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Soil biodiversity in action at ecosystem level

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Genomics, transcriptomics, and proteomics

- >>> generate enormous data sets
- >>> possibility of getting drowned in such an “ocean” of data and possibly conclude, at last, that differences among samples are small.

Multiplexed enzyme assay (Cowie et al., 2013; Bardelli et al., 2017),

dsDNA-based quantitation of soil microbial biomass (Fornasier et al., 2014)

Assessment of extracellular and intracellular DNA (Gómez-Brandón et al., 2017)

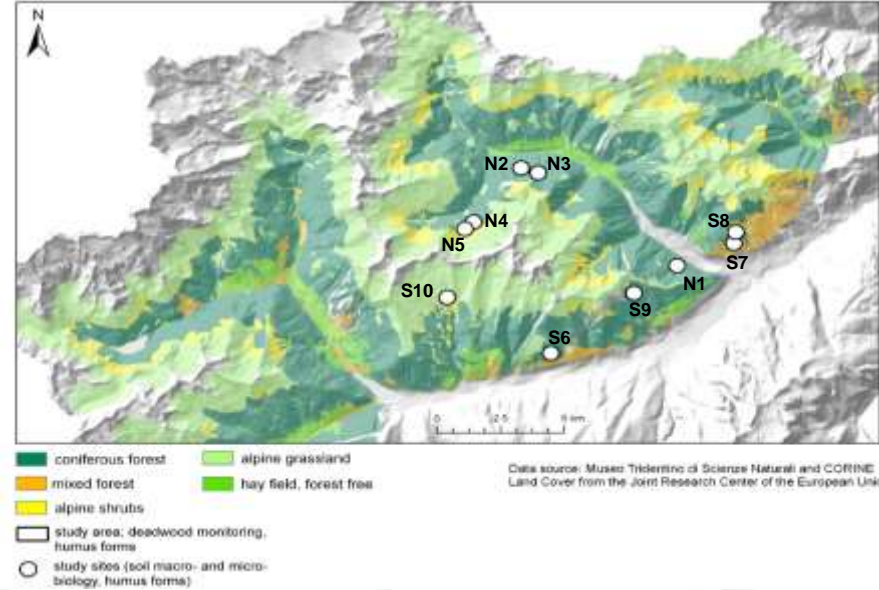
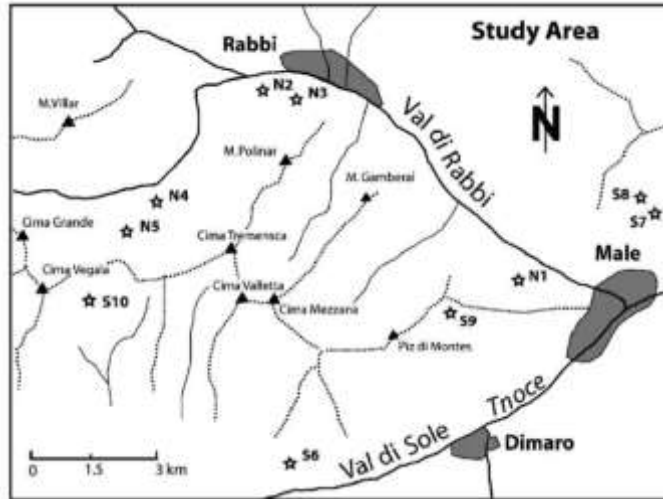
- >>> Time- and cost-effective high throughput techniques



