Exploring Challenges and Opportunities in Inferring Spatial Genetic Patterns for Conservation Planning:

A Case Study With Reptiles Across Six Global Regions






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- Intra-specific genetic diversity (ISD) is one of the three pillars of biodiversity.
- Underlies species' adaptation and survival, ecosystem resilience, and nature's contribution to people.
- Neglected in conservation policy and spatial conservation planning.
- Shortfall of:
  - broadscale patterns of ISD
  - knowledge about which species contain distinct evolutionary lineages
  - underlying evolutionary and ecological processes
- Hinders the evaluation of the effectiveness of current Protected areas in representing ISD

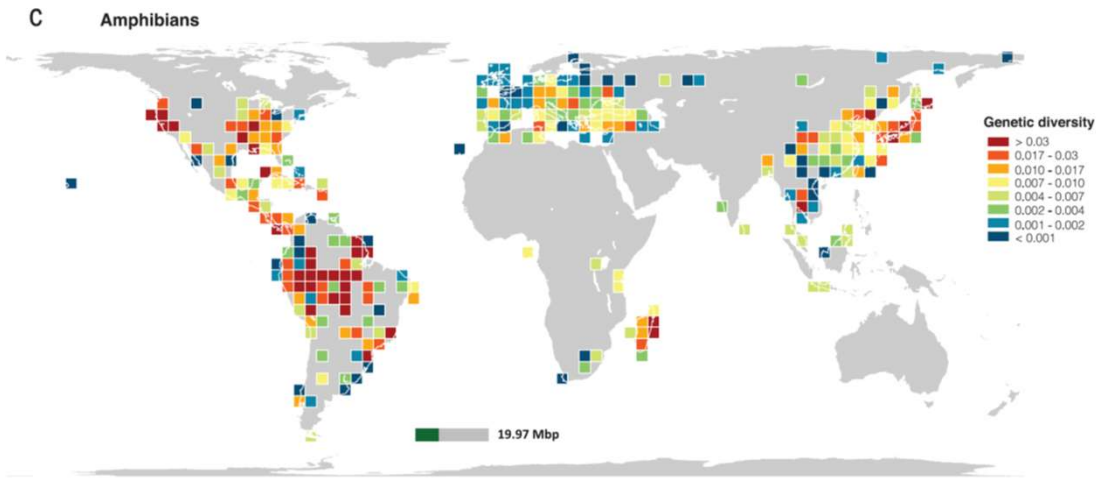
Previous attempts to map global genetic diversity with automated pipelines:

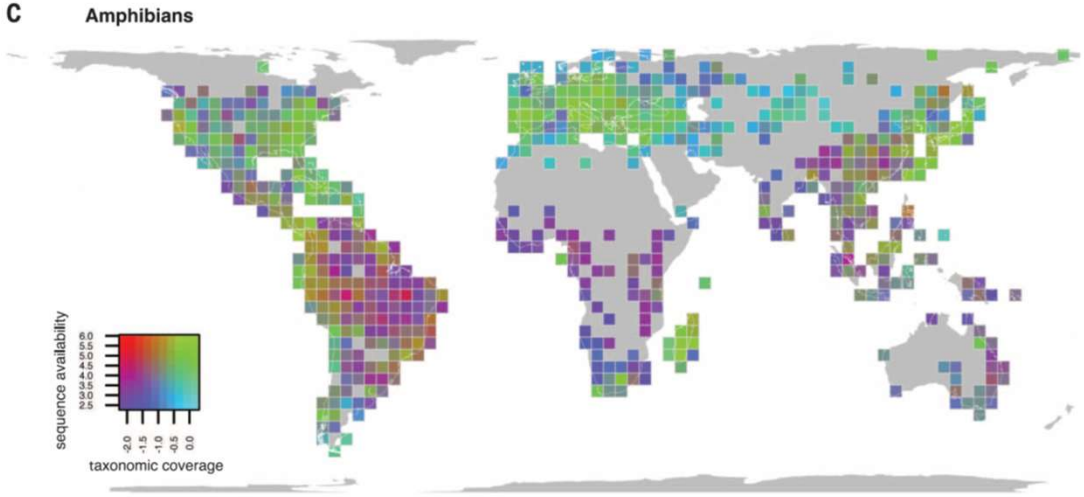
- ~ 32% of sequences georeferenced
- Large regions without sequences
- Low taxonomic coverage
- Low sequence availability per gene

An Anthropocene map of genetic diversity

Andreia Miraldo,[1*] Sen Li,[1] Michael K. Borregaard,[1] Alexander Flórez-Rodríguez,[1] Shyam Gopalakrishnan,[2] Mirnesa Rizvanovic,[1] Zhiheng Wang,[1,3] Carsten Rahbek,[1,4] Katharine A. Marske,[1] David Nogués-Bravo[1*]

Miraldo et al. (2016). *Science 353*(6307), 1532–1535. https://doi.org/10.1126/science.aaf4381



