



ConnectinGEO



Phylogenetic Diversity on WPS

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Societal Benefit Area: Biodiversity

Names: Saverio Vicario and Francesco Lovergine

Institution: CNR ITB/ISSIA

Coordinating an Observation Network of
Networks EnCompassing saTellite and
IN-situ to fill the Gaps in European
Observations



Use Case WPS for phylogenetic diversity

Diversity (Phylogenetic) diversity are relevant parameters for communities EBVs.

- ▶ Here some sampling from Environmental Swedish Agency in between 1970 and 1995 in the Kattegatt/Skagerrak in the benthos
- ▶ Demo: Chao/Allen Phylogenetic Diversity measure in 60 locations on 89859 observations of Echinodermata using sampling in different time as replicates (data with the courtesy of Matthias Obst Univ. Goteborg)
- ▶ Tree using taxonomy with branch length 1 for each rank



Choice of method do matter

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Assemblage Time Series Reveal Biodiversity Change but Not Systematic Loss

Maria Dornelas,^{1*} Nicholas J. Gotelli,² Brian McGill,³ Hideyasu Shimadzu,^{1,4} Faye Caya Sievers,¹ Anne E. Magurran¹

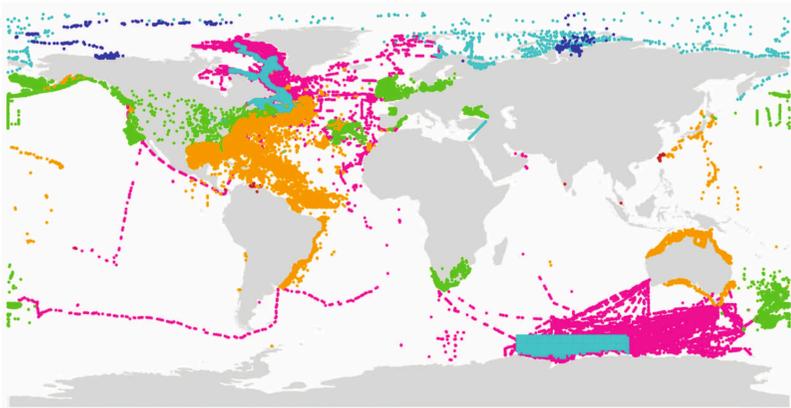


Fig. 1. Distribution of the survey sites included in our analysis. Data sets are color-coded to reflect their climatic region: pink, global; royal blue, polar; light blue, polar/temperate; green, temperate; orange, temperate/tropical; red, tropical. See table S1 for details and sources of the data sets.

