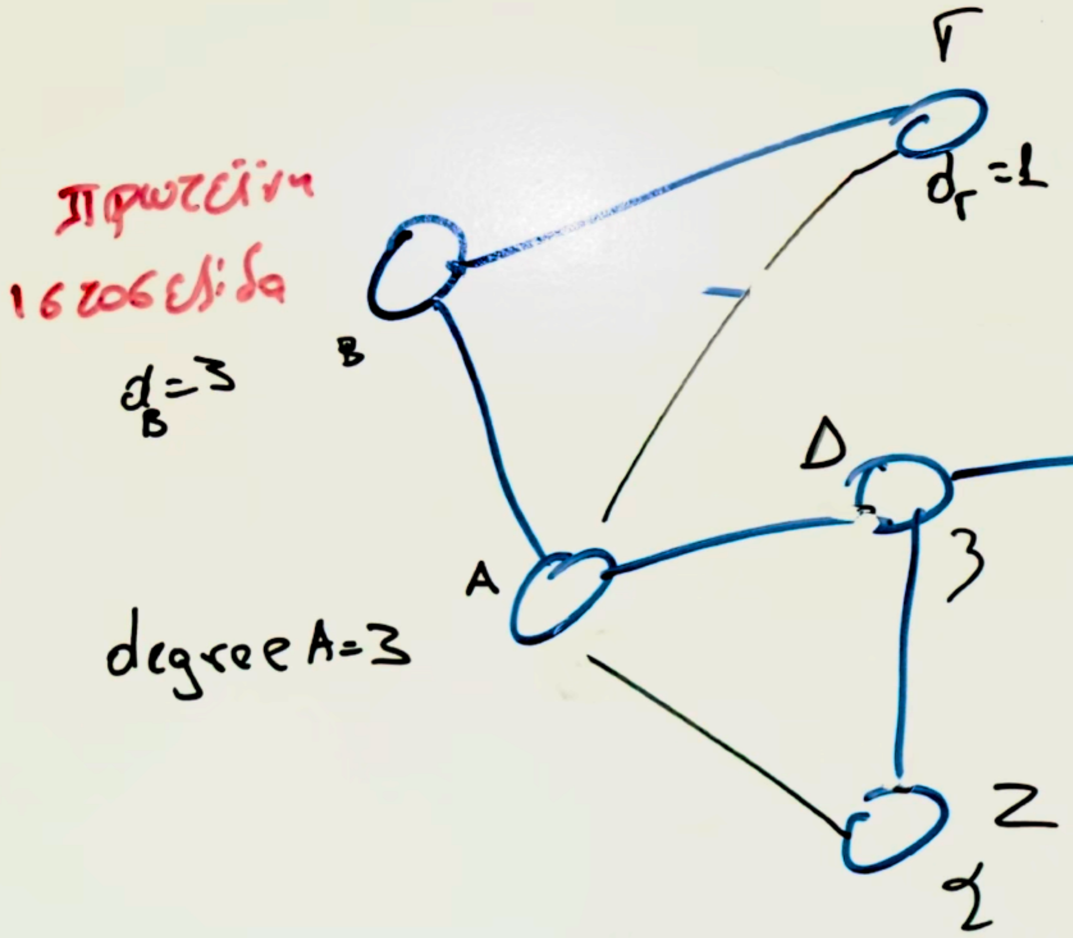


(a) (b)

Figure 6.7: Multilayer and multiplex networks. (a) A multilayer network consists of a set of layers, each containing its own network, plus interlayer edges connecting nodes in different layers (dashed lines). An example is a transportation network with layers corresponding to airlines, trains, buses, and so forth. (b) A multiplex network is a special case of a multilayer network in which the nodes represent the same set of objects or people in each layer. For instance, a social network with several different types of connections could be represented as a multiplex network with one layer for each type. Dynamic or temporal networks are another example, where the layers represent snapshots over time of the structure of a single, time-varying network. In principle one can include interlayer edges in a multiplex network, as here, to represent the equivalence of nodes in different layers, although in practice these are often omitted.

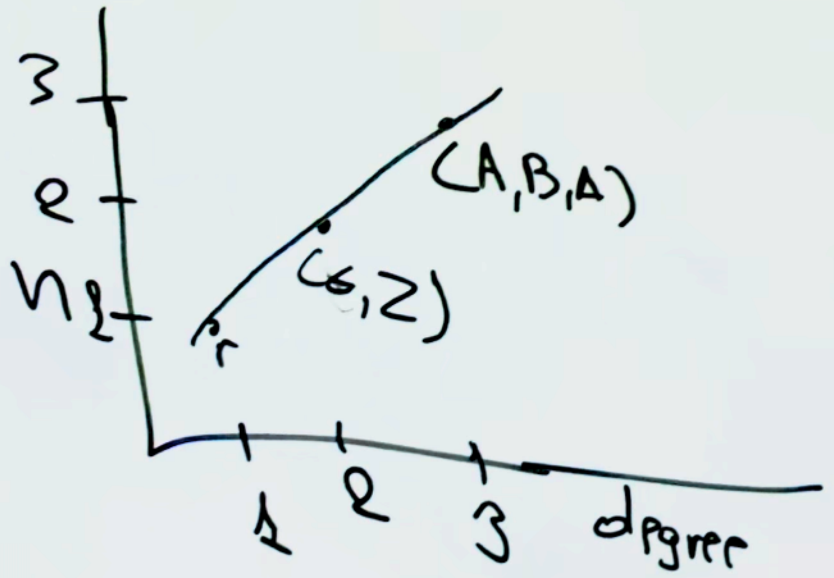
Newman 2018

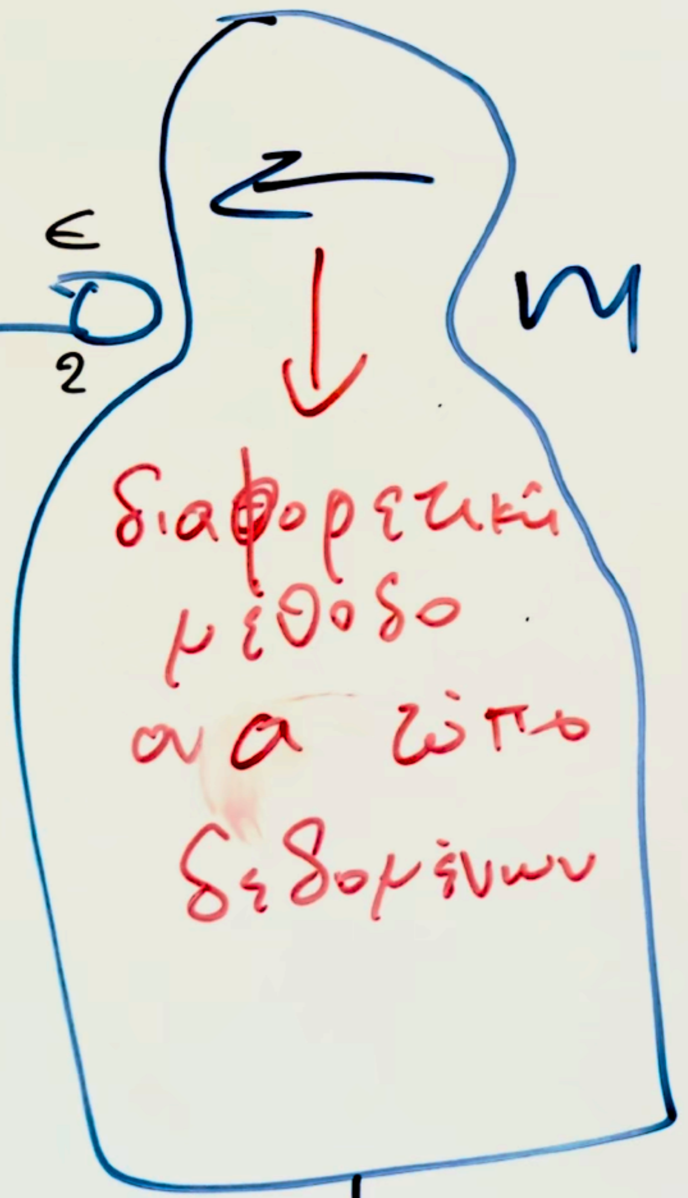
Summary of 21/05/2025



- Τι είναι ο κόμβος
- Τι είναι η σύνδεση

Κατανομή Βαθμού



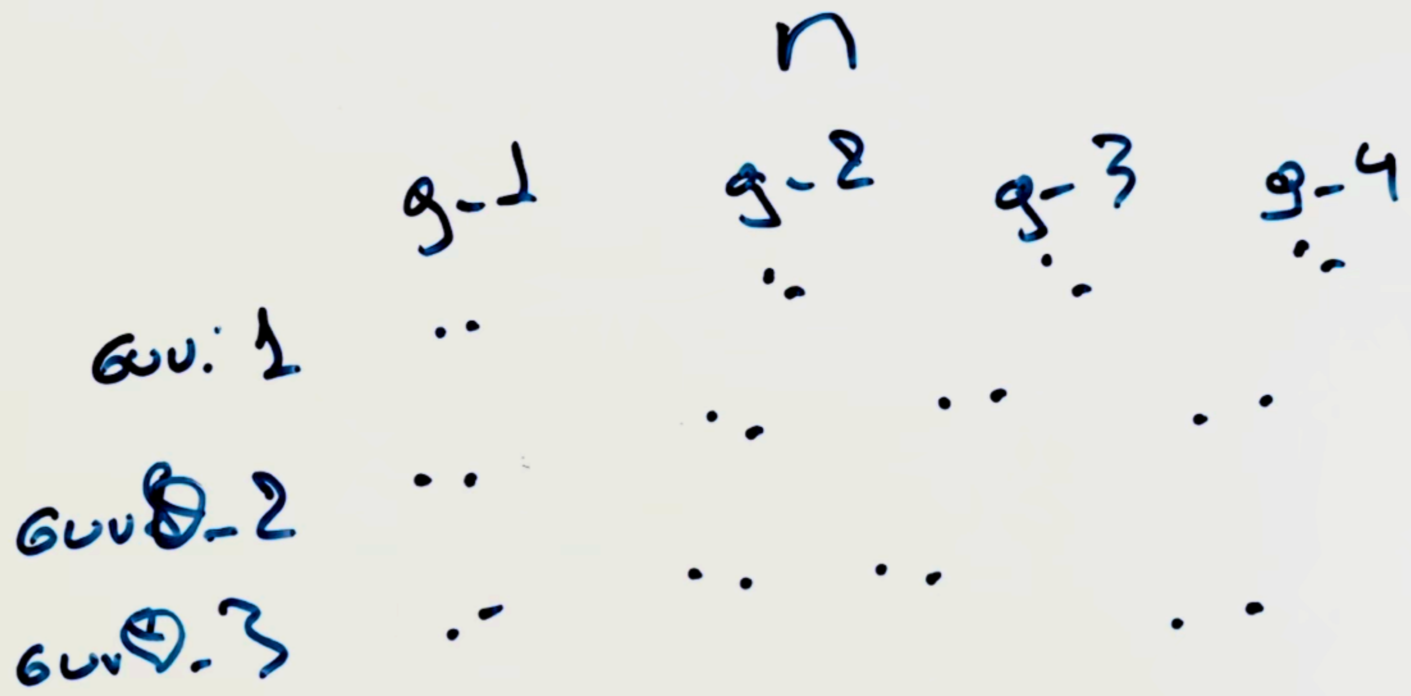


διαφορετική μέθοδο ανα τύπο δεδομένων

↓

Γιατί ο βιολόγος δεν είναι ευχαριστημένος

Pareto Principle 20-80



Text Mining

Entity
word1
word2

Score
score

Πόσο κοντά είναι οι λέξεις

Context
↓
LLM

Μονοπάτια

Z → Γ : ΑΒΓ (3), ΔΕΒΓ (4), ΔΑΒΓ (4)

