Analisi della diversità filogenetica nativa e aliena, ecologia delle comunità e invasibilità di un sito.

Interazione CT Mediterraneo – CT biomolecolare

Paolo Colangelo

MEDITERRANEAN

Misurare la biodiversità

- La biodiversità è generalmente misurata utilizzando la **richness** (n° di specie) e la **evenness** (indici di Simpson e Shannon-Wiener), cioè la ricchezza tassonomica in una determinata area.
  - **alpha** diversity is a measure of diversity at a site
  - **gamma** diversity is a measure of diversity regionally
  - **beta** diversity is a measure of the diversity between two sites
- Whittaker (1972): "If diversity is recognised as an evolutionary product, it may cause no surprise that no single measurement serves all purposes"

Le specie sono tutte uguali?

Le specie sono tutte uguali?
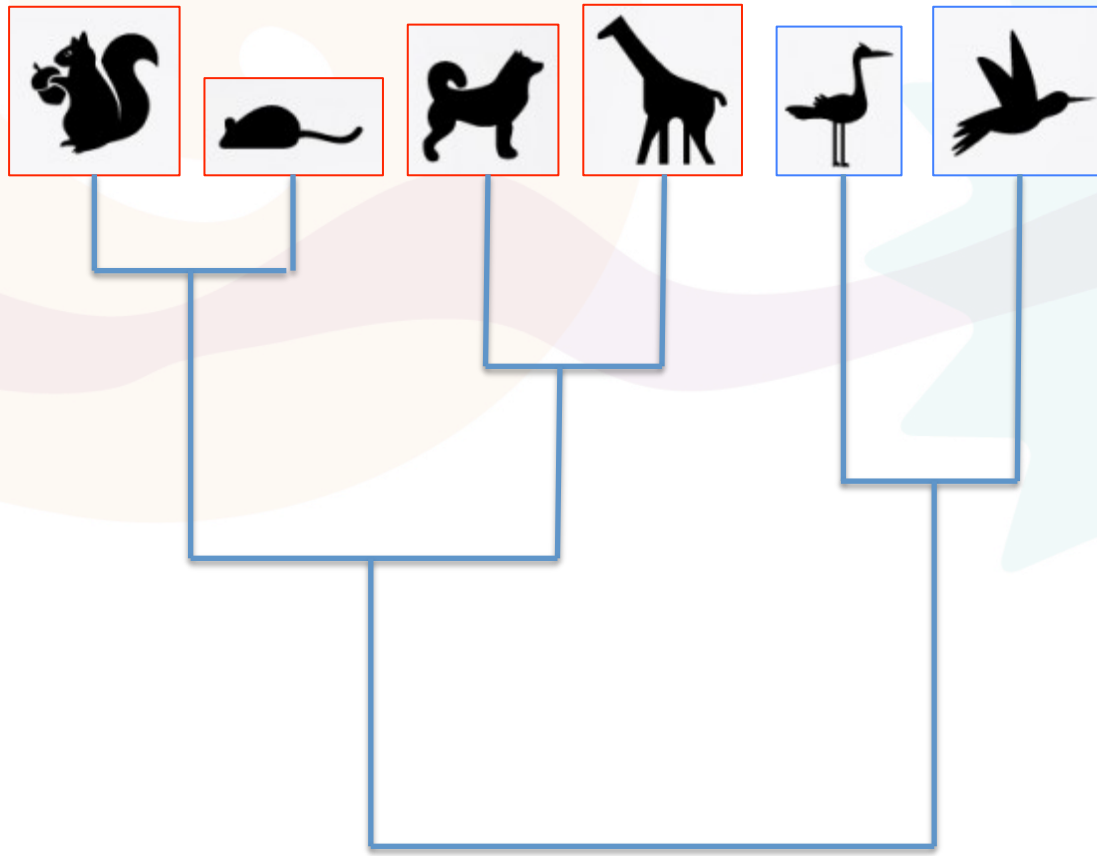
Misurare la biodiversità

- In terms of analyses in community ecology, the incorporation of phylogenetic information has a relatively long history.

- Darwin (1859) first hypothesized that competition should be strongest between close relatives (e.g. congeners), leading subsequent researchers to explore ratios of species-to-genus numbers (or genus-to-family, etc.) as potentially indicative of the role of competition in structuring ecological communities.