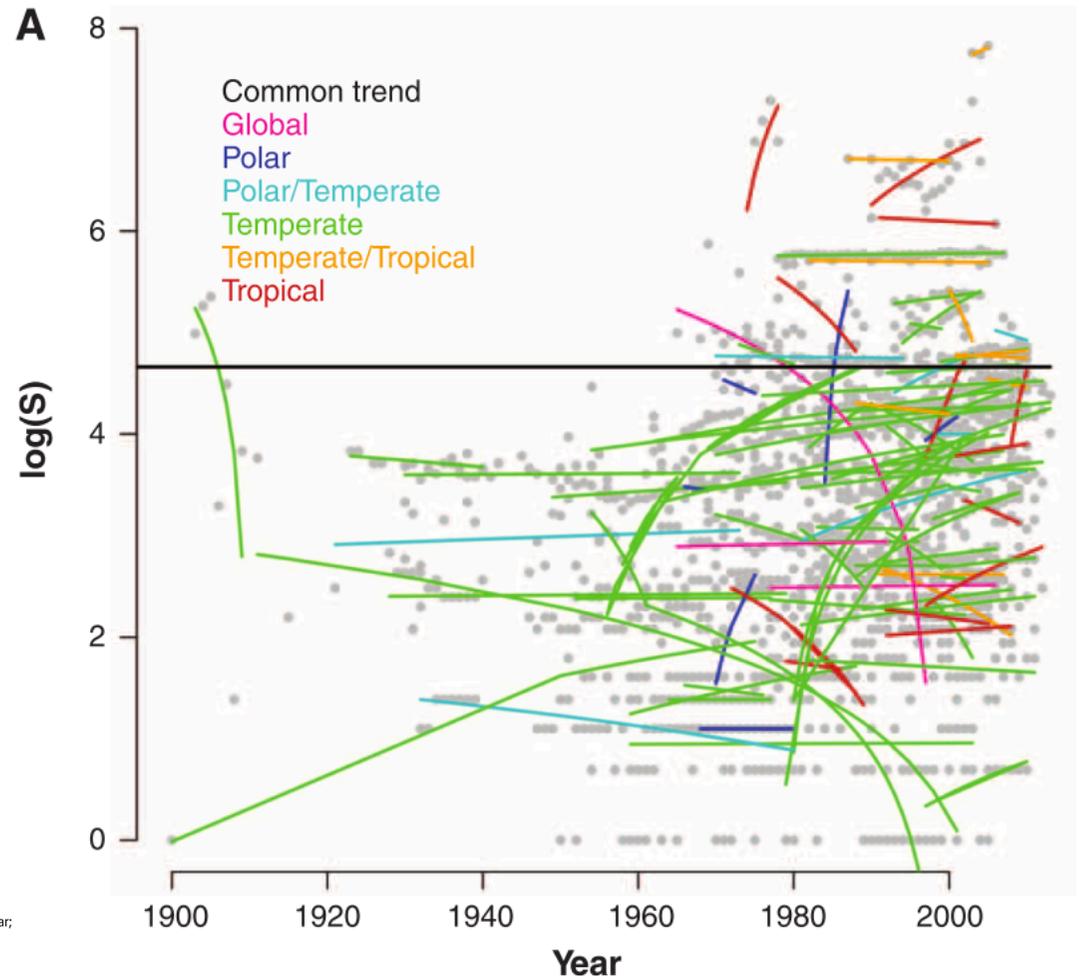


Fig. 2. Temporal change in α diversity and temporal β diversity. (A an

TWDG controlled glossary used

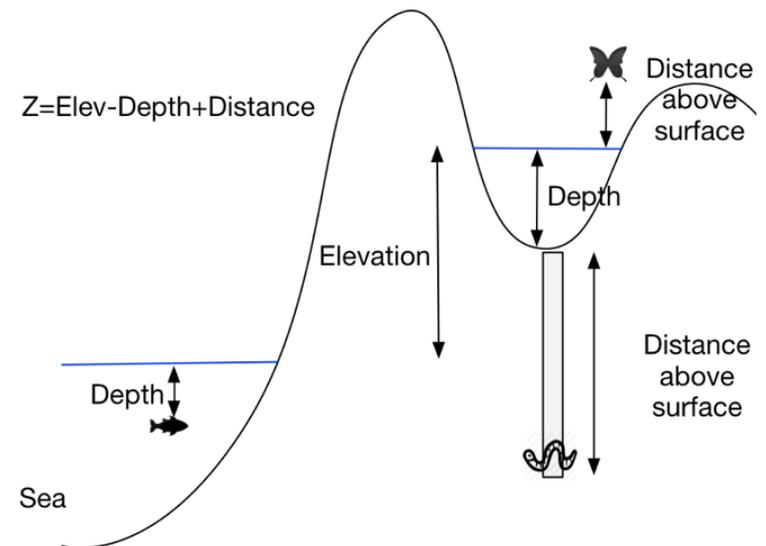
▶ Within the CSV file contemplated headings are:

- Time: EventDate
- Sampling unit: EventID
- Name locality: locationID
- Location: decimalLongitude and decimalLatitude
- Taxon name: nameComplete (or ScientificName)
- Counts: individualCount or organismalQuantity
- Z: several terms (with max and min) that can be combined.