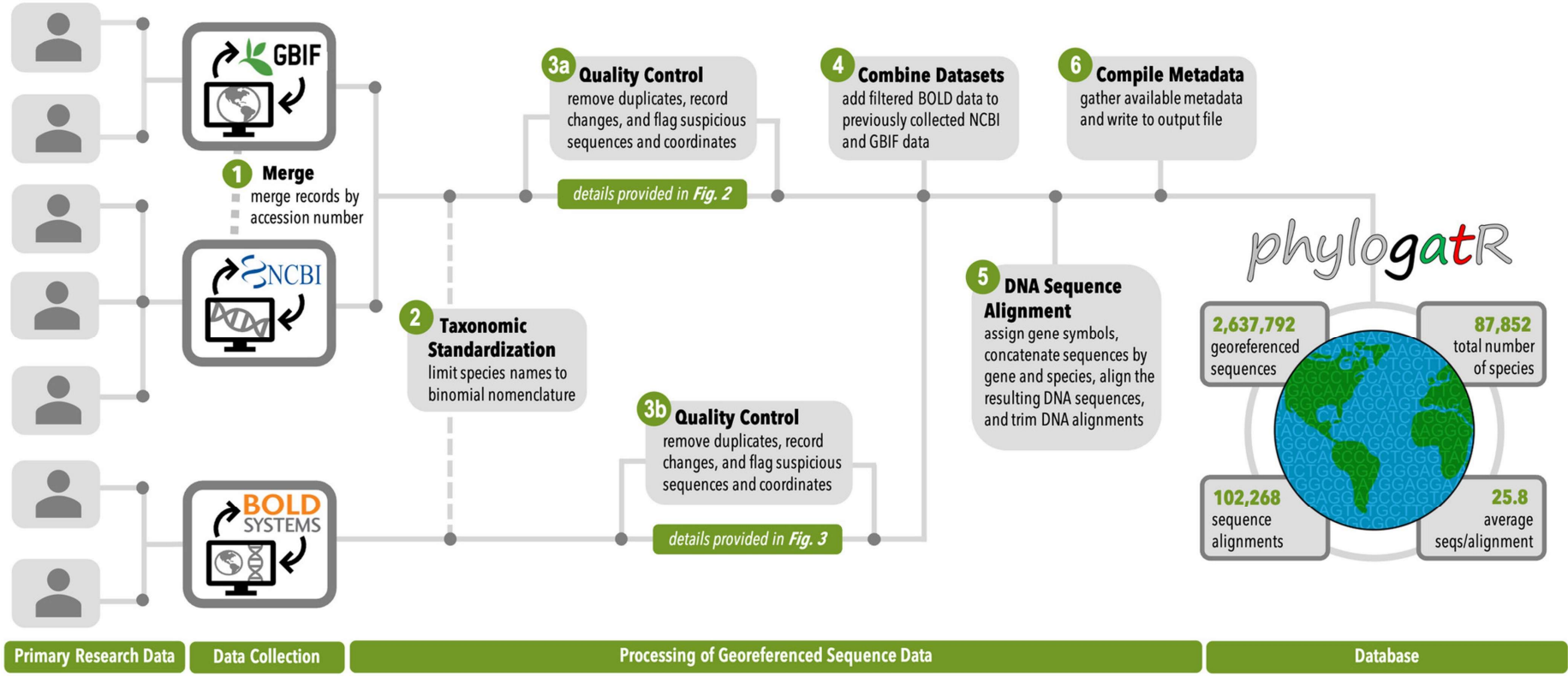


phylogatR

https://phylogatr.org/

phylogeographic data aggre**gat**ion and **r**epurposing

Launch Database

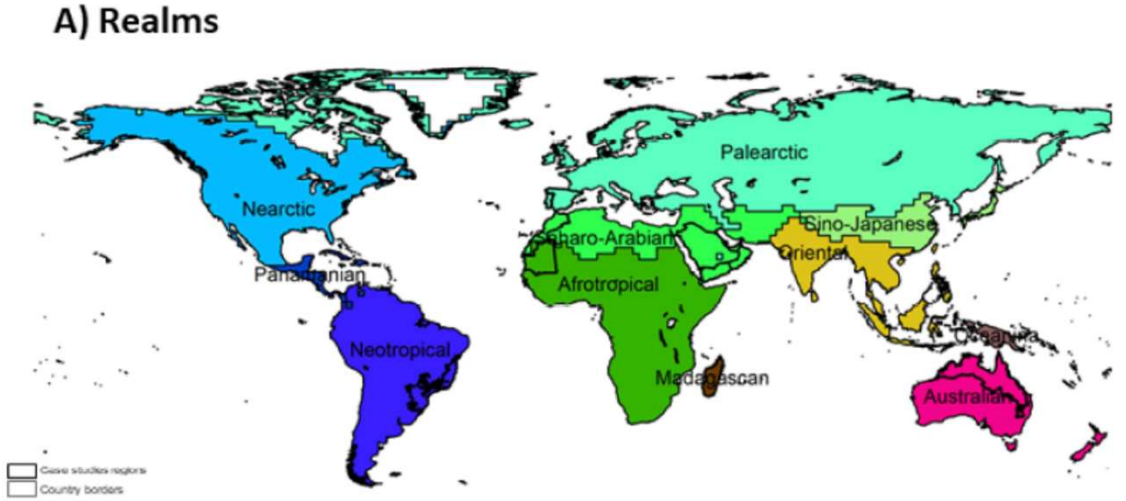


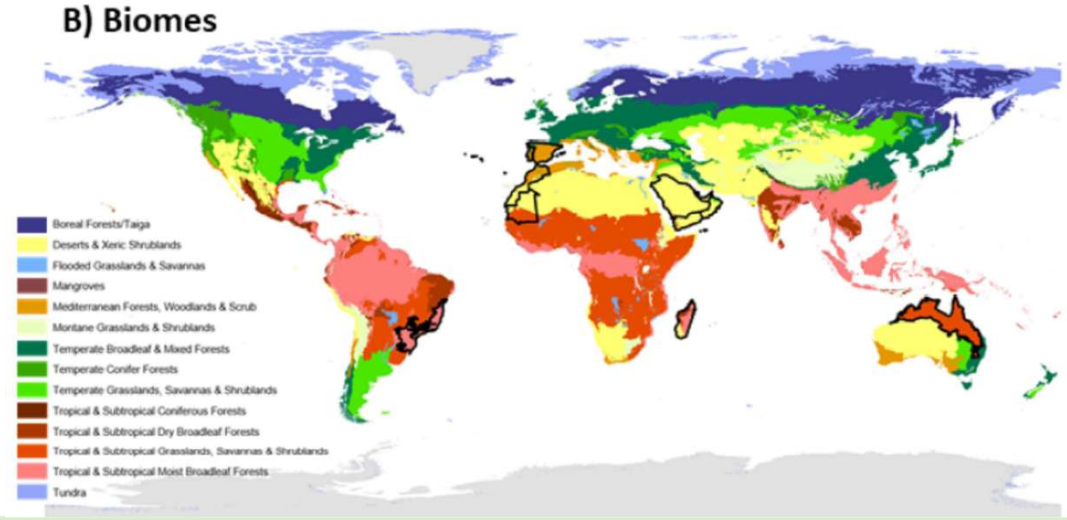
Pelletier et al. 2022)

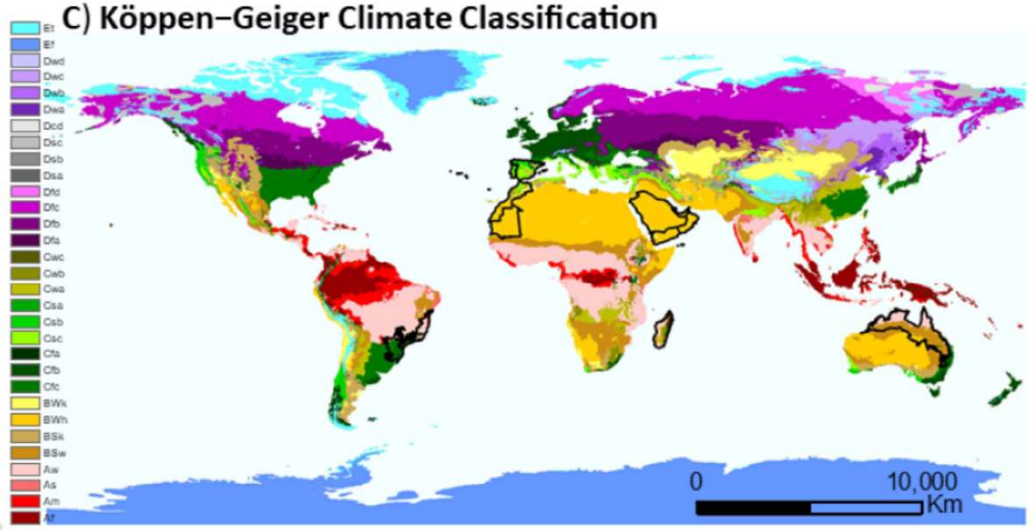
- Reduce the shortfall of knowledge of patterns of Intra specific genetic diversity of Reptiles in 6 World Regions.
- Developed an automated workflow to extract data for species in these regions, encompassing raw genetic data, corresponding geographic locations, and relevant literature.
- Identify spatial patterns of nucleotide diversity with different mitochondrial genes.
- Discuss challenges and opportunities in repurposing existing genetic data for effective conservation planning.