Phylogenetic diversity

- Introdotta da Daniel P. Faith (1992).Conservation evaluation and phylogenetic diversity. *Biological Conservation*

- Phylogenetic diversity (PD) is a biodiversity index that measures the length of evolutionary pathways that connect a given set of taxa

- PD therefore identifies sets of taxa that maximize the accumulation of 'feature diversity'.

- Recent studies, concluded that (at the species-genus taxonomic rank) taxon richness is a good surrogate for PD

Calcolare la PD
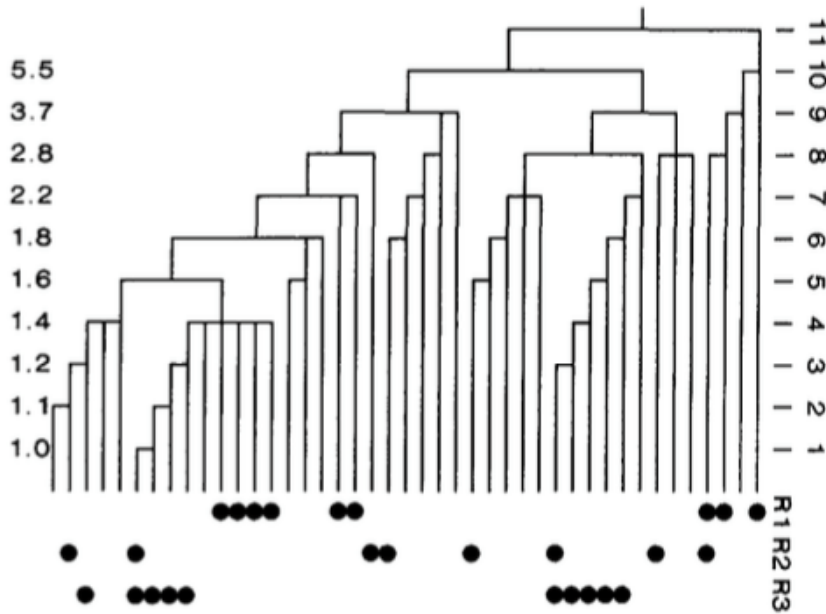
Table 2. Values for phylogenetic diversity and for taxic diversity for each of the three reserve areas, R1, R2, and R3 from Fig. 3(a). Also shown is the number of species for each reserve network

	R1	R2	R3
Number of species	9	8	10
Phylogenetic diversity	66	71	50
Taxic diversity	21·1	15·1	12·7

PD & Conservation Biology

Identificare aree che permettano di mantenere un maggiore potenziale evolutivo su cui indirizzare i maggiori sforzi di conservazione.
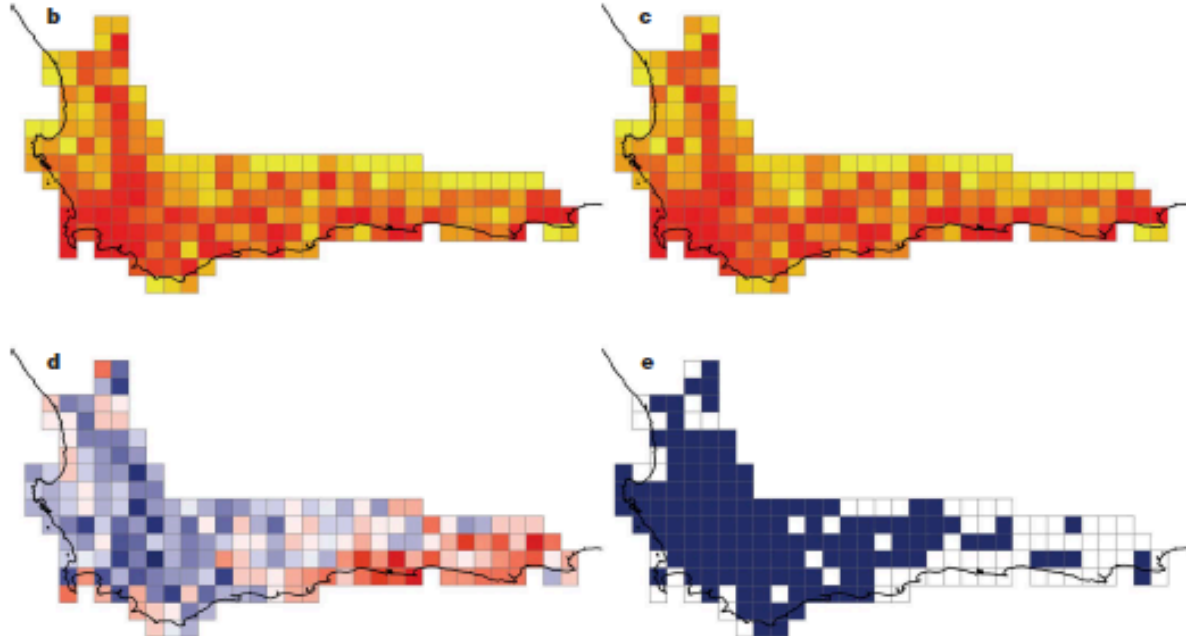
LETTERS