Average Shortest Path

Six degrees of Separation

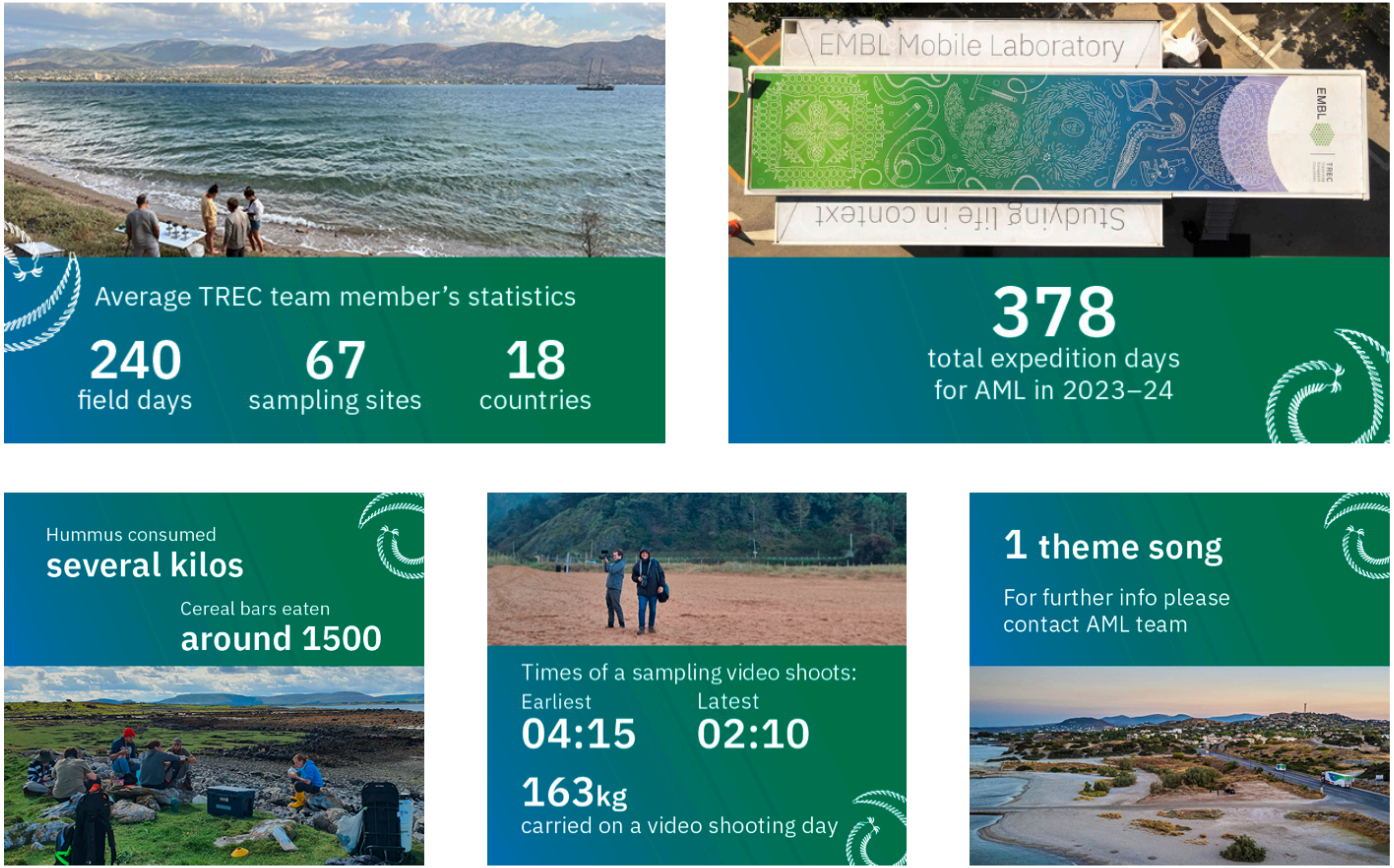
28/05/2025

Rmarkdown - Network Basics

15 minutes Break

Soil Metagenome - From sequences to microbe co-occurrences

- Take a look at Metagenomics course by Dr Lagkouvardos



Average TREC team member's statistics

240 field days

67 sampling sites

18 countries

378
total expedition days
for AML in 2023–24

Hummus consumed
several kilos

Cereal bars eaten
around 1500

Times of a sampling video shoots:

Earliest **04:15**

Latest **02:10**

163kg
carried on a video shooting day

1 theme song

For further info please
contact AML team

The success of this complex international project is a testament to the dedication of all teams involved. Credit: Savvas Parakamian/HCMR, Gerals Pfister, Joanna Zukowska, and Kinga Lubowiecka, Creative Team/EMBL

An expedition where land meets sea

TREC expedition stops 2024

Malaga, Spain	Late February
Mallorca, Spain	Early March
Barcelona, Spain	Mid-March
Banyuls, France	Late March
Villefranche-sur-Mer, France	Early April
Pisa, Italy	Mid-April
Naples, Italy	Late April
Calabria, Italy	Early May
Lesina, Italy	Mid-May
Chioggia, Italy	Late May
Split, Croatia	Early June
Kotor, Montenegro	Mid-June
Athens, Greece	Early-July
Thrace, Greece	Mid-July

Follow the expedition via
our interactive map
https://trec.embl.de/itinerary.cgi

TREC 2023 IN NUMBERS

8
months of expedition

65
land-sea interface and selected species sampling sites (EMBL)

99
sampling sites at sea (*Tara*)

33.000
samples in total

5
sites with advanced mobile lab support

LEGEND

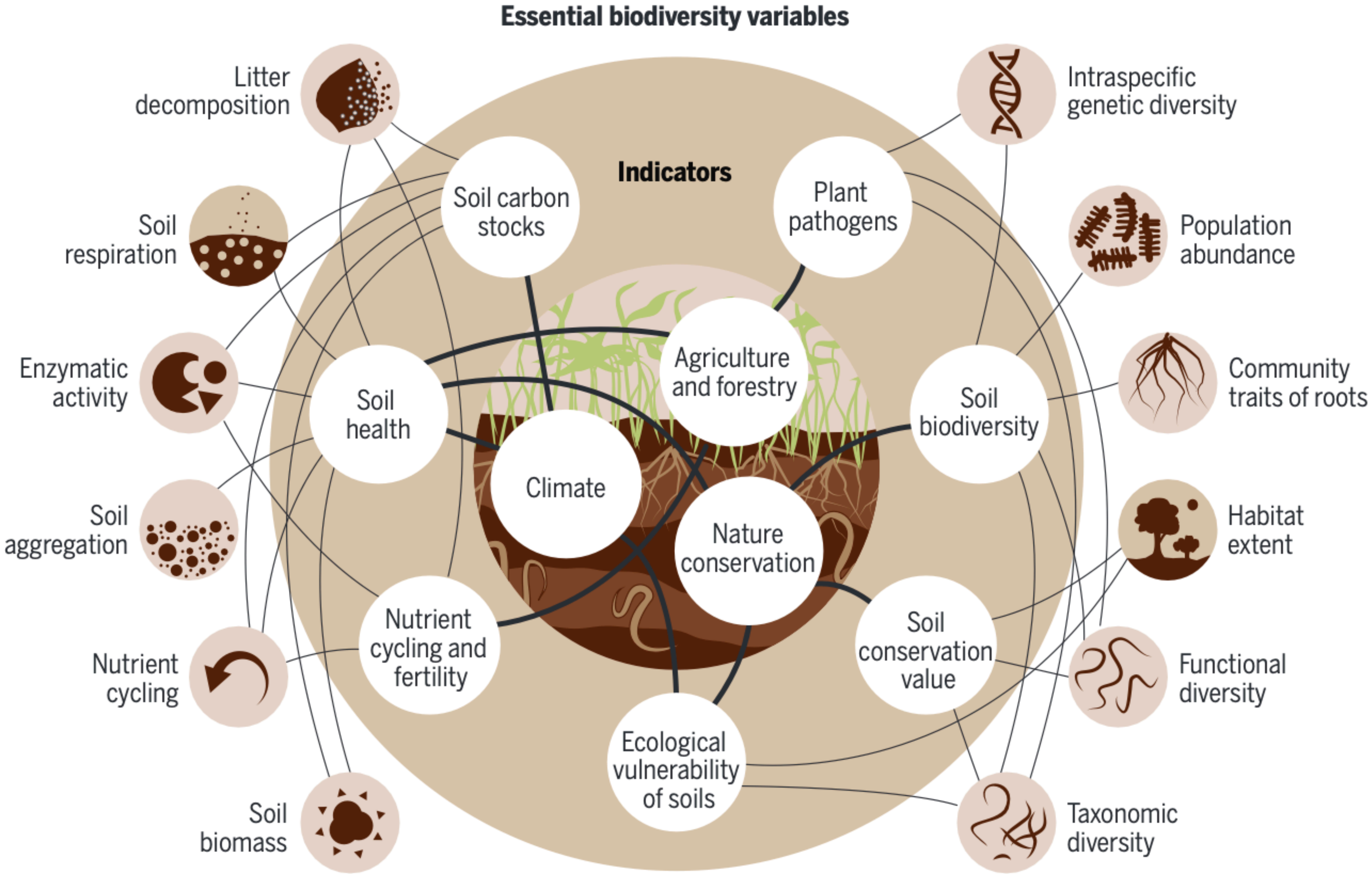
- ● Common stopovers TREC / Tara EUROPA
- ● Port calls Tara EUROPA
- 🟢 Sampling Coastal Sites
- — 2023
- — 2024

The TREC expedition began in Roscoff, France, in spring 2023 and will conclude in Thessaloniki, Greece, in July 2024. During this period, researchers from EMBL, the Tara OceanS consortium, together with the Tara Ocean Foundation, and numerous European collaborating institutes and organisations will be working at 120 sampling sites across 21 European countries.

- TREC https://www.embl.org/about/info/trec/
- Salamina https://www.youtube.com/watch?v=FcYOZWyTmms
- Psatha https://www.youtube.com/watch?v=BQ2hJBeSBwQ

Linking soil biodiversity to policy

Links between global soil essential biodiversity variables (EBVs) (outer ring) are prioritized by the Soil Biodiversity Observation Network (SoilBON) and policy sectors (center) through the use of soil ecological indicators (inner ring; table S3). Thin lines correspond to links between EBVs and soil indicators; thicker lines refer to links between each soil indicator and specific policy sectors. The EBVs for soil systems are proposed as a holistic system approach (table S2), where soil organisms are intertwined with relevant soil chemical, physical, and functional properties, contributing to overall societal well-being. See table S1 for further information on links to specific policy targets and policies. See table S2 for details of the EBVs.



