**Notes for a review paper/thesis chapter on methods of measuring convergence**

Comments come from Natalie’s written notes on a printed copy when we were in Madagascar, April 2014

Write this as a chapter and then consider a paper sometime in the future

Currently this is a review/summary of methods without testing or comparing methods on my own data.

The selling point would be that it’s a combined summary of current methods of measuring convergence.

**Introduction**

* Common pattern, historical interest, repeatability of evolution ([cf. Blount et al., 2008](#_ENREF_4))
* General/conceptual papers on convergence ([Losos, 2011](#_ENREF_18), [Conway-Morris, 2006](#_ENREF_7), [Scheffer and van Nes, 2006](#_ENREF_26)) historical contingency ([Blount et al., 2008](#_ENREF_4))
* Historically (and some current studies) are generally qualitative but increased interest and importance of quantitative approaches, especially since ([Stayton, 2008](#_ENREF_30))
* Distinction between describing patterns of convergence and interest in their adaptive significance ([Tseng, 2013](#_ENREF_31), [Moen et al., 2013](#_ENREF_21), [Elias et al., 2008](#_ENREF_9), [Jones and Holderied, 2007](#_ENREF_15), [Clark et al., 2005](#_ENREF_6), [Donley et al., 2004](#_ENREF_8))
* Three main categories of convergence papers;

1. Papers which don’t specifically quantify convergence (there are lots more references which could be added here) ([Leal et al., 2002](#_ENREF_17), [Ojeda et al., 1999](#_ENREF_23), [Ben-Moshe et al., 2001](#_ENREF_2), [Fleischer et al., 2008](#_ENREF_10)) including recent genomic convergence ([Parker et al., 2013](#_ENREF_24), [Jones et al., 2012](#_ENREF_14))
2. Papers which quantify convergence (usually using simulations); ([Muschick et al., 2012](#_ENREF_22), [Stayton, 2008](#_ENREF_30), [Mahler et al., 2013](#_ENREF_19), [Ingram et al., 2013](#_ENREF_13), [Harmon et al., 2005](#_ENREF_12), [Moen et al., 2013](#_ENREF_21), [Segar et al., 2013](#_ENREF_27), [Alvarado-Cárdenas et al., 2013](#_ENREF_1)) or via comparisons to other closely related species ([Donley et al., 2004](#_ENREF_8), [Jones et al., 2012](#_ENREF_14))
3. Papers which fall somewhere in between; they don’t just look at patterns but don’t measure significance either ([Tseng, 2013](#_ENREF_31), [Wroe and Milne, 2007](#_ENREF_32), [Jones and Holderied, 2007](#_ENREF_15), [Bernal et al., 2001](#_ENREF_3), [Kawahara and Rubinoff, 2013](#_ENREF_16), [Clark et al., 2005](#_ENREF_6))

* Other methods papers (which don’t fall into the categories above): ([Stayton, 2005](#_ENREF_28), [Stayton, 2006](#_ENREF_29))
* Summary of the approaches in the methods papers

**Methods of quantifying convergence**

1. **Across a tree**

**Weighted Count Metric** ([Stayton, 2008](#_ENREF_30))

* Convergence across a tree
* Count the number of taxa whose nearest neighbours in morphospace are not sister taxa
* Multiply that number by the patristic distance separating the two taxa
* Sum those scores over the entire tree
* Standardise by dividing all distances by the maximum patristic distance between taxa remember to define patristic distance and maybe show this on figures where possible

1. **Between species pairs**

**Multidimensional convergence index** ([Stayton, 2006](#_ENREF_29))

* A priori definition of putatively convergent taxa
* Calculate disparity metrics for convergent taxa and their sister groups
* Sister groups are the most closely related clade that don’t share convergent features
* MCI is the ratio of disparity of all sister taxa to the disparity of the convergent taxa
* High values of MCI indicate clustering relative to sister taxa and therefore convergence
* Permutation resampling without replacement to test for significance

**Comparing morphological and phylogenetic distance** ([Muschick et al., 2012](#_ENREF_22))

* Between species, no a priori definitions
* Morphological vs. phylogenetic distance for each species pair
* Compared to simulations of trait evolution (BM and OU)
* Morphological distance from regression of shape against centroid size (MorphoJ)
* Hexagonal binning to deal with over-plotting