Preserving the evolutionary potential of floras in biodiversity hotspots

Félix Forest[1,2,3]*, Richard Grenyer[3]*, Mathieu Rouget[4], T. Jonathan Davies[5,6], Richard M. Cowling[7], Daniel P. Faith[8], Andrew Balmford[9], John C. Manning[1], Şerban Procheş[10], Michelle van der Bank[11], Gail Reeves[1], Terry A. J. Hedderson[2] & Vincent Savolainen[3]

Figure 1 | Taxon richness and phylogenetic diversity in the Cape. a, This biodiversity hotspot, which includes the renowned Cape Peninsula, Cape of Good Hope and Table Mountain (in the distance), dominated by fynbos vegetation, is situated at the southern tip of Africa. Picture credit: A. Proust/iAfrika. **b–e,** Maps of 201 QDS covering the entire Cape region. **b,** Genus richness (ten quantile intervals from yellow to deep red). **c,** PD calculated using NPRS absolute age estimates in million years (colour code as for **b**). **d,** Residuals from a loess regression of PD (calculated using NPRS absolute age estimates) on genus richness. QDS with negative residuals are indicated in blue, and those with positive residuals are shown in red (shading increments of half a standard deviation). **e,** The spatial distribution of unusual PD values, as assessed by comparing the observed PD in each QDS with 10,000 PD values calculated by random selection of the same number of genera from the Cape flora. Cells with significantly lower PD ($P < 0.05$, two-tailed) than expected are shaded in blue. A similar pattern was found when the tree was simplified to reflect the phylogeny-based taxonomy of the Angiosperm Phylogeny Group[30] (Supplementary Information).

PD & Community Ecology

Early PD measures were proposed as a tool to select conservation areas, but later the idea was extended to understand how communities are assembled from a regional pool.

COMMUNITY PHYLOGENETICS AND ECOSYSTEM FUNCTIONING
Phylogenetic patterns are not proxies of community assembly mechanisms (they are far better)

Pille Gerhold*,[1], James F. Cahill Jr[2], Marten Winter[3], Igor V. Bartish[4] and Andreas Prinzing[5,6]
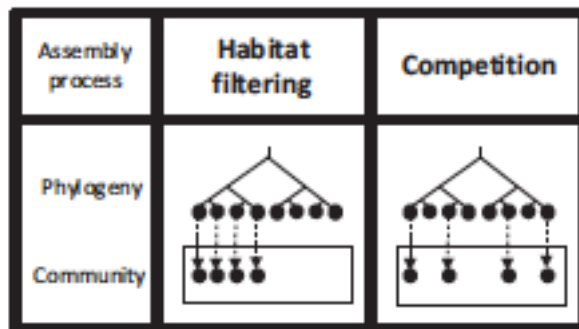
PD & Community Ecology

- Phylogenetic diversity (PD) is a biodiversity measure that accounts for the phylogenetic relationship (hence evolutionary history) among species, whereas functional diversity (FD) represents how species are distributed in a multidimensional niche space defined by ecological traits.