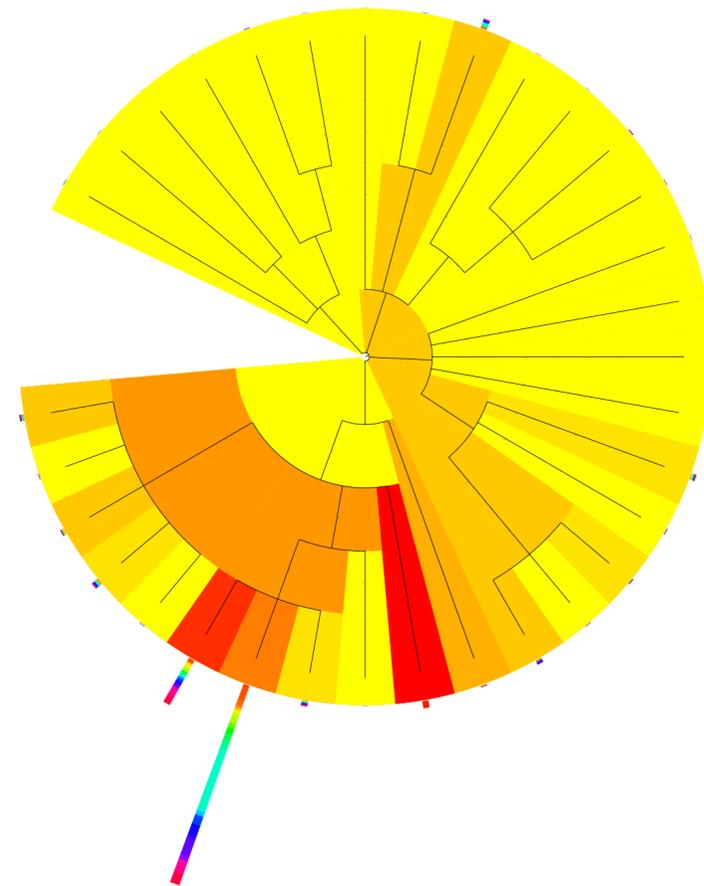
+

Phylogenetic Tree in newick format,
Taxonomy in NCBI format

<http://rs.tdwg.org/dwc/terms/>



Geographical and Phylogenetic Outputs



Demo towards mature EBV

- ▶ Communities diversity is a possible EBV.

Gap:

- ▶ Actual demo requires full phylogenetic tree to produce data. Mature system would produce tree from taxon list. BioVeL and Supersmart/BioVeL posses phylogenetic service that could produce good tree for a good set of eukariotic biodiversity.
- ▶ Observed organism for a given bounding box could be taken from GBIF and formatted in CSV with relevant heading. Source from National/Regional Environmental Agency should be checked.