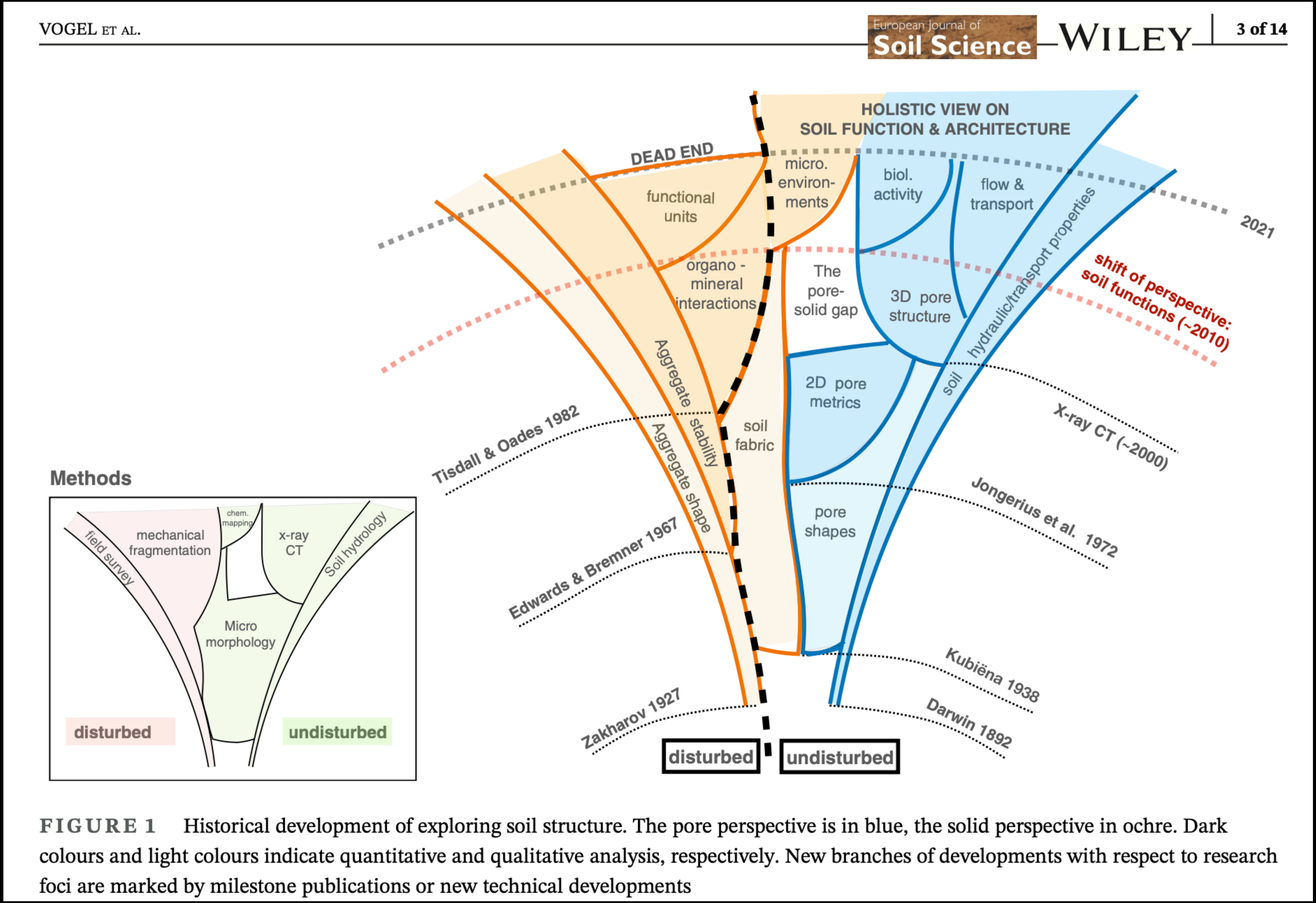
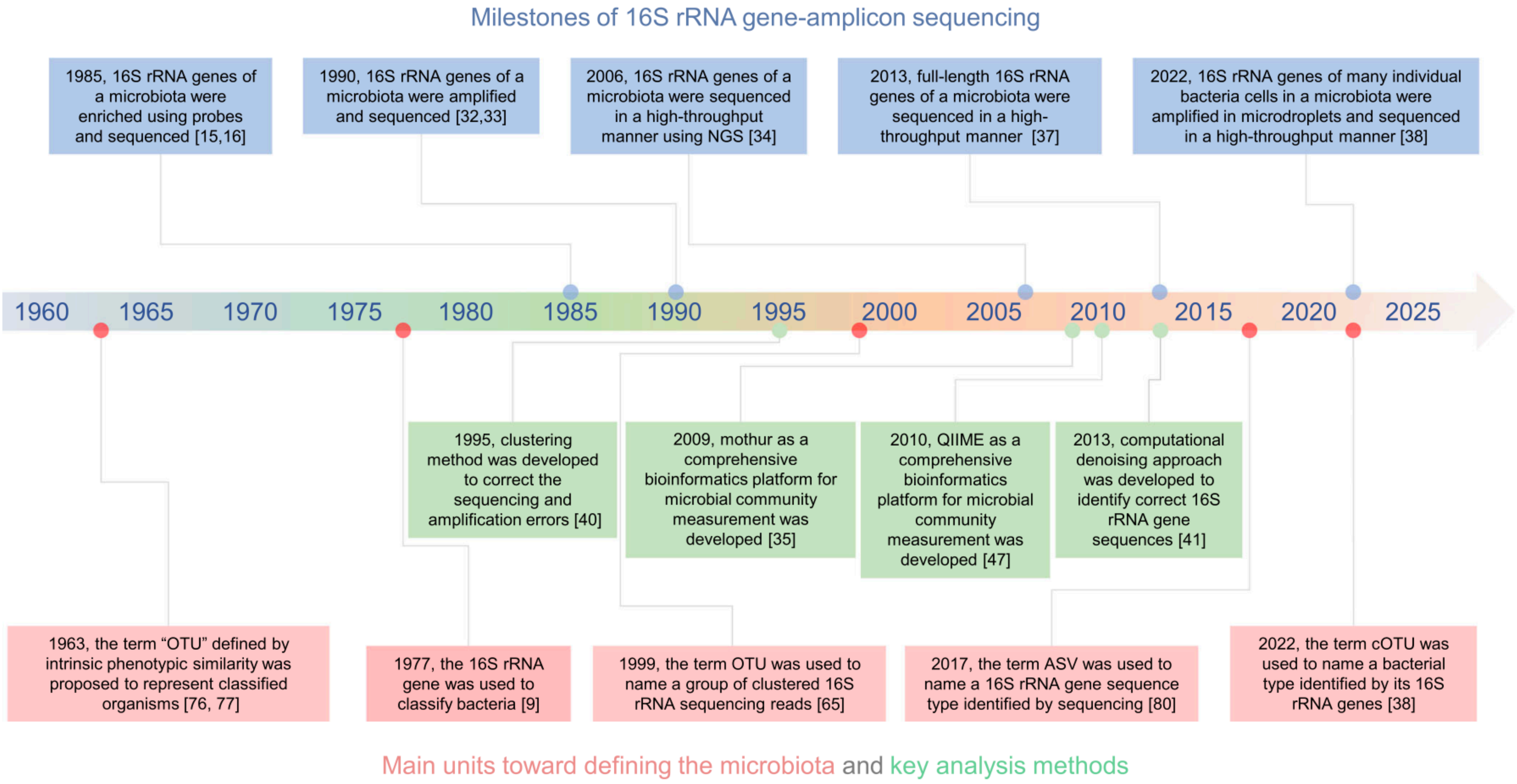


FIGURE 1 Historical development of exploring soil structure. The pore perspective is in blue, the solid perspective in ochre. Dark colours and light colours indicate quantitative and qualitative analysis, respectively. New branches of developments with respect to research foci are marked by milestone publications or new technical developments



Milestones of 16S rRNA gene-amplicon sequencing

1985, 16S rRNA genes of a microbiota were enriched using probes and sequenced [15,16]

1990, 16S rRNA genes of a microbiota were amplified and sequenced [32,33]

2006, 16S rRNA genes of a microbiota were sequenced in a high-throughput manner using NGS [34]

2013, full-length 16S rRNA genes of a microbiota were sequenced in a high-throughput manner [37]

2022, 16S rRNA genes of many individual bacteria cells in a microbiota were amplified in microdroplets and sequenced in a high-throughput manner [38]

1995, clustering method was developed to correct the sequencing and amplification errors [40]

2009, mothur as a comprehensive bioinformatics platform for microbial community measurement was developed [35]

2010, QIIME as a comprehensive bioinformatics platform for microbial community measurement was developed [47]

2013, computational denoising approach was developed to identify correct 16S rRNA gene sequences [41]

1963, the term "OTU" defined by intrinsic phenotypic similarity was proposed to represent classified organisms [76, 77]

1977, the 16S rRNA gene was used to classify bacteria [9]

1999, the term OTU was used to name a group of clustered 16S rRNA sequencing reads [65]

2017, the term ASV was used to name a 16S rRNA gene sequence type identified by sequencing [80]

2022, the term cOTU was used to name a bacterial type identified by its 16S rRNA genes [38]

Main units toward defining the microbiota and key analysis methods

FIGURE 1 History of 16S rRNA gene-amplicon sequencing, key analysis methods, and related classification units. ASV, amplicon sequence variants; cOTU, cell-based operational taxonomic unit; NGS, next-generation sequencing; OTU, operational taxonomic unit; QIIME, quantitative insights into microbial ecology; rRNA, ribosomal RNA.

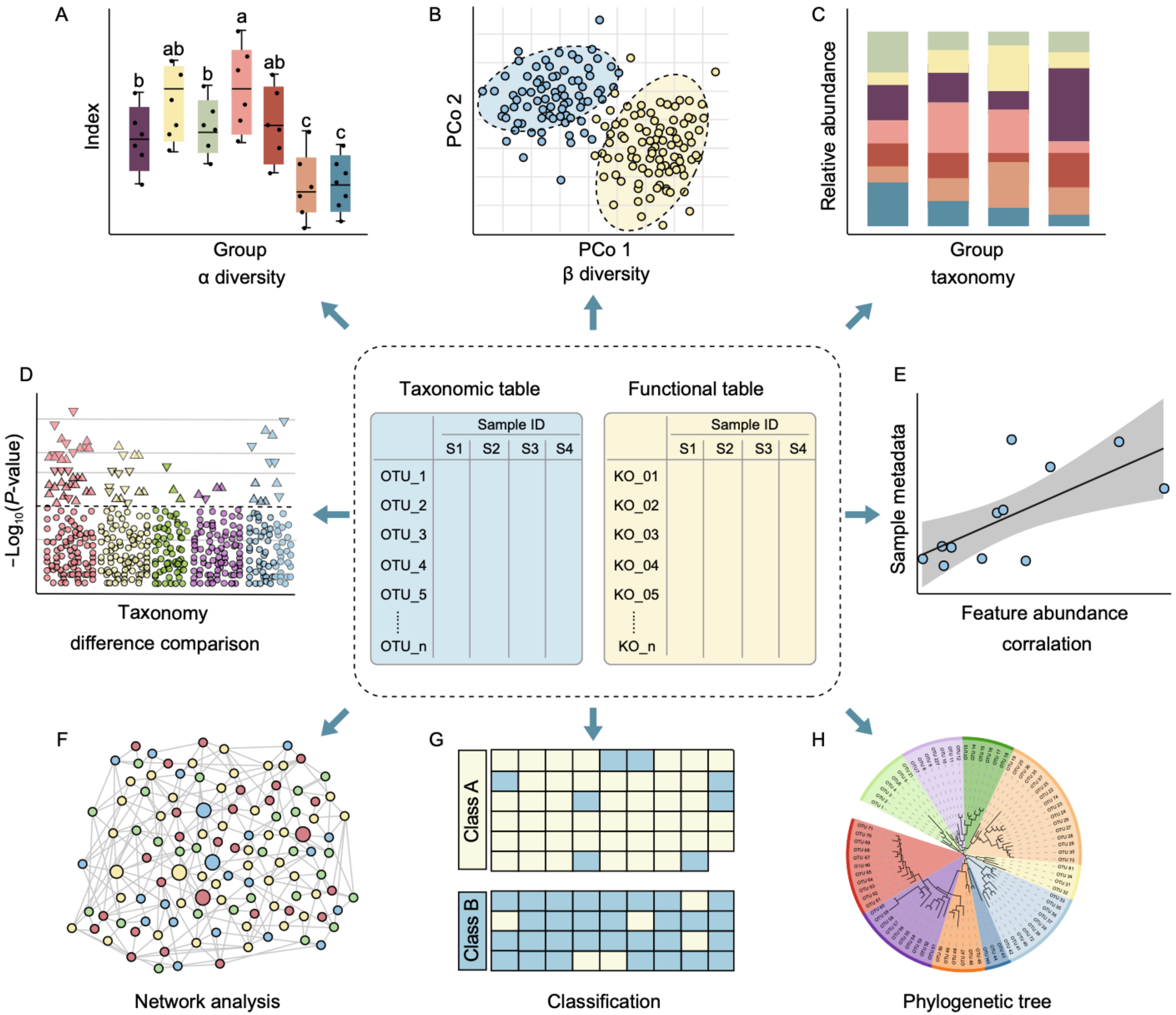


Figure 3. Overview of statistical and visualization methods for feature tables. Downstream analysis of microbiome feature tables, including alpha/beta-diversity (A/B), taxonomic composition (C), difference comparison (D), correlation analysis (E), network analysis (F), classification of machine learning (G), and phylogenetic tree (H). Please see Table 2 for more details.