- closely related species should be ecologically more similar than distant related species and, thus, PD should be a good surrogate for FD.
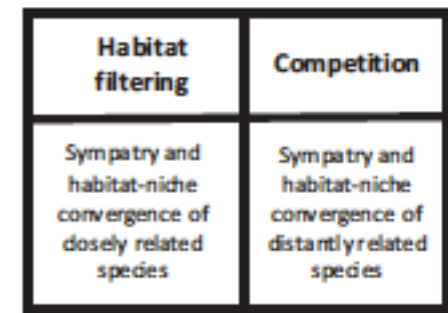
PD & Community Ecology

- Phylogenetic clustering as a proxy for abiotic assembly, that is habitat filtering

- Phylogenetic overdispersion as a proxy for biotic assembly, notably competition

**Phylogenetic-patterns-as-proxy approach:**

Assembly process	**Habitat filtering**	**Competition**
Phylogeny		
Community		

Phylogenetic-patterns-as-result approach:

If « proxy » scenario is true :

Habitat filtering	**Competition**
Sympatry and habitat-niche convergence of closely related species	Sympatry and habitat-niche convergence of distantly related species

Phylogenetic Diversity Theory Sheds Light on the Structure of Microbial Communities

James P. O'Dwyer[1,2]*, Steven W. Kembel[2,3], Jessica L. Green[1,2]
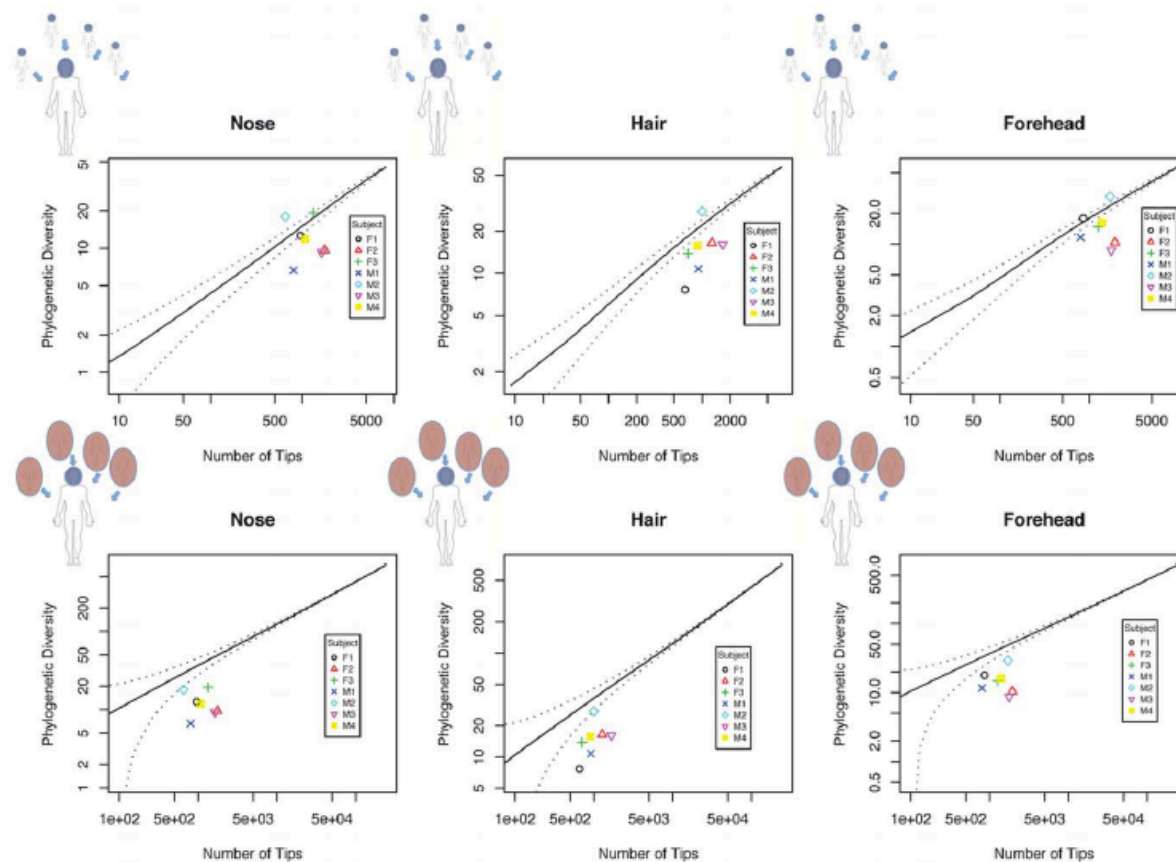
PD e specie aliene

- Does phylogenetic clustering of local communities increase or decrease invasibility?