**Morphological vs. ecomorph convergence** ([Harmon et al., 2005](#_ENREF_12))

* Separate morphological distance matrices for different traits
* Binary ecomorph distance matrix for each species (Anoles!)
* Mantel tests: morphological vs ecomorph distance while controlling for phylogeny (almost the same as ([Melville et al., 2006](#_ENREF_20)))
* Convergence; species are more morphologically similar to other species within the same ecomorph class
* They also did phylogenetic (M)ANOVAs to test whether ecomorph categories differed in morphology

or lineages of species ([Revell et al., 2007](#_ENREF_25)) (NB: I need to finish reading the Revell paper)

1. **Community/faunal convergence (ecological +/- morphological)**

**Environmental niche convergence** ([Alvarado-Cárdenas et al., 2013](#_ENREF_1))

* Environmental niche models using MaxEnt
* Niche equivalence and similarity tests
* ENMTools to quantify environmental niche overlap (e.g. Schoener’s D score)
* Compared the observed D scores to a null distribution

**Ecological niche convergence** ([Elias et al., 2008](#_ENREF_9))

* Mutualism leads to ecological niche convergence in Müllerian mimic butterflies
* Ecological Euclidean distance matrix using five variables, binary mimicry distance matrix
* Partial Mantel test for correlation between ecological and mimicry distances while controlling for phylogeny – this method is dodgy, see Harmon and Glor 2010 – I have this in ReadCube but I haven’t read it yet
* Two ways of testing for ecological convergence and divergence

1. Calculated the average ecological distance among co-mimics, standardised by the average ecological distance for the tree and tested the significance against character simulations
2. Regressed ecological against phylogenetic distances, permuted the residual ecological distances among species pairs to determine whether observed residuals were more –ve or +ve than expected by chance for the co-mimics and non-co-mimics respectively

**SURFACE** ([Ingram et al., 2013](#_ENREF_13), [Mahler et al., 2013](#_ENREF_19))

* Faunal convergence – this is the same as community convergence
* Adaptive radiation, measuring convergence with OU models
* One or more continuous traits, assumes independent evolution of traits
* Simulate null models for each trait separately

**(Intercontinental) community convergence** ([Melville et al., 2006](#_ENREF_20))

* Morphological and microhabitat distance matrices (detailed Anole data)
* Partial Mantel tests to compare morphological and microhabitat distances while controlling for phylogeny (but problems with Mantel tests ([Harmon and Glor, 2010](#_ENREF_11)))
* Compare distances to expected differences under a null model of traits under BM

**(Intercontinental) community convergence** ([Moen et al., 2013](#_ENREF_21))

* Two reasons for species from different regions to have similar traits; convergent evolution vs. ecologically conservative dispersal
* Ecological, morphological and performance convergence (detailed frog data)
* Phylogenetic MANOVA on PC scores for morphology and performance to test their associations with particular habitats
* Test for conservatism
* Tested for effects of previous history – requires that you identify a focal group with ancestral ecology – so not directly applicable for me
* Convergence is shorter distance between two groups sharing the same microhabitat than between two groups that are closely related

**(Intercontinental) community convergence** ([Segar et al., 2013](#_ENREF_27))

* Specific wasp/fig system; three hypotheses to explain community structure – inheritance, convergence and constraint.
* Each hypothesis has makes specific predictions about the relative roles of ecology and phylogeny
* Clustered species into functional guilds and estimated ecological distance (not applicable for me)
* Tested for phylogenetic niche conservatism
* Phylogenetic eigenvector regression to quantify the relative contributions of ecological role and phylogeny to community structure
* New index; proportion of phylogenetic distance/proportion of ecological distance occupied by each species pair. Pairs within the 95% quantile are examples of phylogenetic>>ecological distance and therefore ecologically convergent species

([Burd et al., 2014](#_ENREF_5))

**Discussion**

* Variety of methods reflecting increased interest in quantifying convergence
* Importance of expanding and developing approaches to non-traditional study groups
* Make a comparison table with method, data required, suitability for different questions?

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