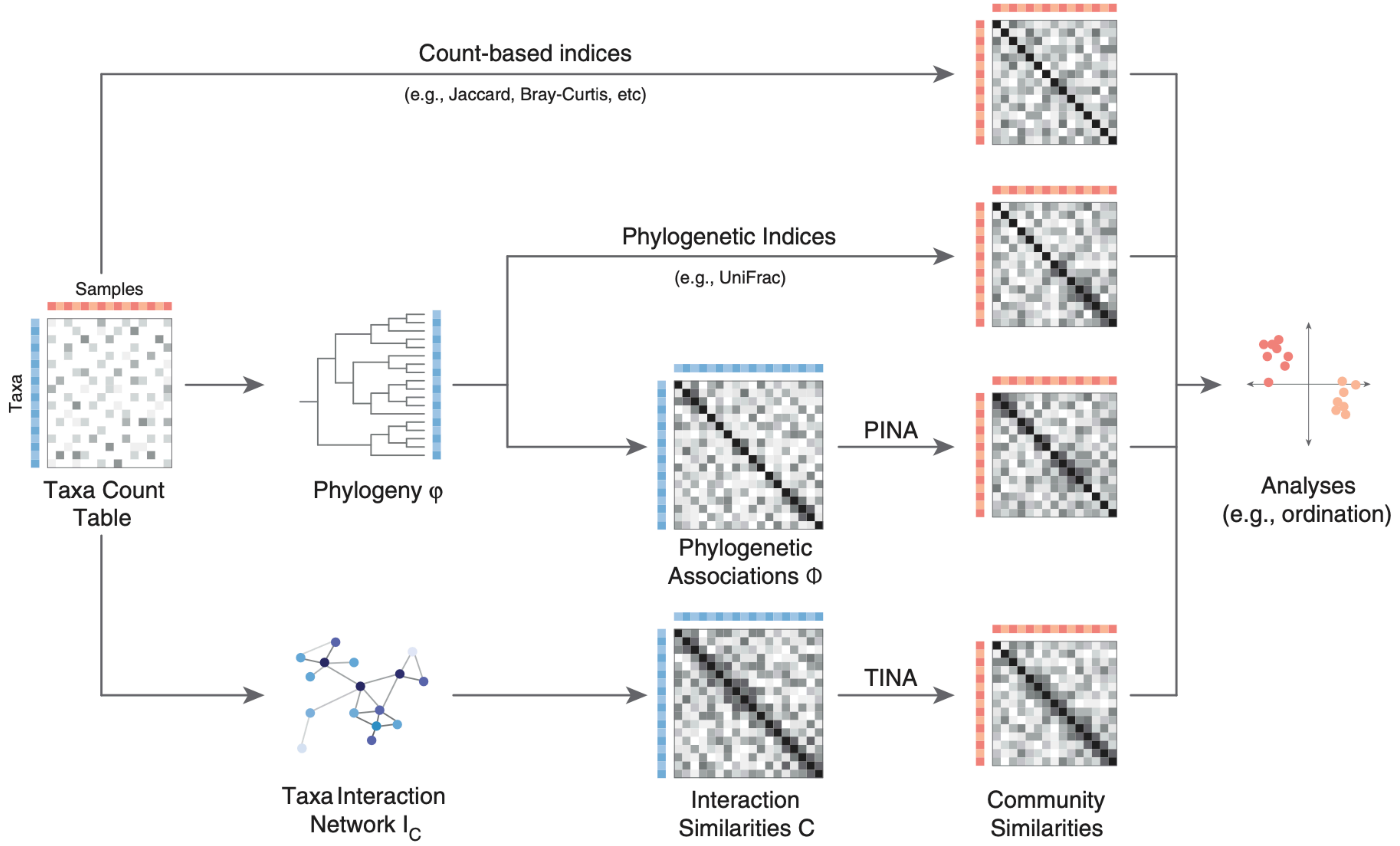


Figure 1 Overview of different approaches to quantifying community similarity. Based on a taxa-sample count table, traditional count-based indices such as Jaccard and Bray–Curtis quantify community similarity from the overlap in taxa composition (upper branch). In contrast, phylogenetic indices such as UniFrac take into account taxa relationships, quantifying community similarity as shared evolutionary history, based on taxa phylogeny (middle branch). Our proposed Taxa INteraction-Adjusted (TINA) and Phylogenetic INteraction-Adjusted (PINA) indices, in contrast, take into account similarities on a taxa co-occurrence network, codified in an interaction similarity matrix C, or in terms of cophenetic phylogenetic distances, represented in a phylogenetic association matrix Φ.

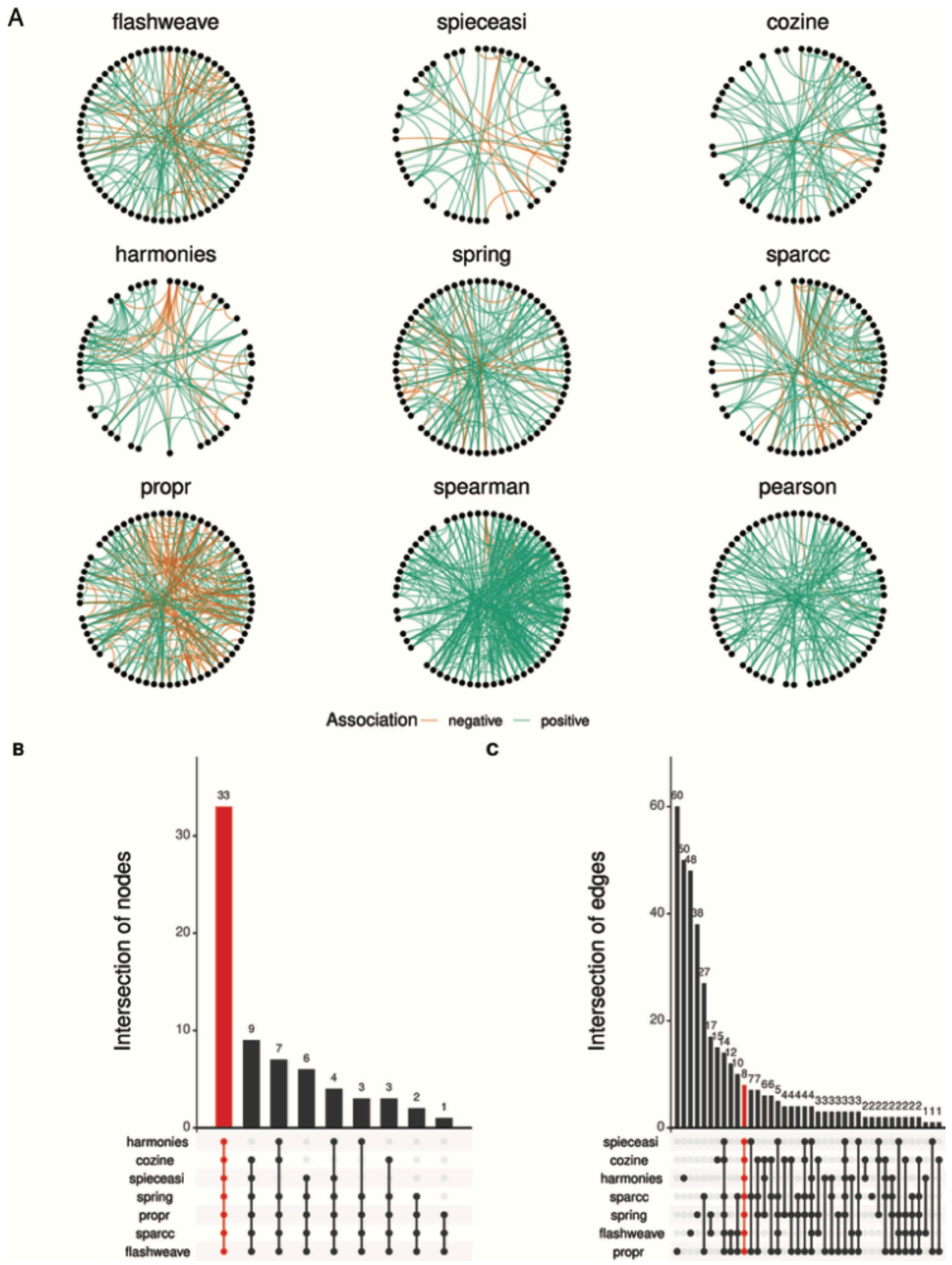
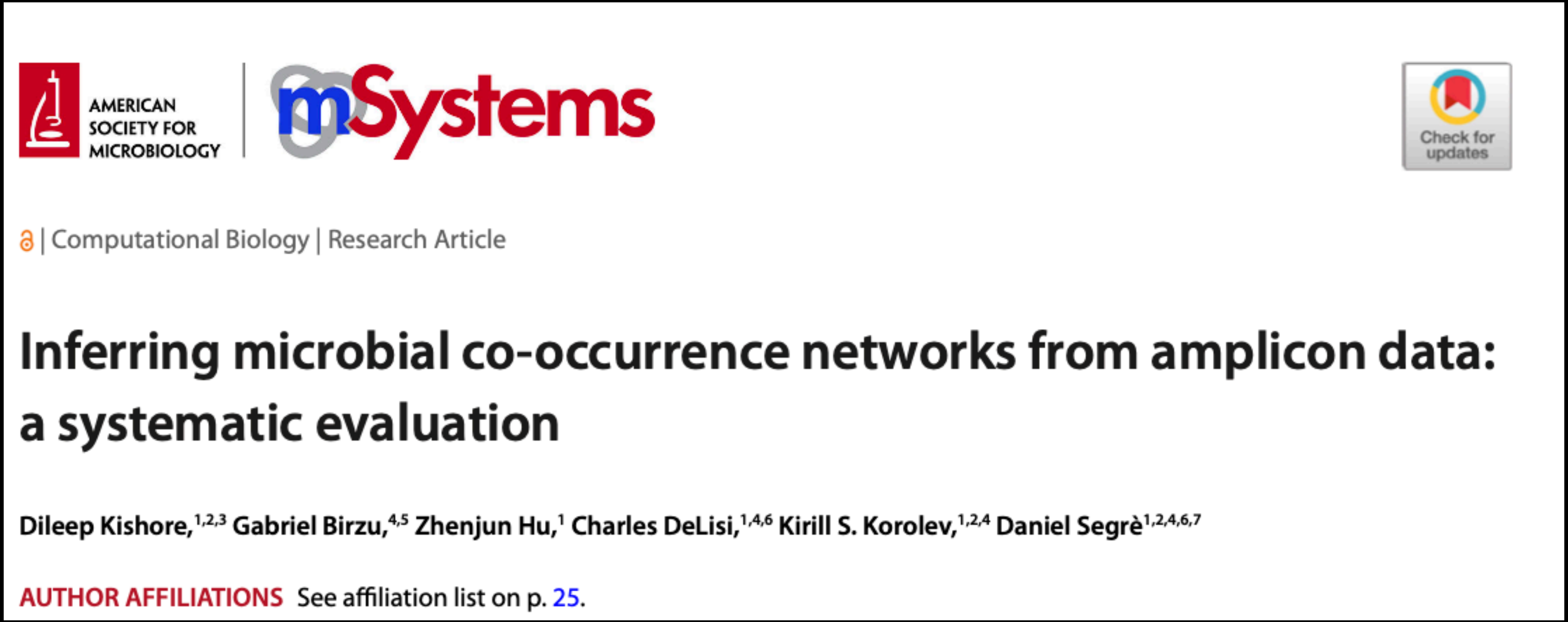


FIG 4 Networks generated using different network inference methods show notable differences in terms of edge-density and connectivity. (A) The nine different networks generated by the different network inference methods (excluding mLDM). The nodes for each network (representing taxa) are arranged in the same positions in a circular layout, and the differences in the connections can be directly visualized and compared. The green links are positive associations, and the orange links represent negative associations. The networks look dissimilar and vary widely in terms of connectivity, and it is notable that the correlation-based methods generally produce networks with higher edge-densities. A threshold of 0.3 was set for the correlation-based methods (sparcc, propr, spearman, and pearson), and a threshold of 0.01 was set for the direct association methods (flashweave, spieceasi, cozine, harmonies, and spring). (B) The node overlap Upset plot indicates that all the networks have a large proportion of common nodes involved in connections (33 out of 68). Conversely (C), the edge overlap Upset plot shows that a very small fraction of these connections are actually shared (8 out of 202). The data used in this analysis were the healthy stool samples from the FMT data set. mLDM is not shown in the comparisons because the algorithm failed to converge for the particular network combination used here (default setting of the MiCoNE pipeline).