- Successful establishment of aliens may be more likely for aliens with no close relatives in the recipient native community, due to lack of competitive exclusion ('Darwin's naturalization hypothesis')

Diversification of a single lineage and resulting phylogenetic clustering in isolated regional species pools.

Present-day local communities sampled from these isolated habitat species pools are more receptive to aliens as many of them belong to lineages not represented within the local community.

Assembly
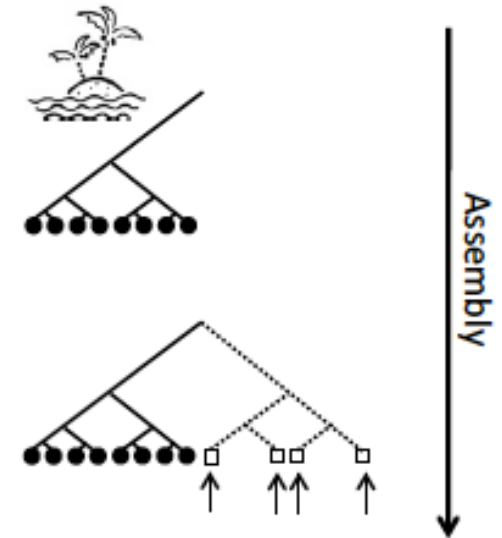
Phylogenetically Poor Plant Communities Receive More Alien Species, Which More Easily Coexist with Natives

Pille Gerhold,[1] Meelis Pärtel,[1] Oliver Tackenberg,[2] Stephan M. Hennekens,[3] Igor Bartish,[4,5] Joop H. J. Schaminée,[3] Alexander J. F. Fergus,[4,6] Wim A. Ozinga,[3,7] and Andreas Prinzing[3,4,*]
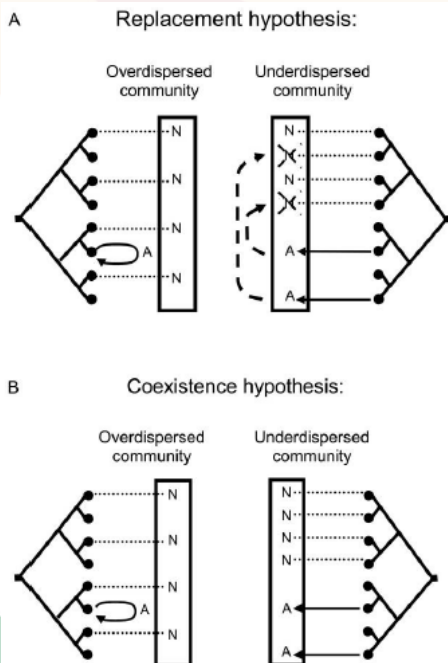
Community types composed of species from phylogenetically distinct lineages (i.e., phylogenetically rich or overdispersed communities) are less receptive to alien establishment. In contrast, community types consisting of closely related species (i.e., phylogenetically poor or underdispersed) are more receptive to aliens.

Fish species introductions provide novel insights into the patterns and drivers of phylogenetic structure in freshwaters

Angela L. Strecker[1] and Julian D. Olden[2]

- Phylogenetic clustering and overdispersion of native and non-native fishes of a large river basin in the American Southwest were quantified to test for the mechanisms (environmental filtering versus competitive exclusion) and spatial scales influencing community structure.

- Contrary to expectations, non-native species were phylogenetically clustered and related to natural environmental conditions.

- The species that are most invasive (in terms of ecological impacts) tended to be the most phylogenetically divergent from natives across watersheds, but not within watersheds, supporting the hypothesis that Darwin's naturalization conundrum is driven by the spatial scale.
  - Phylogenetic distinctiveness may facilitate non-native establishment at regional scales
  - Environmental filtering restricts local membership to closely related species with physiological tolerances for current environments.