Climosequence approach



Val di Rabbi, Trentino, Italy



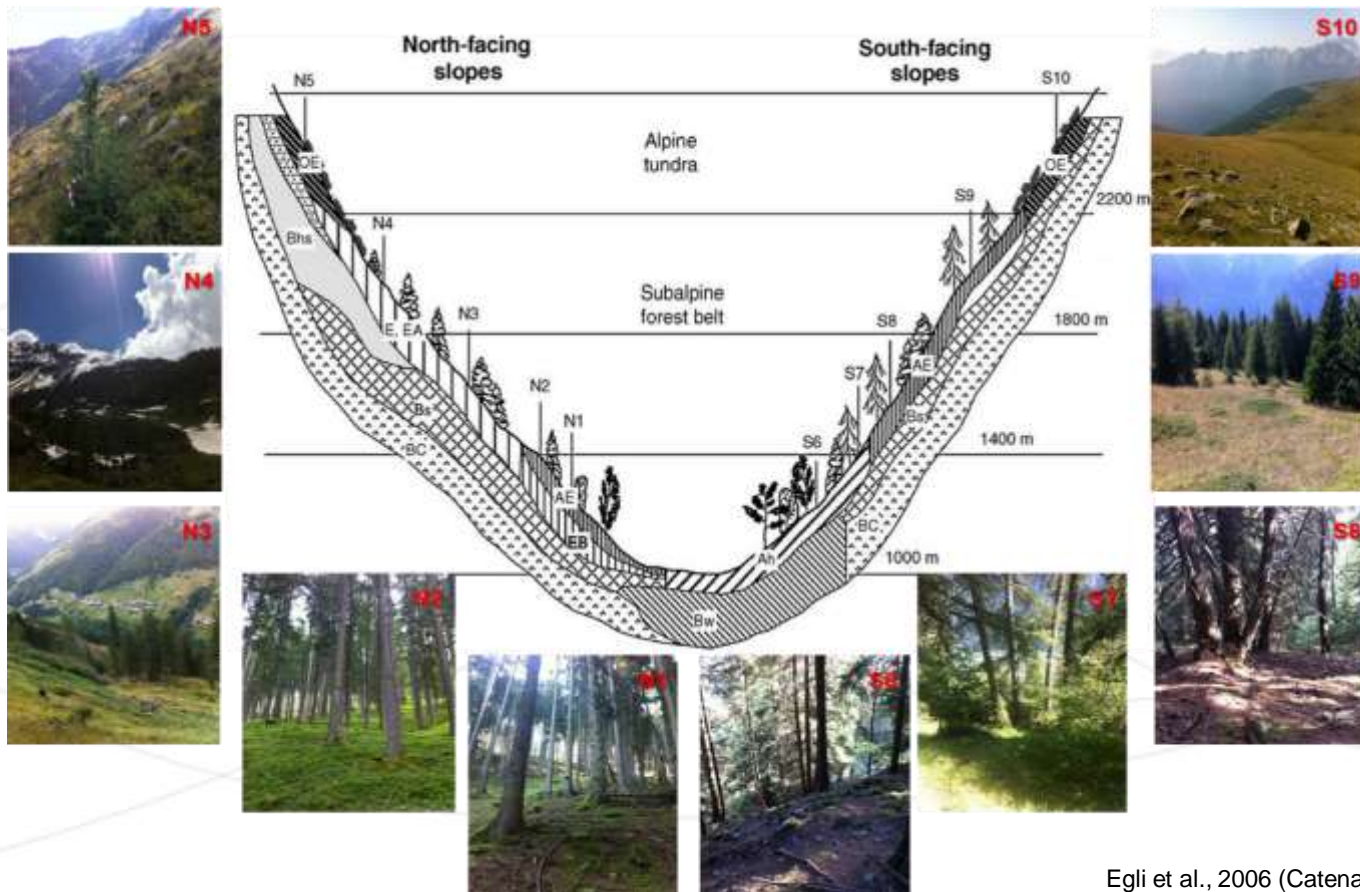
- **Parent material** Paragneiss debris
 - **Forest type** Natural forest (subalpine sites)
 - **Land use** Natural grassland (alpine sites)
 - **Soil type** Cambisols to Umbrisols or Podzols
- from the **warmest** to the **coldest** sites

the **sites** do not differ with respect to the state factors (**Jenny, 1941**), except for **climate** (different **thermal conditions** due to different exposure and altitude)

❖ **Climate** ≠ **S6** > S7 > S8 = N1 > N2 > N3 = S9 > N4 > S10 > **N5**

(Mean Annual Temperature; Egli et al., 2006; Petrillo et al., 2015)