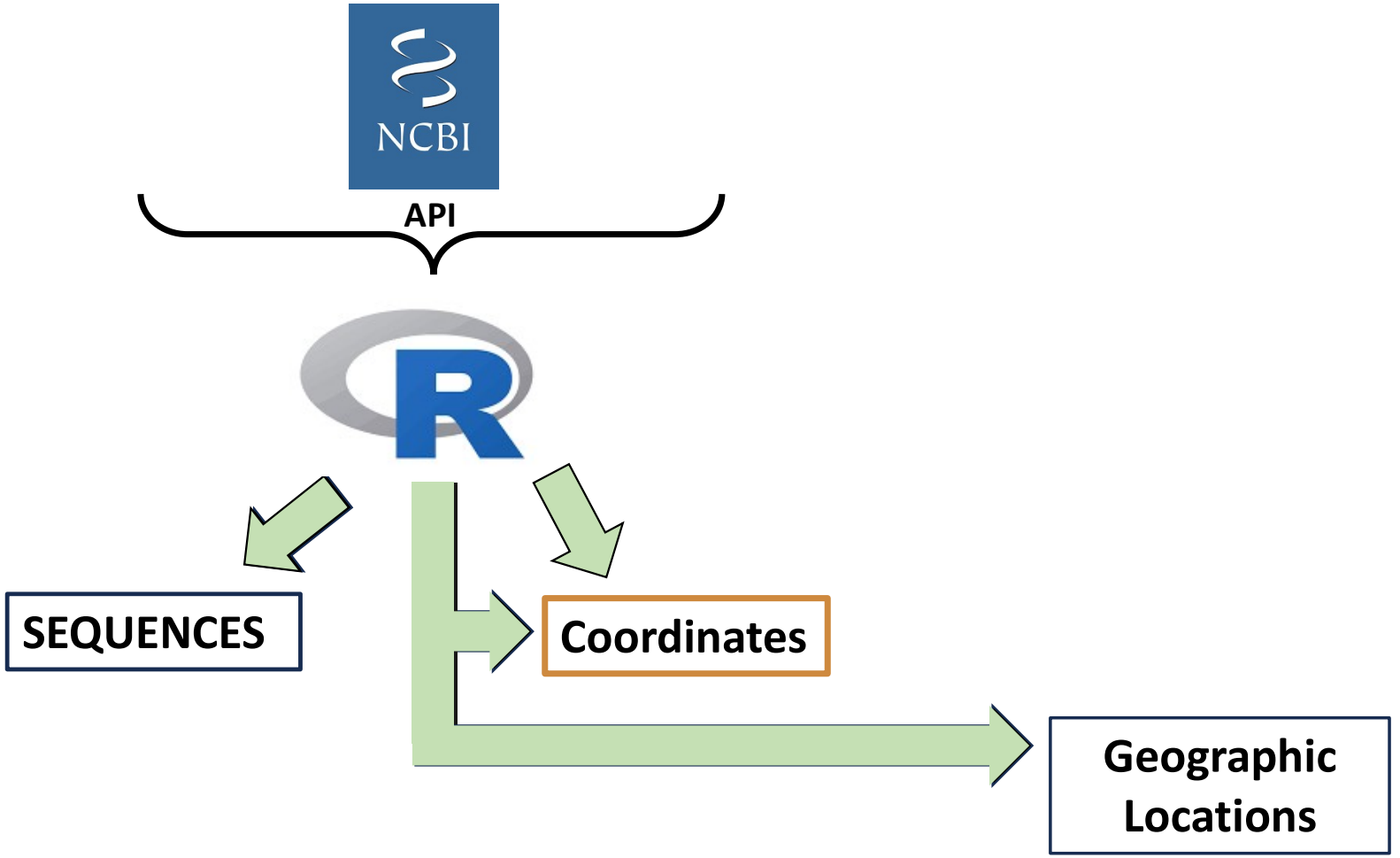
6 World regions

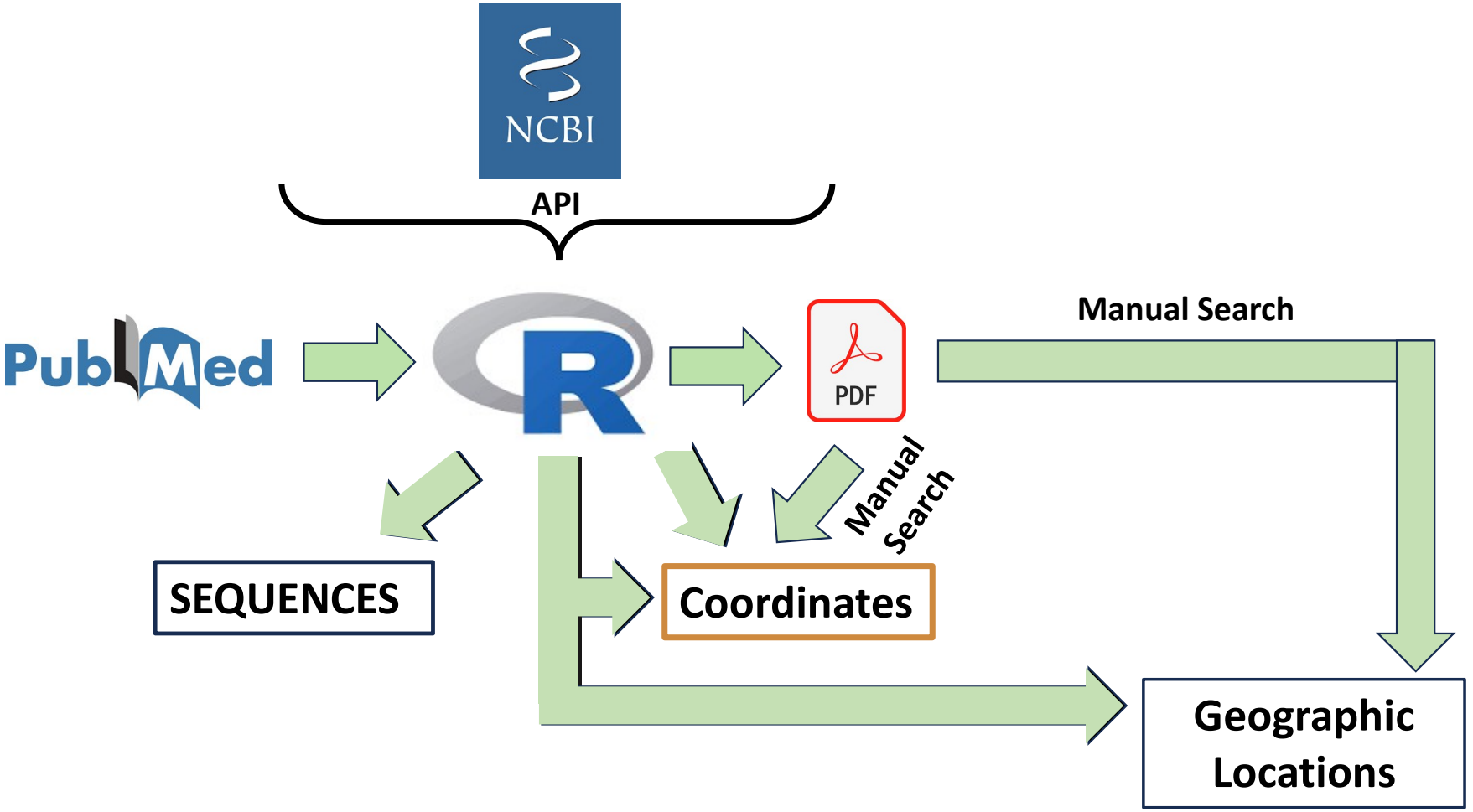
- Iberia Peninsula
- NW Africa
- Arabian Peninsula
- Madagascar
- Australia Tropics
- Brazilian Atlantic Forest