Applicazione per Lifewatch

- Ambiti di applicazione per i casi studio LW
  - Hotspot biodiversità
  - Specie aliene
    - Alien species are phylogenetically clustered or phylogenetically overdispersed
      - In diversi gruppi tassonomici
      - In diversi ambienti?
      - In diversi ambienti x gruppi tassonomici?
    - Alien lineages are phylogenetically close or not to native lineages?
 - Struttura di comunità

PD in pratica

- ## Cosa serve:
  - ### Gruppi tassonomici per le specie native
    - Selezionare gruppi tassonomici con un buon coverage in differenti habitat per I quali è disponibile un buon numero di sequenze in genebank
  - ### Filogenesi
    - Single marker (COX1, CYT-B)
    - Supertree
    - Supermatrix
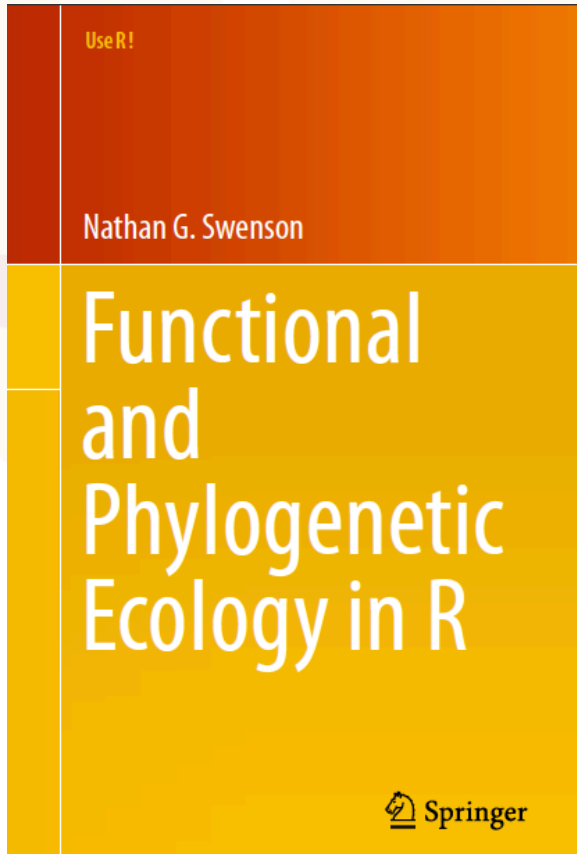   - Total-evidence (4-5 marcatori+morfologia?)

Outcomes

- Statistical Workflow

- Tools (per analisi filogenetica e assessment della PD)

- Mappe (diversità filogenetica per areaXgruppo tassonomico di interesse)

- Papers

Mappe
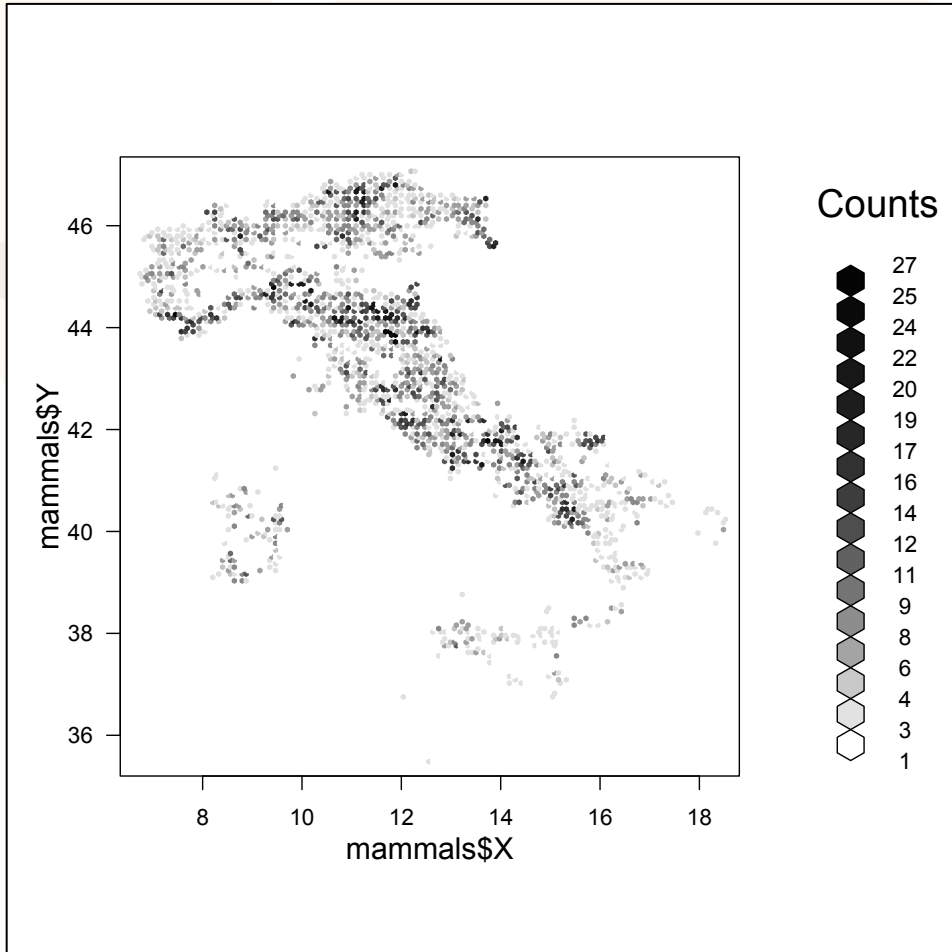
Diversità Filogenetica?