AMERICAN SOCIETY FOR MICROBIOLOGY | mSystems

| Computational Biology | Research Article

Inferring microbial co-occurrence networks from amplicon data: a systematic evaluation

Dileep Kishore,[1,2,3] Gabriel Birzu,[4,5] Zhenjun Hu,[1] Charles DeLisi,[1,4,6] Kirill S. Korolev,[1,2,4] Daniel Segrè[1,2,4,6,7]

AUTHOR AFFILIATIONS See affiliation list on p. 25.

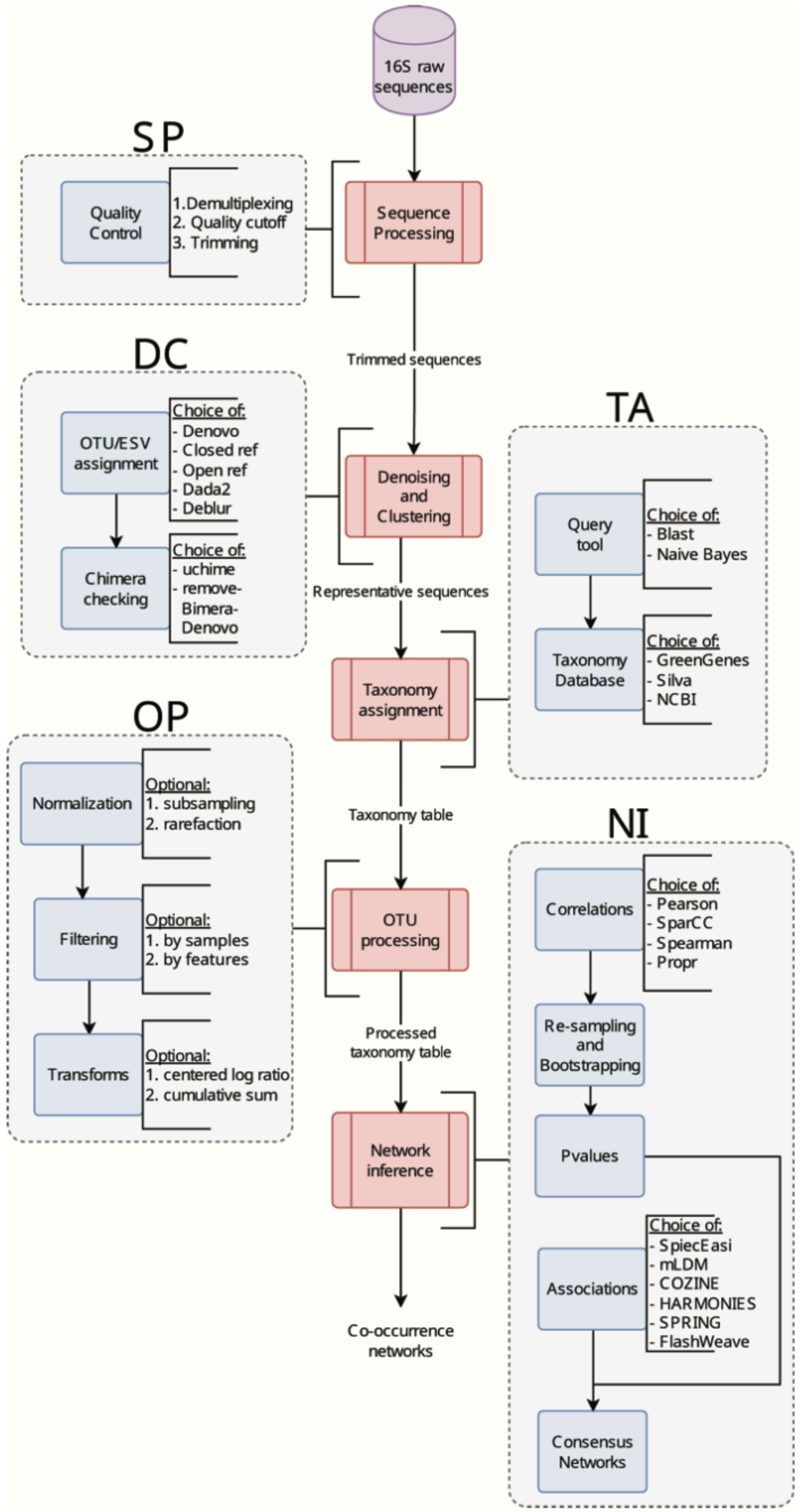


FIG 1 The workflow of the MiCoNE pipeline. The steps of the workflow can be broken down into five major groups: (SP) sequence processing, (DC) denoising and clustering, (TA) taxonomy assignment, (OP) OTU and ESV processing, and (NI) network inference. Each step incorporates several processes (blue boxes), each of which, in turn, has several alternative algorithms for the same task (indicated by the text to the right of the blue boxes). Each arrow describes the data that is being passed from one step to another. The inputs to the pipeline are 16S rRNA sequencing reads, and the final output is the consensus network generated from the inferred co-occurrence networks. For details on each process and the different outputs, see Methods.

Microbiome Datasets Are Compositional: And This Is Not Optional

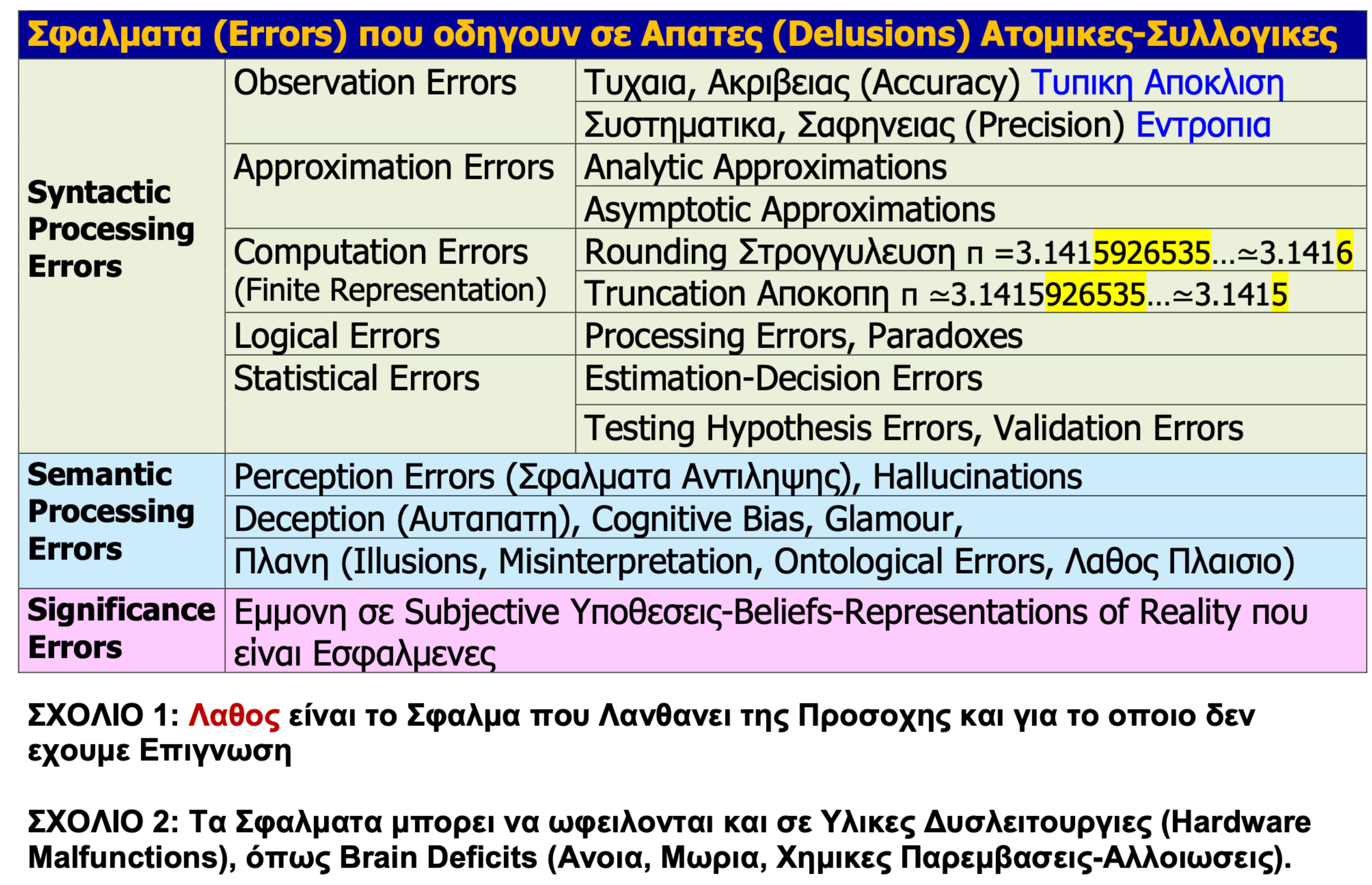
Gregory B. Gloor[1], Jean M. Macklaim[1], Vera Pawlowsky-Glahn[2] and Juan J. Egozcue[3]*

[1] Department of Biochemistry, University of Western Ontario, London, ON, Canada, [2] Departments of Computer Science, Applied Mathematics, and Statistics, Universitat de Girona, Girona, Spain, [3] Department of Applied Mathematics, Universitat Politècnica de Catalunya, Barcelona, Spain