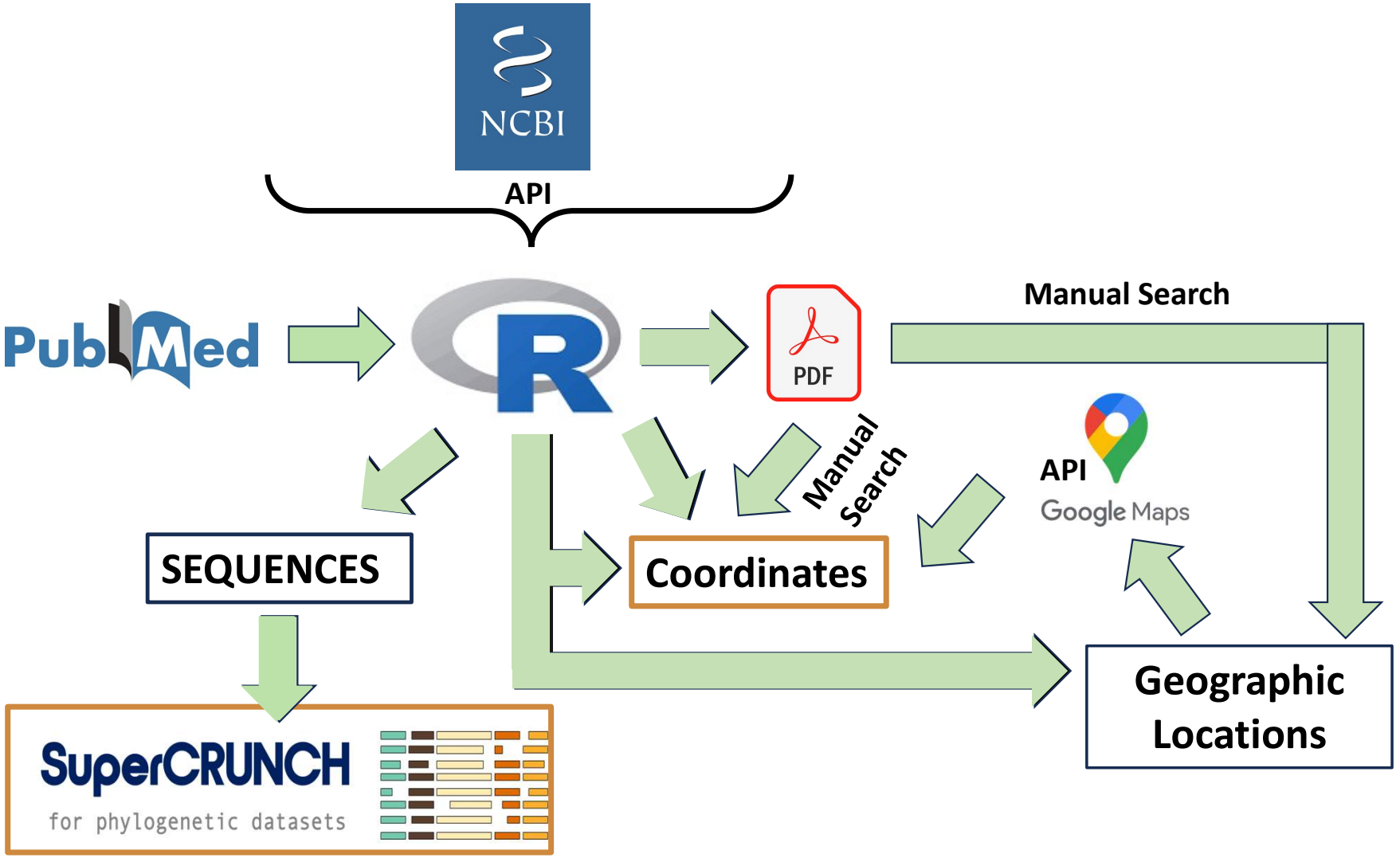







NCBI
API
SEQUENCES
Coordinates
Geographic Locations


NCBI
API
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PDF
Manual Search
Manual Search
SEQUENCES
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Geographic Locations


NCBI
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Google Maps
SEQUENCES
Coordinates
Geographic Locations
SuperCRUNCH
for phylogenetic datasets