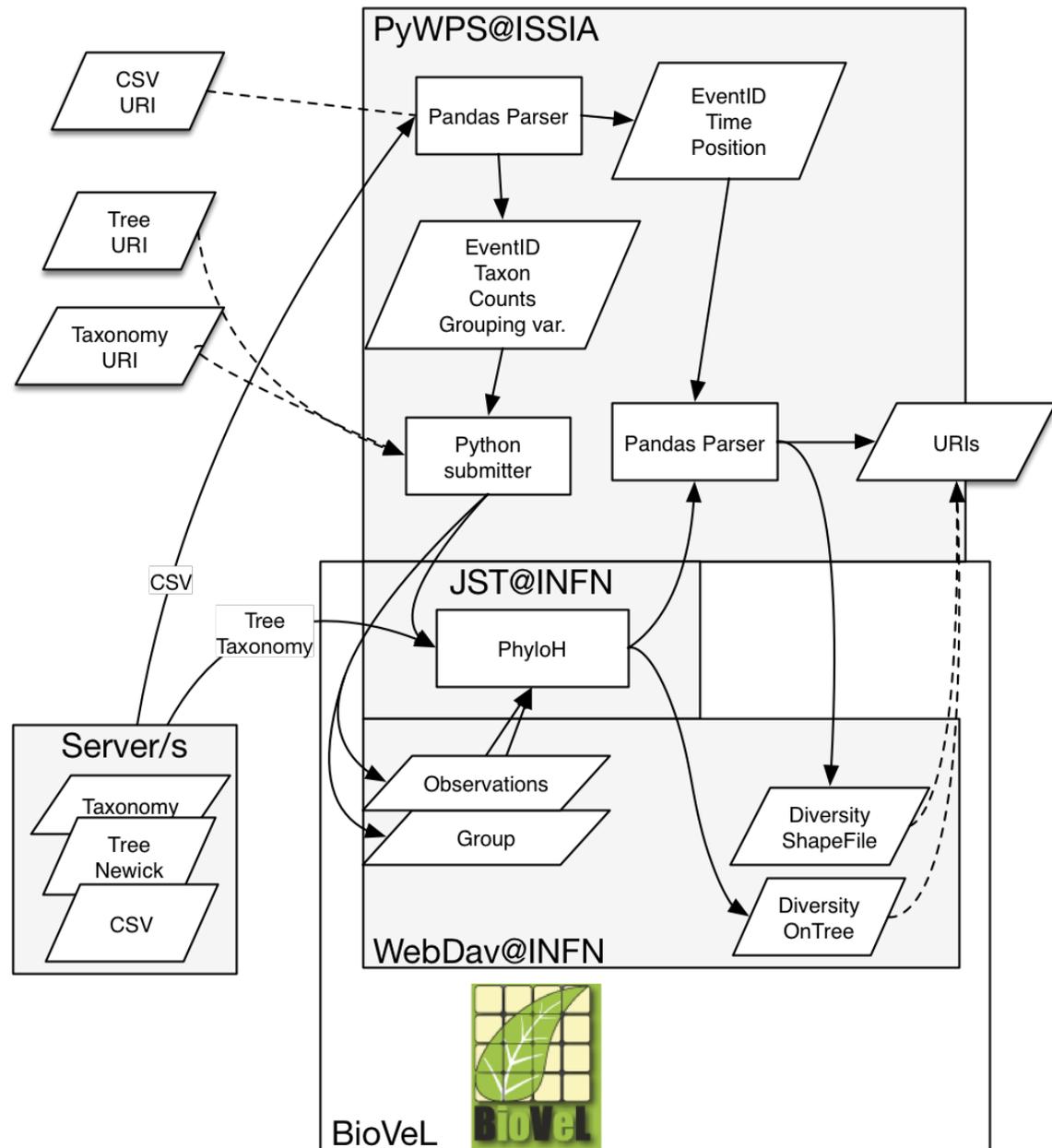


Schema

Flow of File and Refs within Web Service

CSV files using heading and format taken from DarwinCoreArchive.

User server can be of all kind (DropBox, public folder)



Asynchronous service what to do?

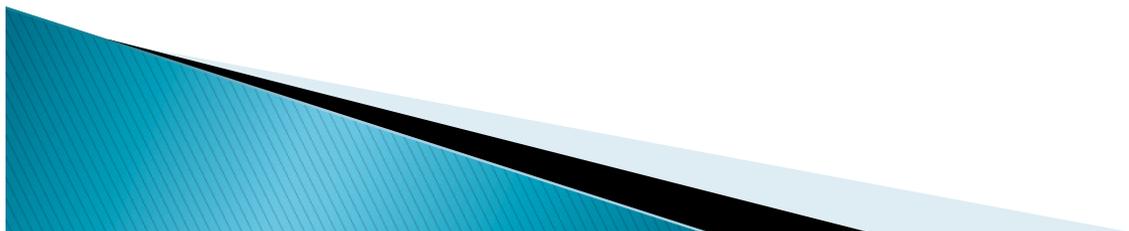
- ▶ Explicit loop on client:

- One service for submission, one for retrieval within loop (<http://www.myexperiment.org/workflows/3941.html>?)

★ One service for all, with ID submission to track job across requests (as proposed in WPS 1.0). Loop to repeat submission with proper ID.

- ▶ No loop on client:

- Service only for submission, output the foreseen address to retrieve results. Address will be filled when job completed. Client will checkout with separate tool.



Technical Demo Gap/prospectives

- ▶ Demo is based on PyWPS that is actually working on WPS 1.0. Upgrade should be done this summer to WPS 2.0. Then our services should be updated.
- ▶ Add bounding box filtering
- ▶ Add taxonomic and temporal filtering
- ▶ Only point locations in CSV format as input are accepted. Transept and Quadrant would require geographical format. It could be easily done but difficult to be generic and handy to field biologist.
- ▶ Define best strategy with Client/ workflow engine



Calling

```
http://salina.ba.issia.cnr.it/cgi-bin/pywps?  
Service=WPS&Version=1.0.0&Request=Execute&id  
entifier=phyloH&DataInputs=html=0;jobid=0;Nam  
eGroupCol=locationID;sample=http://  
testjst.ba.infn.it/openaccess/InputExamples/  
ExamplePhyloHGeo/  
allPMK1970-1996ll.tab;output_prefix=BellaPupo;X  
MLoutputType=nexml;Nrandomization=2;taxonom  
y=http://testjst.ba.infn.it/openaccess/  
InputExamples/ExamplePhyloHGeo/  
taxEchino.tabular;qparamHill=1;tree=http://  
testjst.ba.infn.it/openaccess/InputExamples/  
ExamplePhyloHGeo/Echinodermata.tree
```