Statistical workflows

Use R!

Nathan G. Swenson

Functional
and
Phylogenetic
Ecology in R

Springer

Methods in Ecology and Evolution

Methods in Ecology and Evolution 2015, **6**, 232–236

doi: 10.1111/2041-210X.12310

British Ecological Society

APPLICATION

BAT – Biodiversity Assessment Tools, an R package for the measurement and estimation of alpha and beta taxon, phylogenetic and functional diversity

Pedro Cardoso[1,2]*, François Rigal[2] and José C. Carvalho[2,3]

Picante: R tools for integrating phylogenies and ecology

About Picante

The Picante package provides tools for **P**hylocom **i**ntegration, **c**ommunity **a**nalyses, **n**ull-models, **t**raits and **e**volution in R.

The package includes functions for analyzing the phylogenetic and trait diversity of ecological communities, comparative analyses, and the display and manipulation of phenotypic and phylogenetic data.
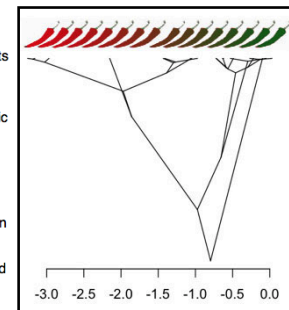
Package maintainer: Steven Kembel

Developers: Peter Cowan, Matthew Helmus, Steven Kembel

Contributors: David Ackerly, Simon Blomberg, Will Cornwell, Peter Cowan, Matthew Helmus, Steven Kembel, Helene Morlon, Cam Webb
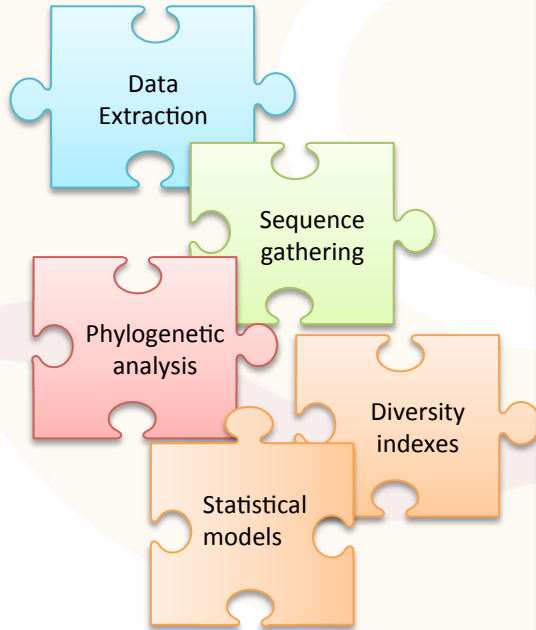
Development of picante has been supported by NSERC, NESCent, the Google Summer of Code, and the Gordon and Betty Moore Foundation.

Thanks to Jonathan Davies, Kyle Dexter, Catherine Graham, Nathaniel Hallinan, Nick Matzke, Alain Paquette, Emmanuel Paradis, Juan Parra, Dan Rabosky, and Marten Winter for feedback and bug reports. Thanks to R-Forge for hosting the project.

R-Shiny Apps

Data Extraction
Sequence gathering
Phylogenetic analysis
Diversity indexes
Statistical models

Usare R per produrre singole applicazioni Shiny che possono essere usate per comporre un workflow

Data Extraction | Sequence gathering | Phylogenetic analysis | Diversity index | Statistical Models