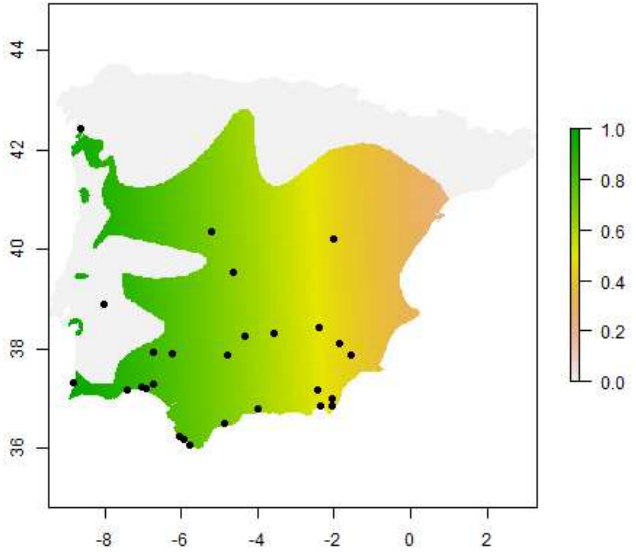
SuperCRUNCH for phylogenetic datasets

Coordinates

RED LIST Species Distributions

Thin Spline Interpolation of nucleotide diversity

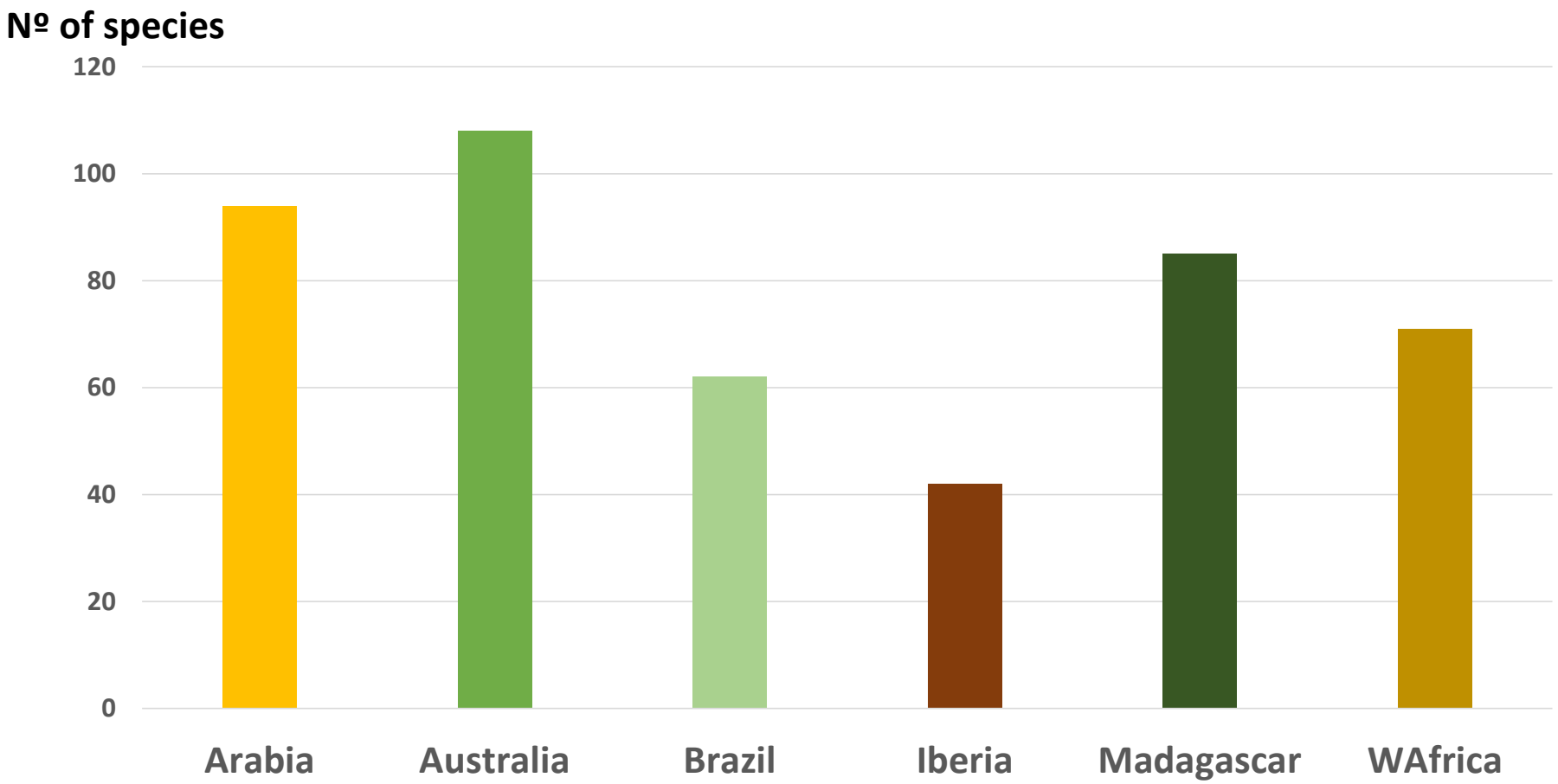




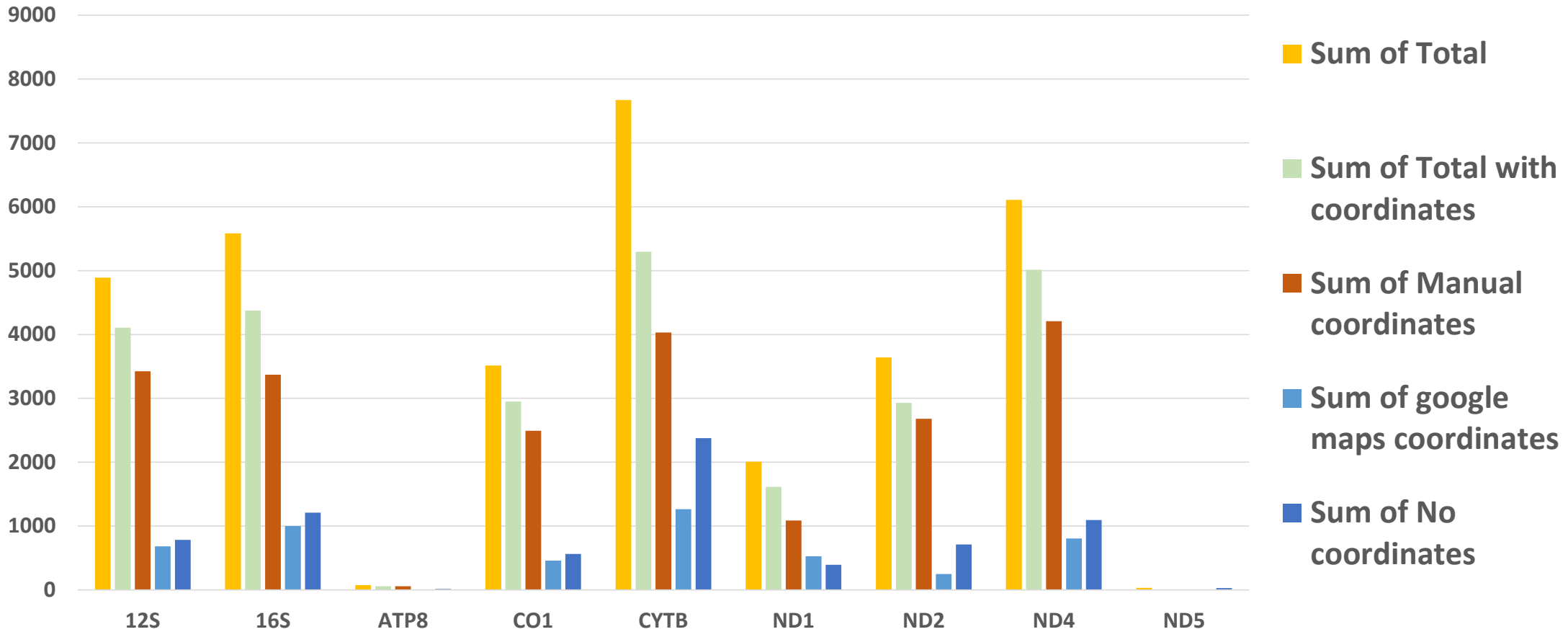


Chalcides bedriagai

322 species analyzed



322 species analyzed
33526 Sequences

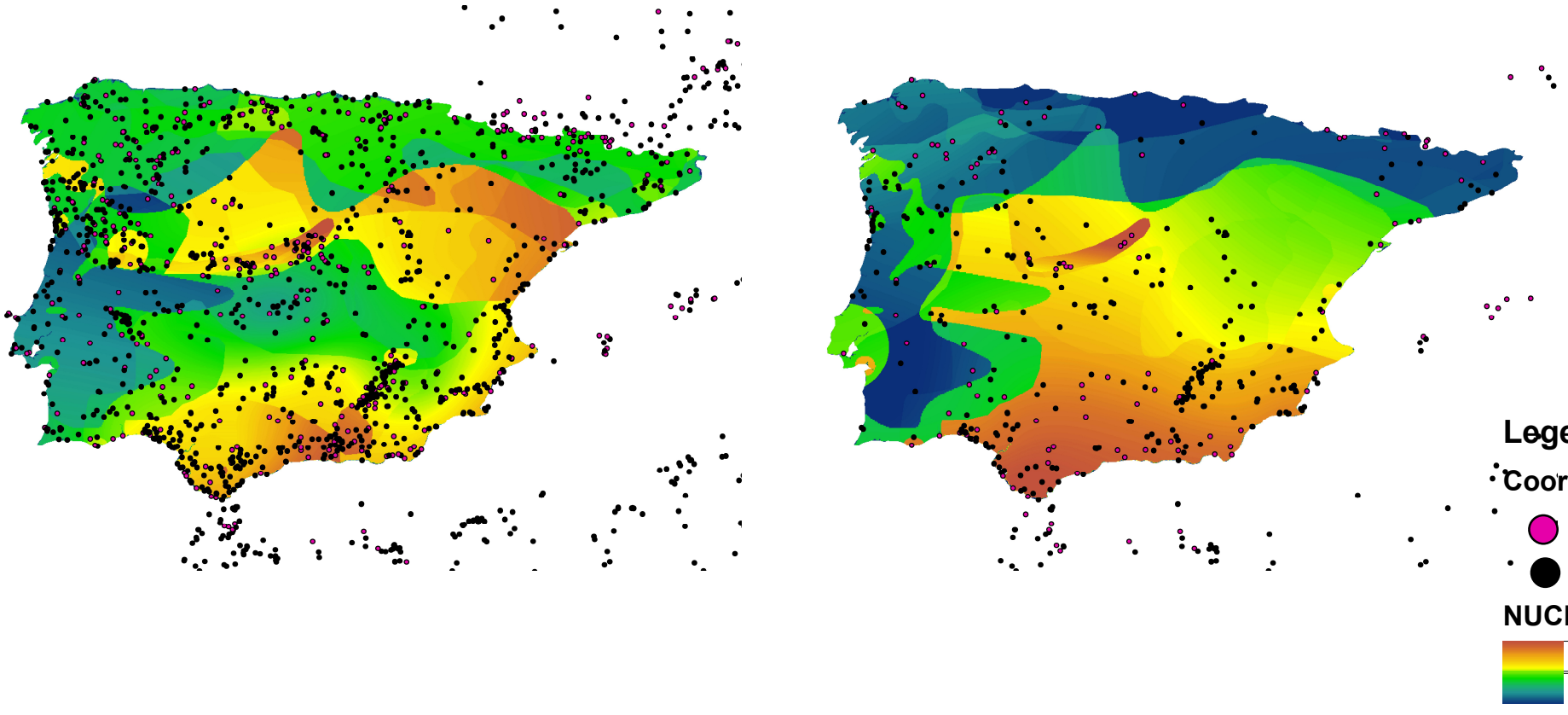


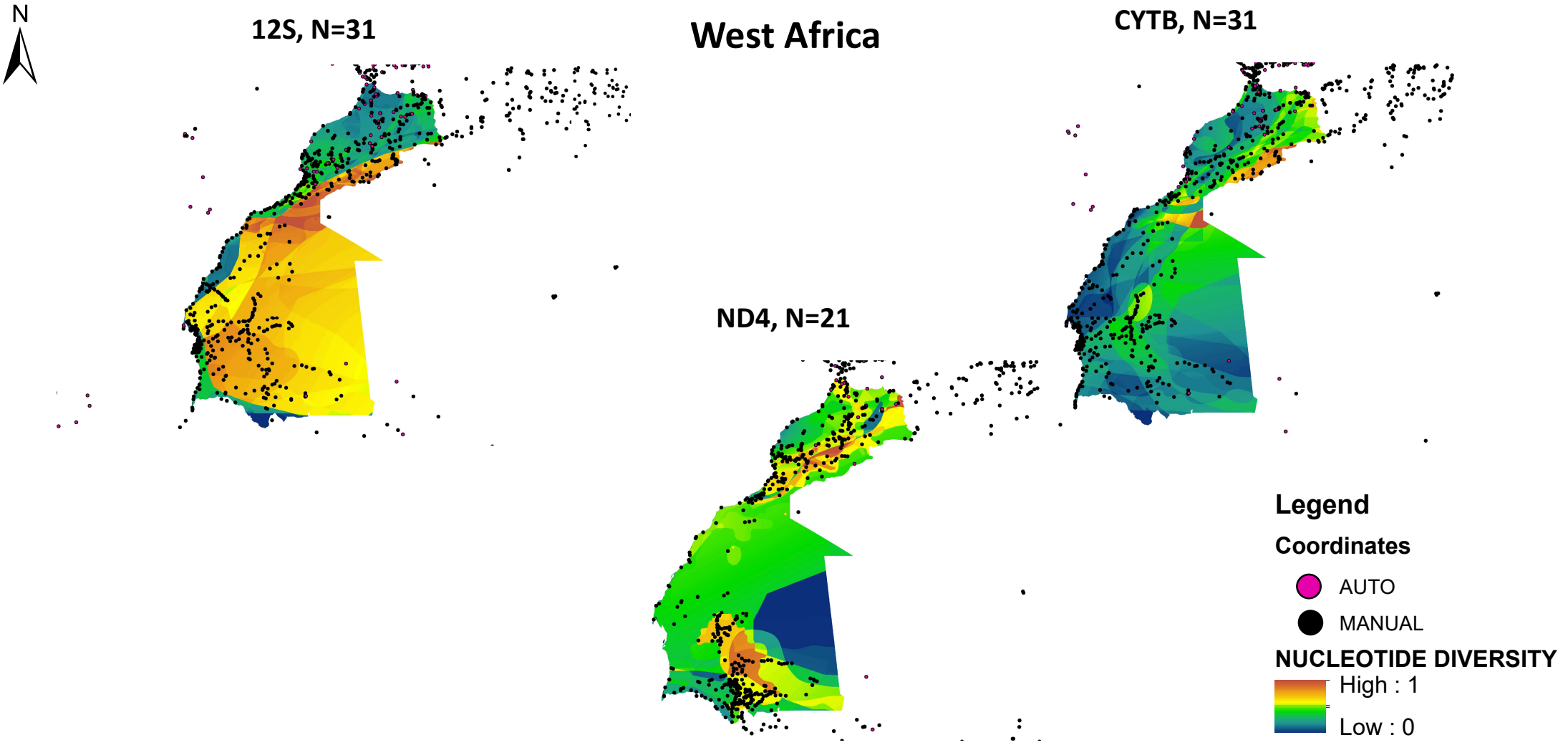
Iberia

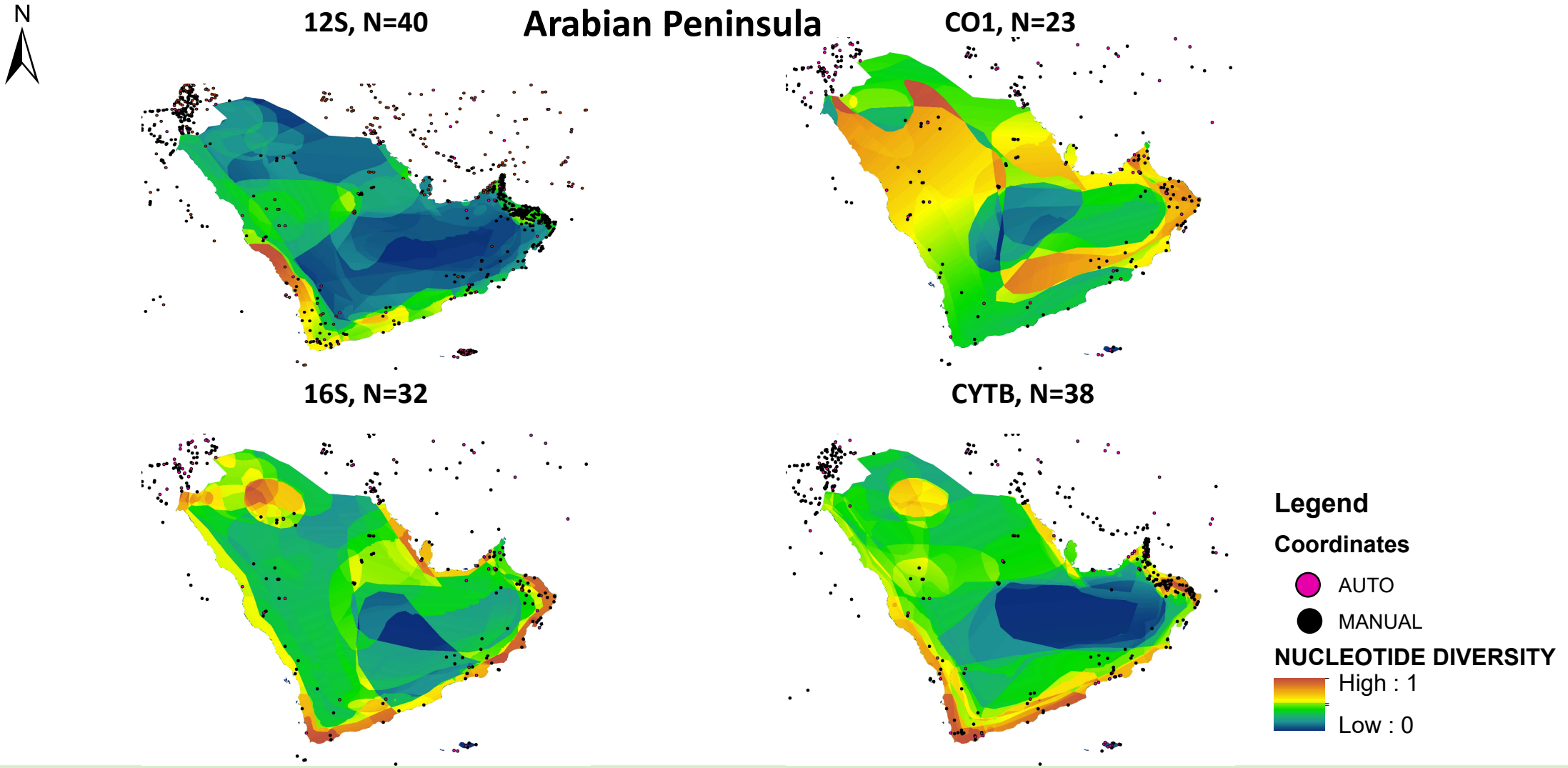
N

CYTB, N=20

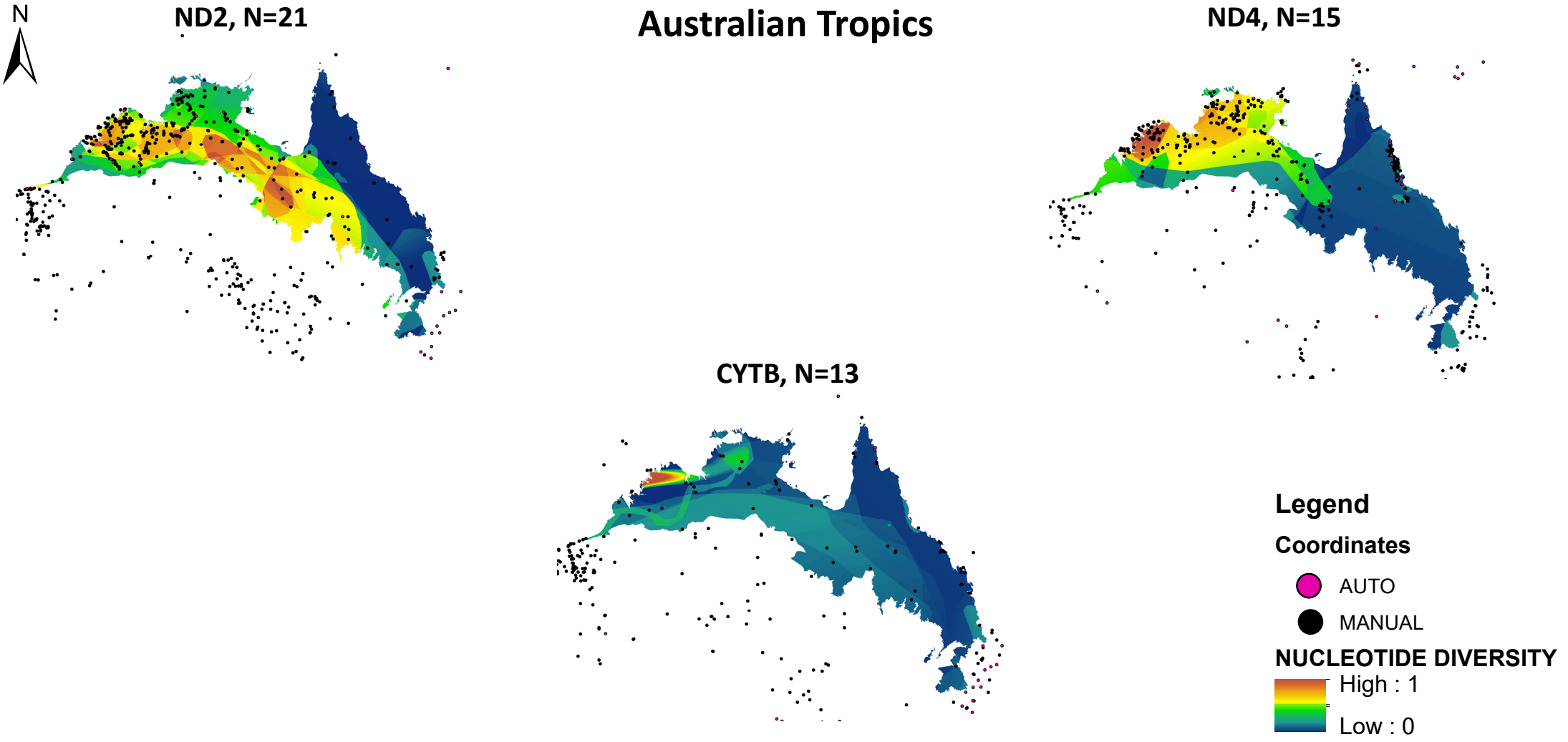
12S, N=12

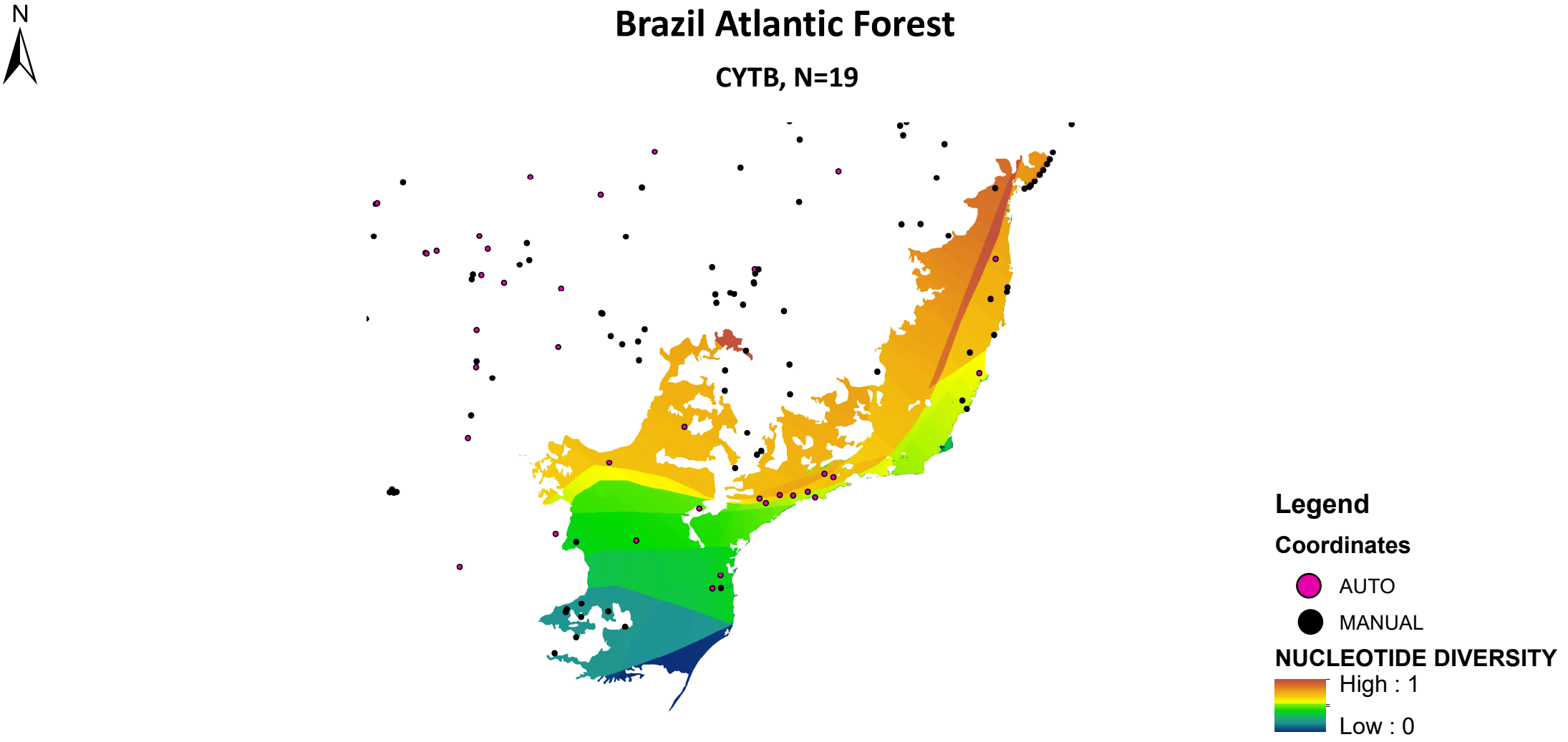



N
12S, N=31
West Africa