16s amplicon workflow

Or How I Learned to Stop Worrying and Love the Errors

1. **Current Challenges and Pitfalls in Soil Metagenomics**
2. Pitfalls in the statistical analysis of microbiome amplicon sequencing data
3. **Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform**
4. The choice of the DNA extraction method may influence the outcome of the soil microbial community structure analysis
5. **Biases in Prokaryotic Community Amplicon Sequencing Affected by DNA Extraction Methods in Both Saline and Non-saline Soil**
6. Examining Sources of Error in PCR by Single-Molecule Sequencing, Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies
7. Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies
8. **Groundtruthing Next-Gen Sequencing for Microbial Ecology–Biases and Errors in Community Structure Estimates from PCR Amplicon Pyrosequencing**
9. Examining Sources of Error in PCR by Single- Molecule Sequencing
10. Reducing the Effects of PCR Amplification and Sequencing Artifacts on 16S rRNA-Based Studies
11. Batch effects removal for microbiome data via conditional quantile regression
12. Parsing ecological signal from noise in next generation amplicon sequencing
13. Comparison of Oxford Nanopore Technologies and Illumina MiSeq sequencing with mock communities and agricultural soil
14. Insight into biases and sequencing errors for amplicon sequencing with the Illumina MiSeq platform
15. **Ten quick tips for effective dimensionality reduction**
16. **Double indexing overcomes inaccuracies in multiplex sequencing on the Illumina platform**
17. Handling of targeted amplicon sequencing data focusing on index hopping and demultiplexing using a nested metabarcoding approach in ecology
18. Normalization and microbial differential abundance strategies depend upon data characteristics
19. Analysis of microbial compositions/ a review of normalization and differential abundance analysis
20. Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data
21. Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data
22. Broadscale Ecological Patterns Are Robust to Use of Exact Sequence Variants versus Operational Taxonomic Units
23. **Ranking the biases: The choice of OTUs vs. ASVs in 16S rRNA amplicon data analysis has stronger effects on diversity measures than rarefaction and OTU identity threshold**
24. Uniform Manifold Approximation and Projection (UMAP) Reveals Composite Patterns and Resolves Visualization Artifacts in Microbiome Data
25. **Blocking Factors and Hypothesis Tests in Ecology: Is Your Statistics Text Wrong?**
26. **Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations**
27. **Parsing ecological signal from noise in next generation amplicon sequencing**
28. **Batch effects removal for microbiome data via conditional quantile regression**
29. Exact sequence variants should replace operational taxonomic units in marker-gene data analysis
30. Amplicon Sequence Variants Artificially Split Bacterial Genomes into Separate Clusters
31. **A field guide for the compositional analysis of any-omics data**
32. A family of interaction-adjusted indices of community similarity
33. Analysis of compositions of microbiomes with bias correction
34. Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data
35. **Microbiome Datasets Are Compositional: And This Is Not Optional**
36. Microbiome differential abundance methods produce different results across 38 datasets
37. Normalization and microbial differential abundance strategies depend upon data characteristics
38. Improved normalization of species count data in ecology by scaling with ranked subsampling (SRS)/ application to microbial communities
39. **From hairballs to hypotheses–biological insights from microbial networks**
40. Inferring microbial co-occurrence networks from amplicon data: a systematic evaluation
41. Rapid Inference of Direct Interactions in Large-Scale Ecological Networks from Heterogeneous Microbial Sequencing Data
42. **Phylogenies of the 16S rRNA gene and its hypervariable regions lack concordance with core genome phylogenies**



Σφαλματα (Errors) που οδηγουν σε Απατες (Delusions) Ατομικες-Συλλογικες

Syntactic Processing Errors	Observation Errors	Τυχαια, Ακριβειας (Accuracy) Τυπικη Αποκλιση
		Συστηματικα, Σαφηνειας (Precision) Εντροπια
	Approximation Errors	Analytic Approximations
		Asymptotic Approximations
	Computation Errors (Finite Representation)	Rounding Στρογγυλευση $\pi = 3.1415926535\ldots \simeq 3.1416$
		Truncation Αποκοπη $\pi \simeq 3.1415926535\ldots \simeq 3.1415$
	Logical Errors	Processing Errors, Paradoxes
	Statistical Errors	Estimation-Decision Errors
		Testing Hypothesis Errors, Validation Errors
Semantic Processing Errors	Perception Errors (Σφαλματα Αντιληψης), Hallucinations	
	Deception (Αυταπατη), Cognitive Bias, Glamour,	
	Πλανη (Illusions, Misinterpretation, Ontological Errors, Λαθος Πλαισιο)	
Significance Errors	Εμμονη σε Subjective Υποθεσεις-Beliefs-Representations of Reality που είναι Εσφαλμενες	

ΣΧΟΛΙΟ 1: Λαθος είναι το Σφαλμα που Λανθανει της Προσοχης και για το οποιο δεν εχουμε Επιγνωση

ΣΧΟΛΙΟ 2: Τα Σφαλματα μπορει να ωφειλονται και σε Υλικες Δυσλειτουργιες (Hardware Malfunctions), όπως Brain Deficits (Ανοια, Μωρια, Χημικες Παρεμβασεις-Αλλοιωσεις).

Slide from
Prof I. Antoniou

Island Sampling Day

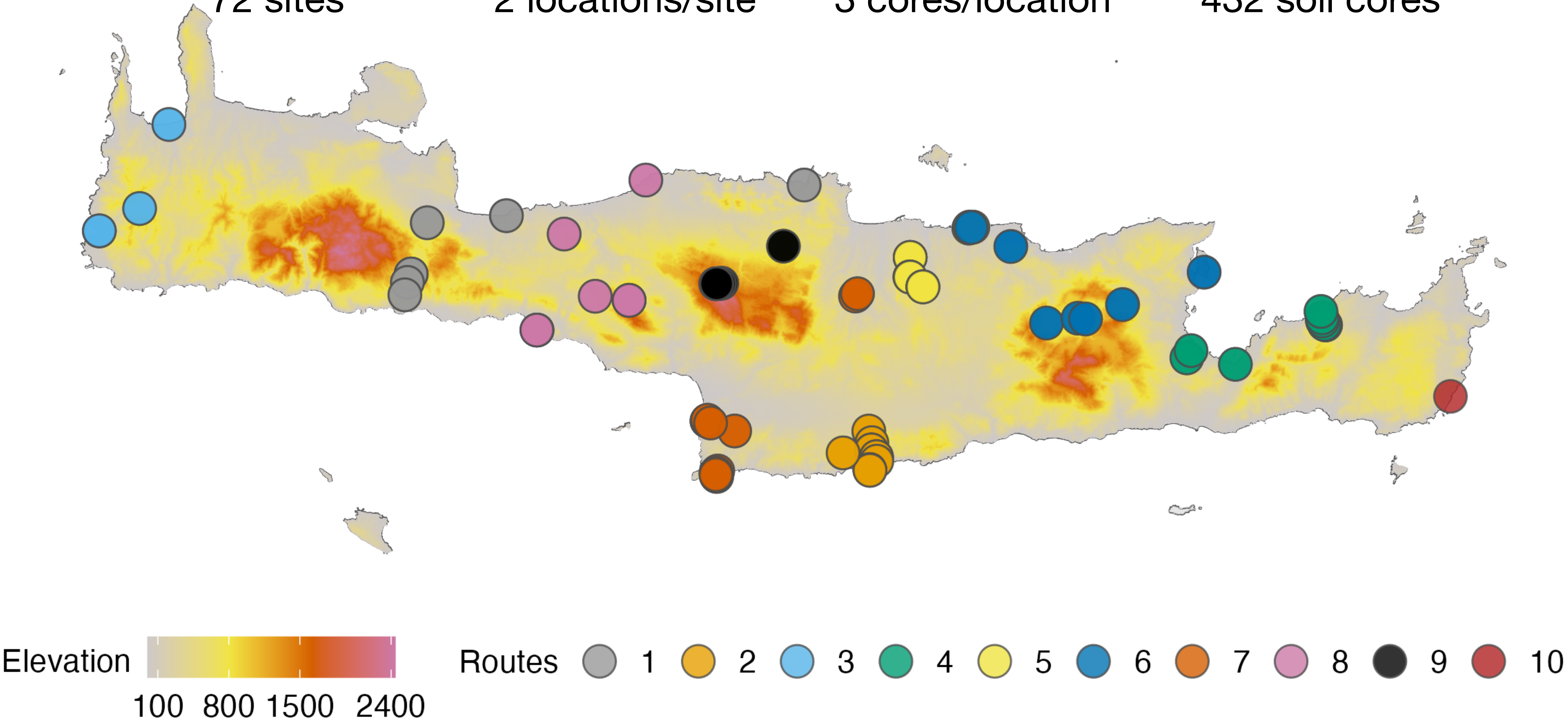
Crete

1 day
72 sites

26 participants
2 locations/site

10 routes
3 cores/location

2400 km
432 soil cores



Island Sampling Day 2016

One Day, One Island - 15th June 2016, Crete - GSC18

16s rRNA amplicon study

26 participants, 10 teams/routes

72 predefined locations across the island of Crete

Second time point in 2022, same locations

Sampling

Topsoil cores

72 sites (2 sub-sites in each)

Each sub-site 3 replicates

DNA - Chemistry - HCMR

Designed for Citizen science by experts

Single day event to avoid seasonality

Capture as much ecosystem diversity as possible

Sequences

- **Open data with immediate release**
- Available at ENA project PRJEB21776
- 140 samples available (Illumina HiSeq 2500) using Amplicon 16s rRNA V3V4 regions
- 3 Samples NOT sequenced
- Dr Lynn Schriml, University of Maryland

Reads	60.6×10^6
Ns	76.000
Filtered	50.1×10^6
denoisedF	45.9×10^6
denoisedR	48.5×10^6
merged	35.0×10^6
nonchim	33.3×10^6

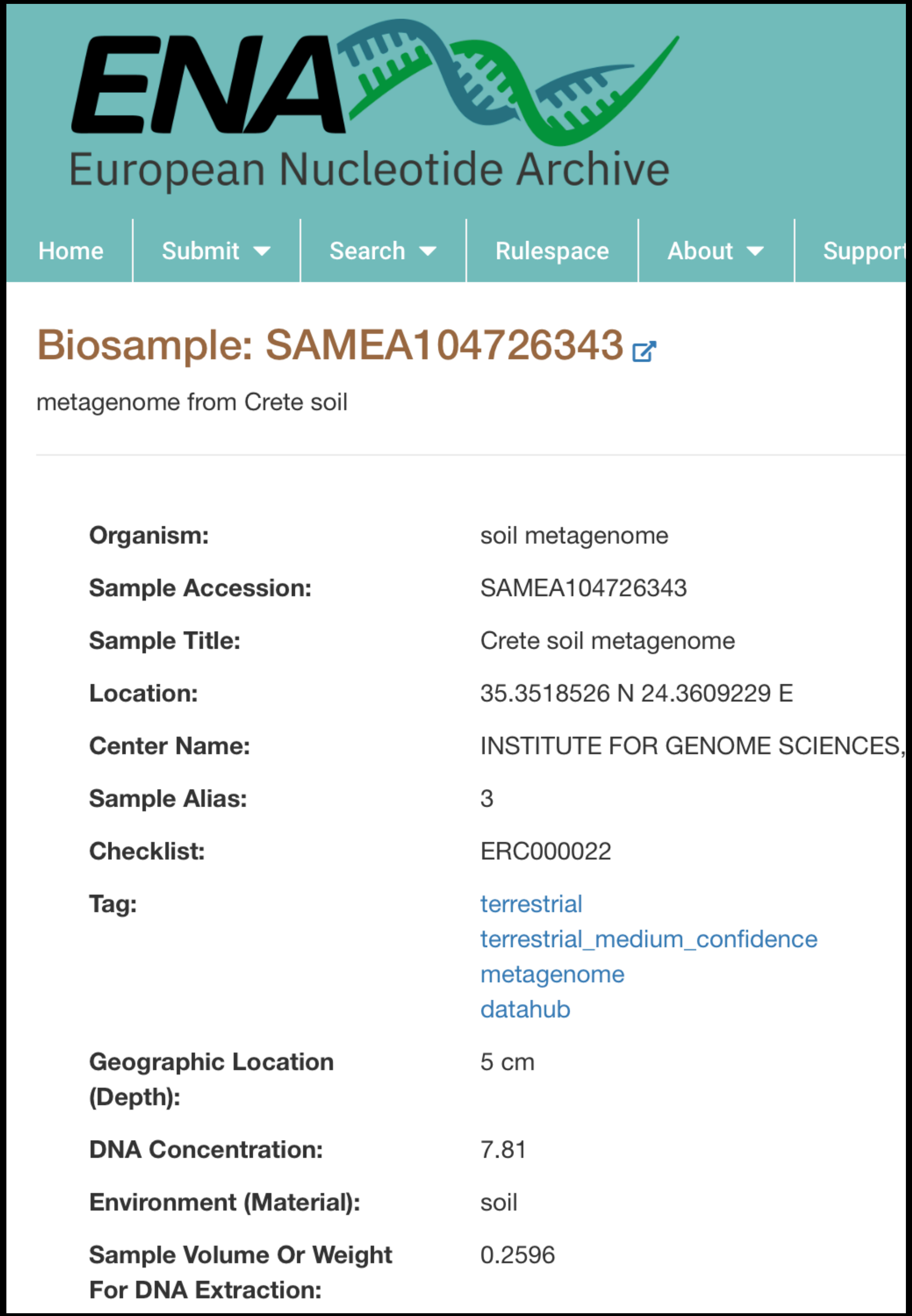
Metadata

Onsite measurements
GPS coordinates
nearest plant
Etc

total nitrogen
water content
total organic carbon
pH

Dr Stephanie A Yarwood, University of Meryland

FAIR Data by Design - Findable - Accessible - Interoperable - Reusable



Biosample: SAMEA104726343

metagenome from Crete soil

Organism:	soil metagenome
Sample Accession:	SAMEA104726343
Sample Title:	Crete soil metagenome
Location:	35.3518526 N 24.3609229 E
Center Name:	INSTITUTE FOR GENOME SCIENCES,
Sample Alias:	3
Checklist:	ERC000022
Tag:	terrestrial terrestrial_medium_confidence metagenome datahub
Geographic Location (Depth):	5 cm
DNA Concentration:	7.81
Environment (Material):	soil
Sample Volume Or Weight For DNA Extraction:	0.2596