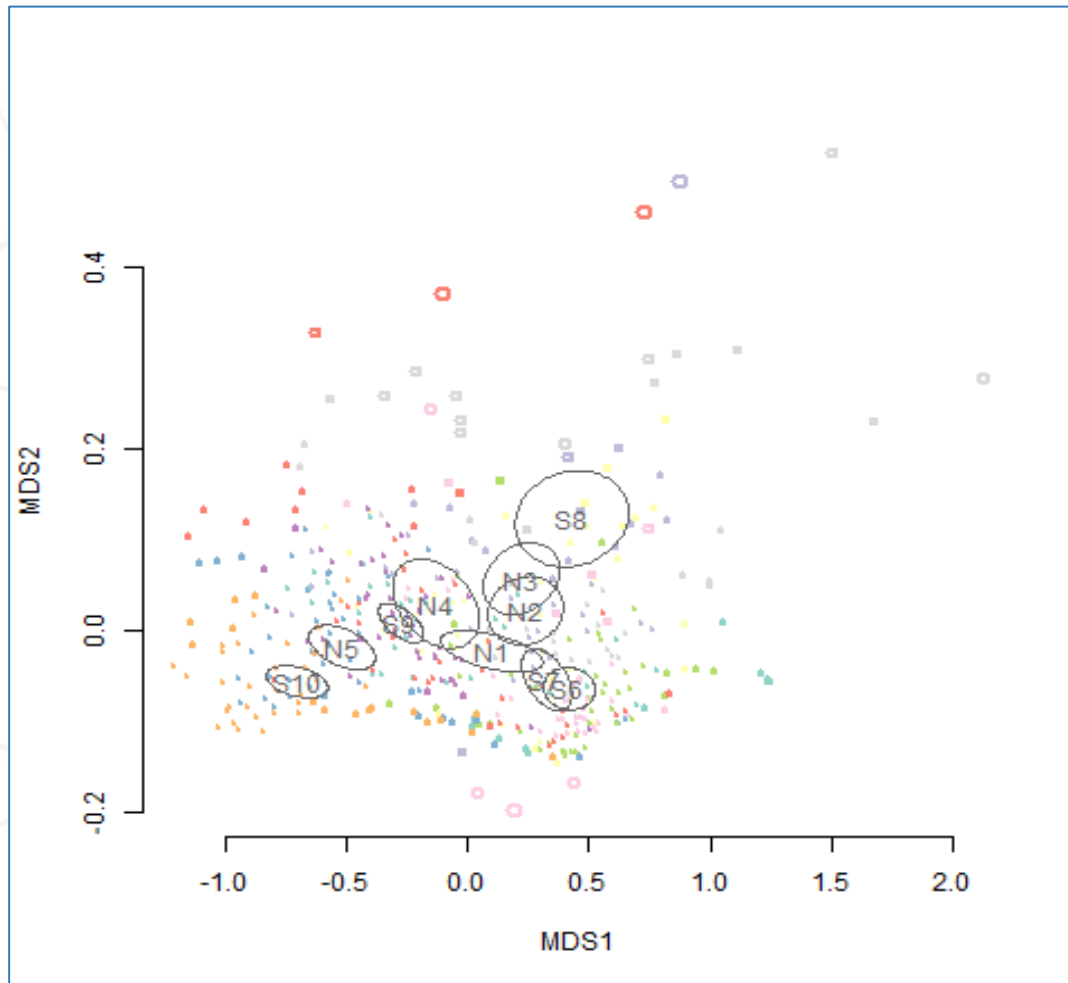


Egli et al., 2006 (Catena 67:155-177)