CYTB, N=31
ND4, N=21
Legend
Coordinates
AUTO
MANUAL
NUCLEOTIDE DIVERSITY
High : 1
Low : 0


N
12S, N=40
Arabian Peninsula
CO1, N=23
16S, N=32
CYTB, N=38
Legend
Coordinates
AUTO
MANUAL
NUCLEOTIDE DIVERSITY
High : 1
Low : 0

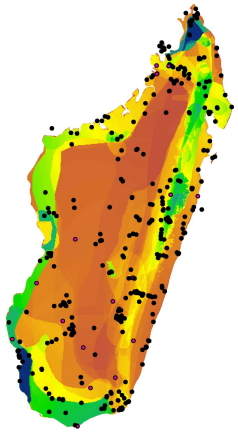
Australian Tropics




N
Brazil Atlantic Forest
CYTB, N=19
Legend
Coordinates
AUTO
MANUAL
NUCLEOTIDE DIVERSITY
High : 1
Low : 0

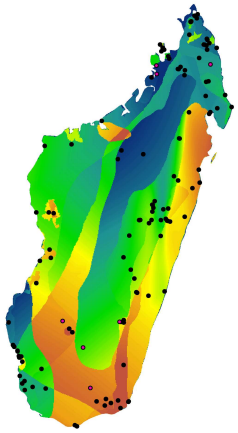
N

16S, N=33

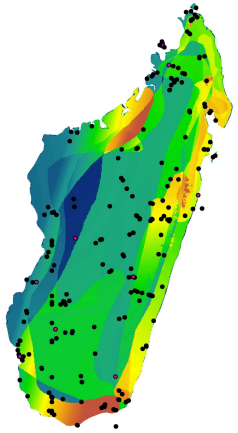


Madagascar

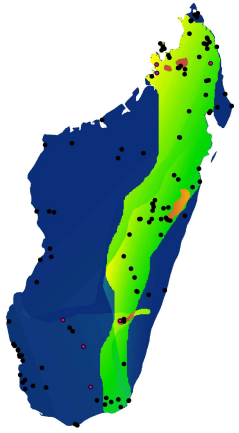
CYTB, N=13



ND4, N=15



ND2, N=8



Legend

Coordinates

AUTO

MANUAL

NUCLEOTIDE DIVERSITY

High : 1

Low : 0

Issues with repurposing genetic data

- Great amount of genetic information which are not deposited in centralized databases.
- Many studies only deposit unique haplotypes in NCBI.
- Geographic coordinate are missing in many studies.
- Some studies report coordinates but without the link to NCBI accession numbers.
- Sample sizes and sample biases affect detection of spatial patterns of nucleotide diversity.
- For the same species there are a variety of different markers for different locations – difficult to optimize and homogenize all the information available.
- For the same marker there is a lot of variation between size and length of sequences for the same gene.
- The spatial structure of genetic diversity varies expressively within the same region when using different genes and sampling.
- Discordant spatial patterns between *mt*DNA diversity and genomic diversity.
- Urgent need to reduce the shortfall of knowledge of spatial patterns of genetic diversity to inform conservation planning.
- Need for a generalized framework to incorporate genetic information in conservation planning.

TEAM MEMBERS



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