ISD Crete - Reproducible analysis

GET

API
sequences (fastq)
metadata (xml)

ENA
European Nucleotide Archive

INFER

DADA2
Amplicon Sequencing. **Exactly.**

PEMA
a pipeline for eDNA metabarcoding analysis

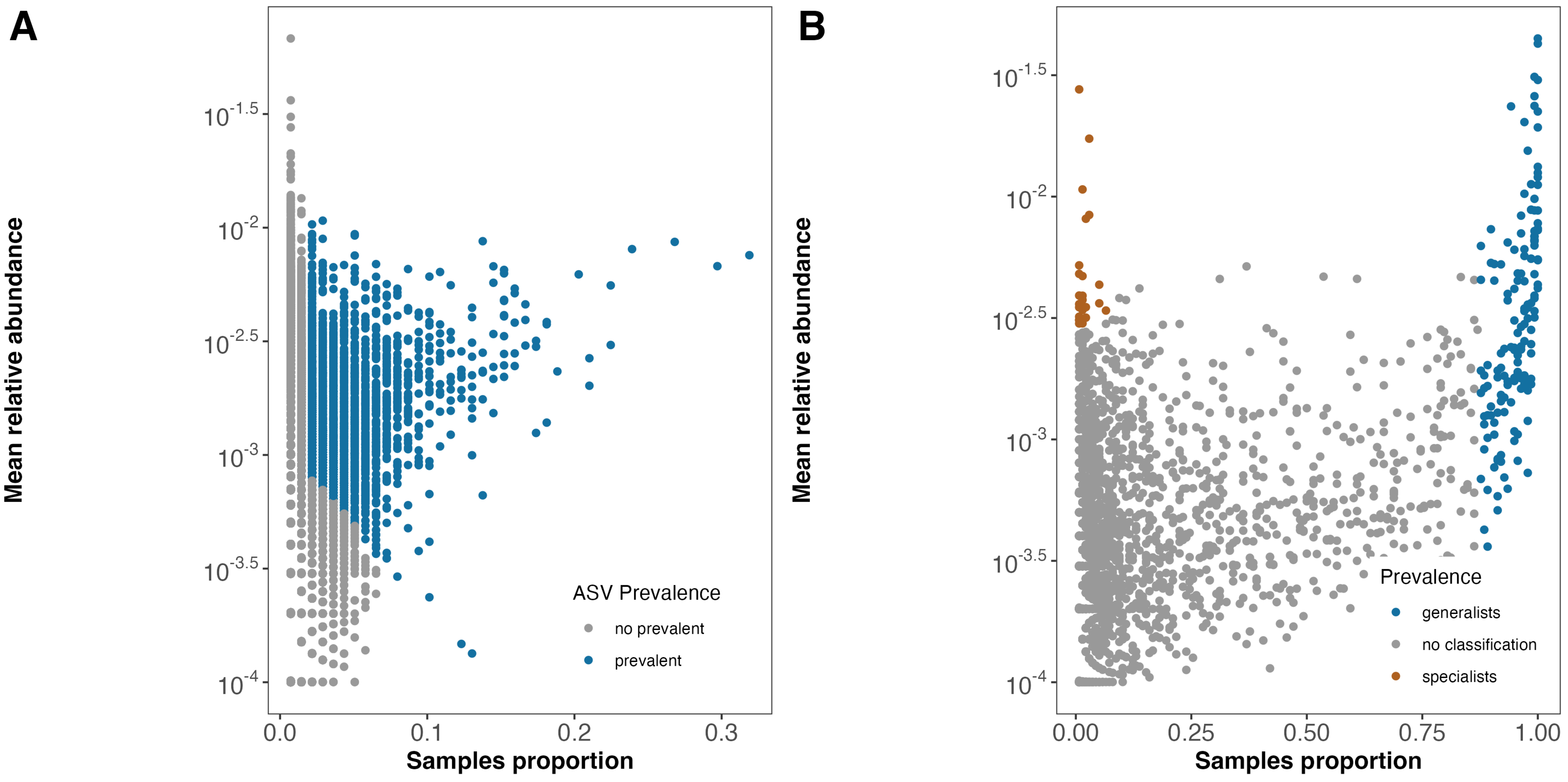
ANALYZE

Drivers
Ordination
Figures
Community matrix
Diversity
Soil Metadata
Maps
Taxonomy

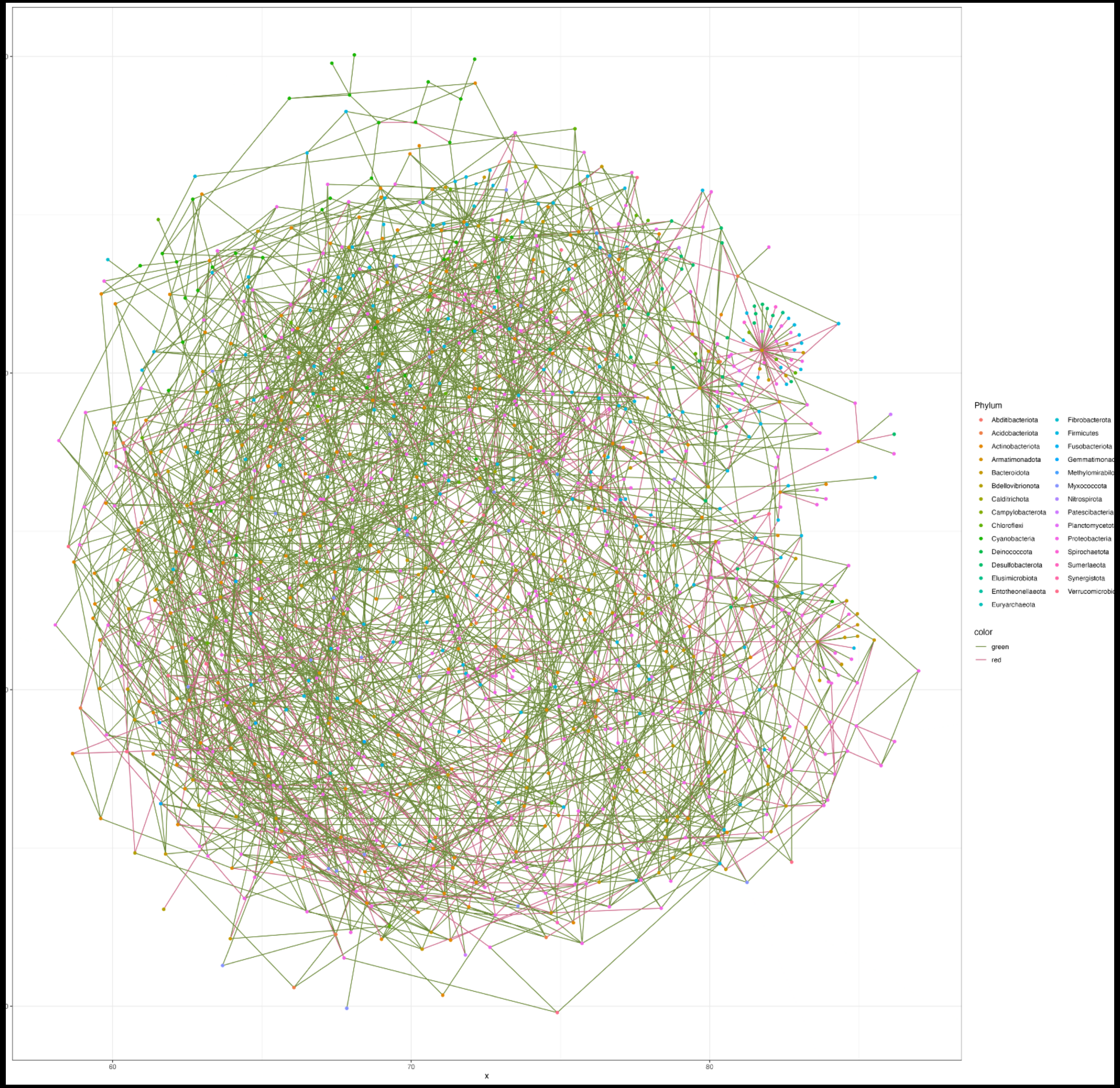
Taxonomic assignment

- **DADA2**
  - Taxonomy - Silva 138
  - ASVs = 239000
  - Taxa = 3102
- **PEMA (VSEARCH)**
  - Taxonomy - Silva 132
  - OTUS 6890
  - Taxa = 1057

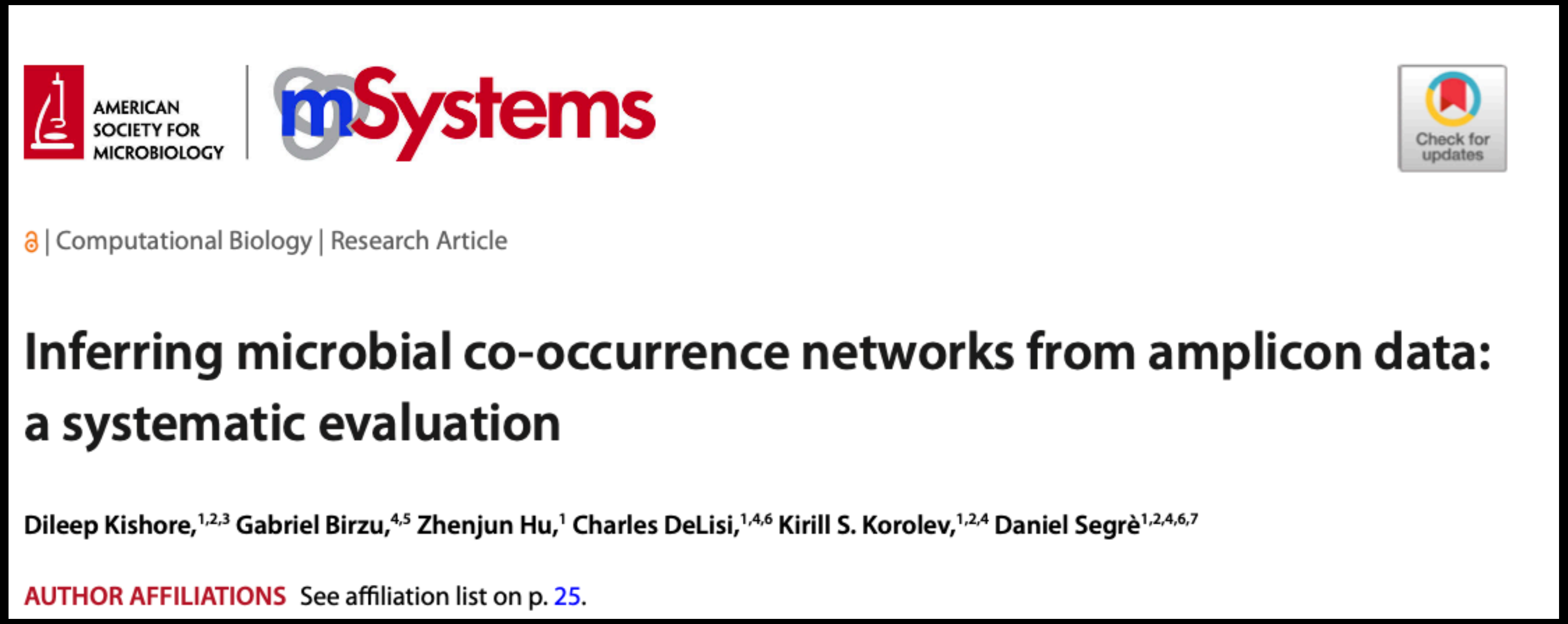
Classification depth	**DADA2**		**PEMA**	
	ASVs	**Taxa**	**OTUs**	**Taxa**
Kingdom	1974	2	284	2
Phylum	4034	33	121	15
Order	38517	193	1224	135
Class	24157	83	978	62
Family	71355	287	2319	218
Genus	90137	1166	1920	582
Species	9120	1338	44	43
Total	~ 239000	3102	6890	1057