10 sites x 3 soil depth x 3 independent field replicates x 5 subsamples

450 SOIL SAMPLES

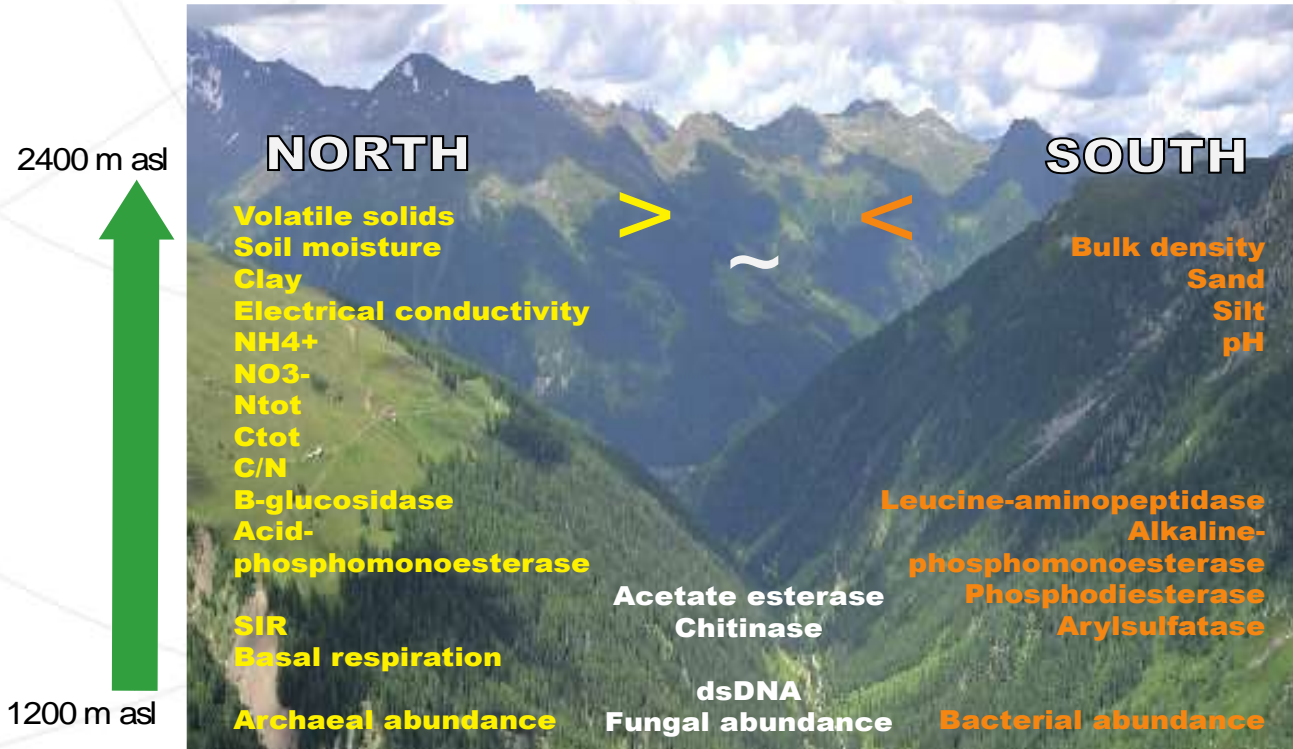




Non-metric multidimensional scaling (NMDS) of soil enzymatic activities and microbial biomass estimated by dsDNA contents. Ellipses embracing sample groups were drawn at a confidence interval of 95% around group centroid.



CLIMOSEQUENCE APPROACH



complex, altitude dependent and microbial domain specific EXPOSURE EFFECTS (thermal signal) on soil microbiota

helpful to predict future climate scenarios (global warming) in mountain ecosystems



A comprehensive picture of both the microbiota and complexity of biogeochemical cycling was achieved by :

Next Generation Sequencing (NGS)

>> huge, very detailed data sets and specific information for each sample

High-throughput methods:

exDNA/iDNA ratio

dsDNA-microbial biomass

multiplexed enzyme assay

>> able to process **hundreds of samples** in a very short time at minimal cost

>> rather than being an alternative to costly high-end methods, serve as a tool to select samples for deeper analysis.

Suitable sampling strategy and Statistics methods





**Thank you for
your attention**