A
Mean relative abundance
$10^{-1.5}$
10^{-2}
$10^{-2.5}$
10^{-3}
$10^{-3.5}$
10^{-4}
0.0
0.1
0.2
0.3
Samples proportion
ASV Prevalence
● no prevalent
● prevalent
B
Mean relative abundance
$10^{-1.5}$
10^{-2}
$10^{-2.5}$
10^{-3}
$10^{-3.5}$
10^{-4}
0.00
0.25
0.50
0.75
1.00
Samples proportion
Prevalence
● generalists
● no classification
● specialists

Networks



- Network analysis (FlashWeave v0.19.2)
- Focus on Richtis gorge


AMERICAN SOCIETY FOR MICROBIOLOGY | mSystems

Check for updates

| Computational Biology | Research Article

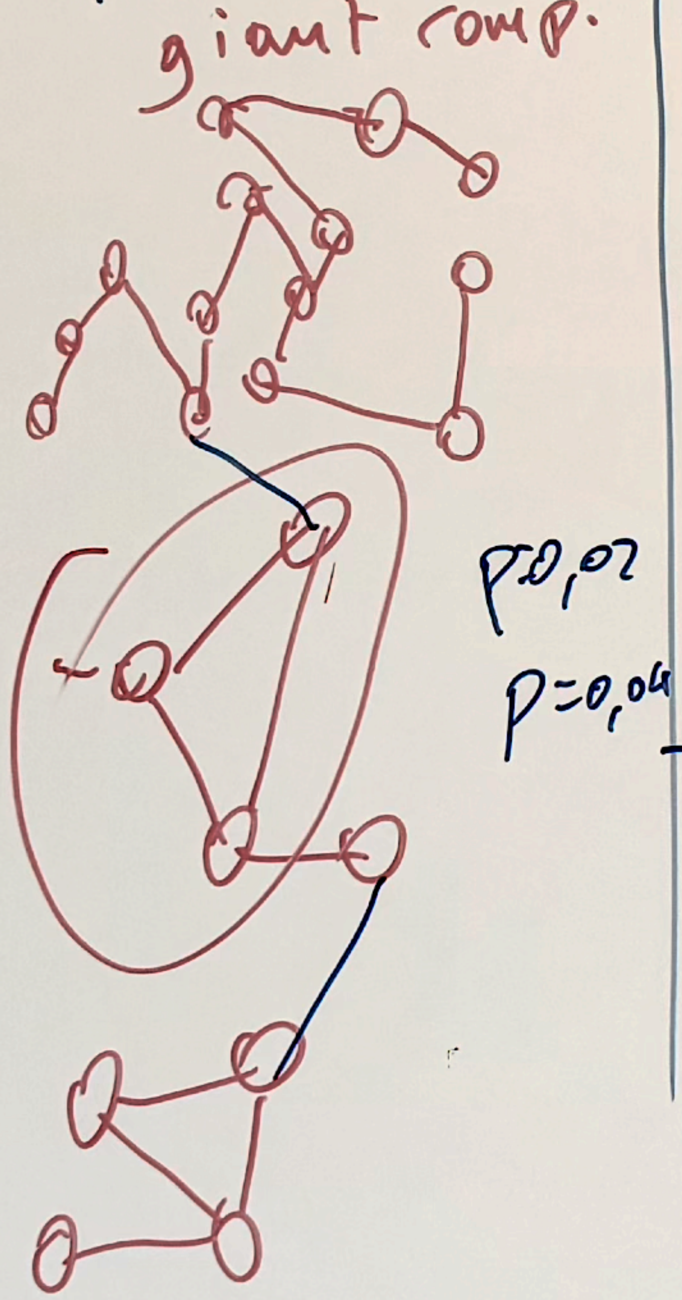
Inferring microbial co-occurrence networks from amplicon data: a systematic evaluation

Dileep Kishore,[1,2,3] Gabriel Birzu,[4,5] Zhenjun Hu,[1] Charles DeLisi,[1,4,6] Kirill S. Korolev,[1,2,4] Daniel Segrè[1,2,4,6,7]

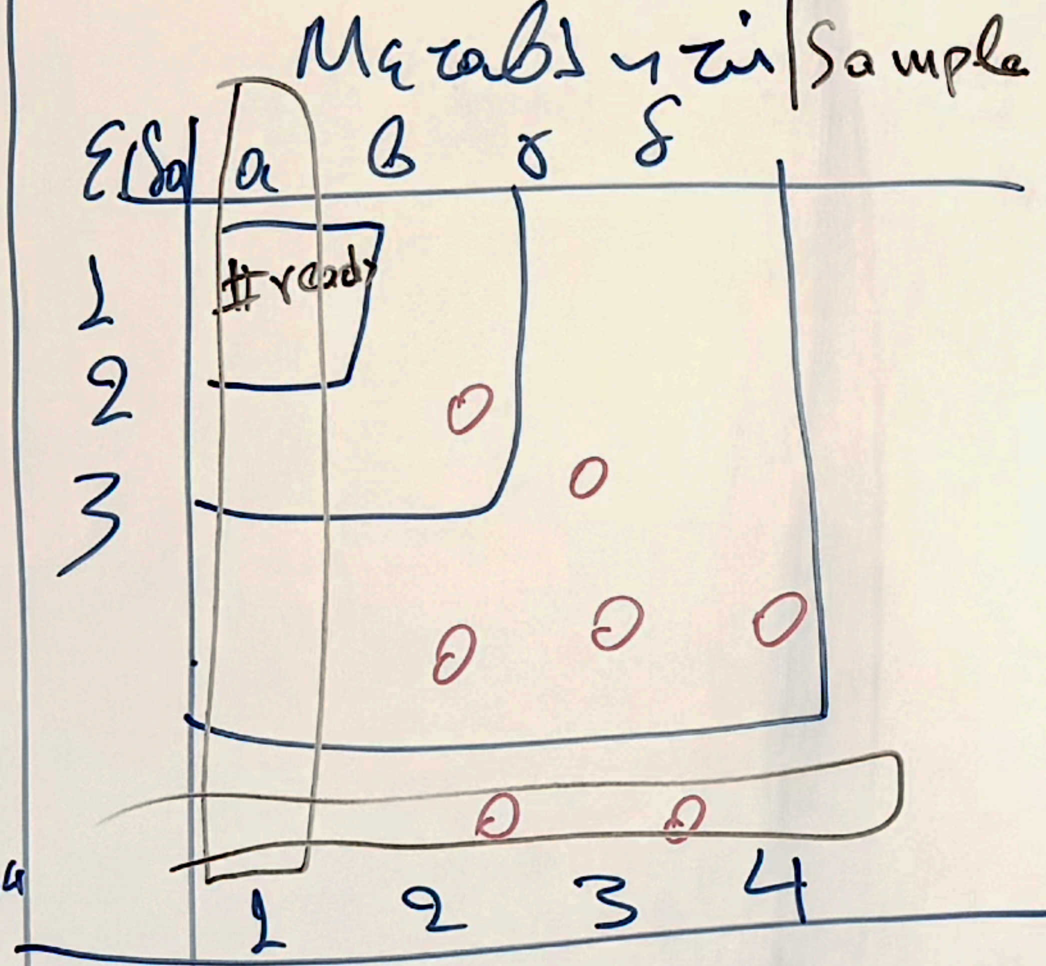
AUTHOR AFFILIATIONS See affiliation list on p. 25.

Edgelist long format

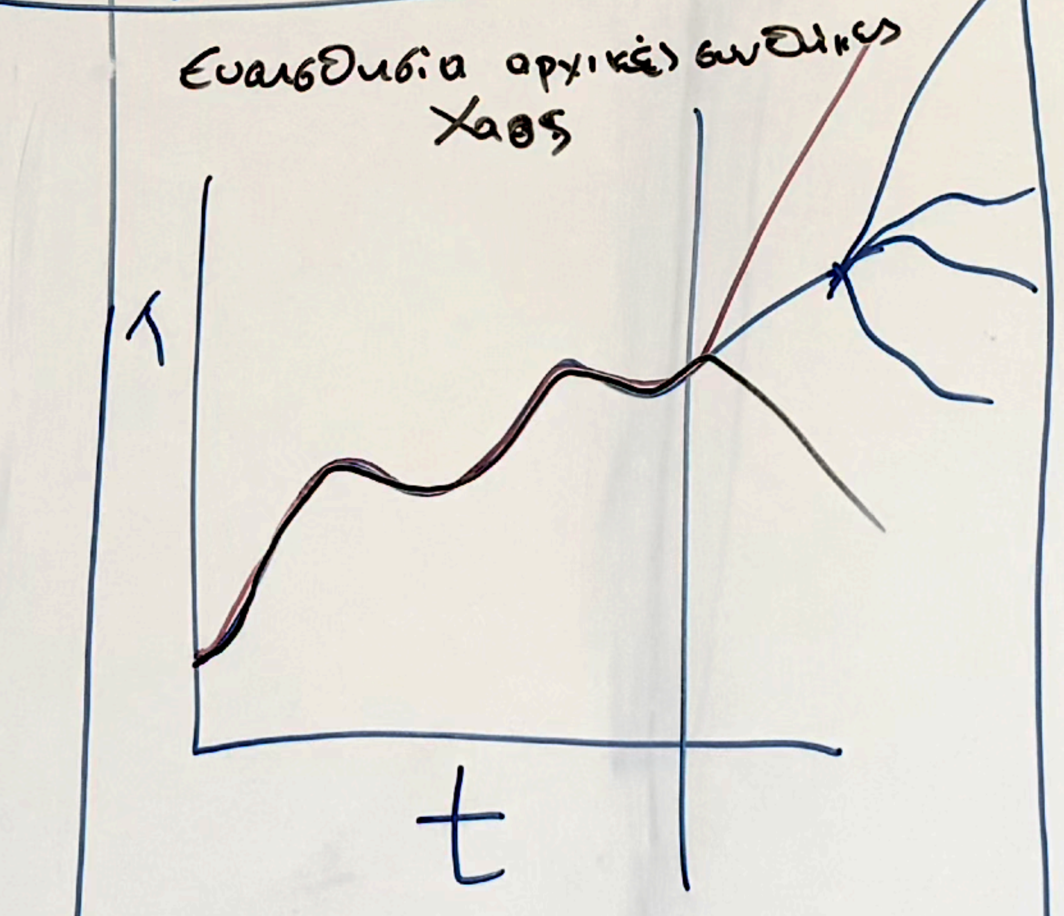
κόμβος 1 είδος οργ.	κόμβο 2. μεταβλητή φύτο	Βάρος τιμή
1	a	
1	a	
1	a	
2	a	
2	b	
3	a	
3	b	
3	b	



Wide



Ευαισθησία αρχικές συνθήκες
Χάος



Bioinformatics

κατηγορίες εργασιών
σε Metagenomics

Ποιο είναι το ερώτημα

Τι	Omics
Γιατί	
Πως	

$$g(x) = f(x) + \rho$$