Genetic diversity's twin aspects: what sequence (or expression, etc), and how many of each sequence? New tricks for combining these.

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TAGC-PEQG

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Genetic diversity
-
crucial to
Evolution
& Conservation
Differences of:

Frequency P_i
+/OR
Function
- % nucleotide Diff.
- Expression Diff.

HOW To Combine These?

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Function (expression) diff:
Transcriptomes of
two major pest flies:
- Sympatric, interfertile
- Kept apart by time-of-day for mating.
- Only one is invasive

WITHOUT counterintuitive effects, eg:
- **Negative diversities!**
- **Similar** diversity despite **different** function
- **Unwanted Dependencies** EG % variation between-pop (AMOVA, Fst)
  - Decreases if the variation within-location increases
  - Even if the populations still share no sequences!

2 Functional Diversity Solution: 2

Two Complementary Profiles

Frequency: *q*-Profile (low *q* emphasizes rare alleles)

$q = 0$	$q = 1$	$q = 2$
Number of alleles, S	Shannon Entropy/Info	Heterozygosity / Nt diversity etc
$^0H = 1-S$	$^1H = -\Sigma\, p_i \log p_i$	$^2H = 1-\Sigma p_i^2$
$^0D = S$	$^1D = e^{(^1H)}$	$^2D = 1/(1-^2H)$

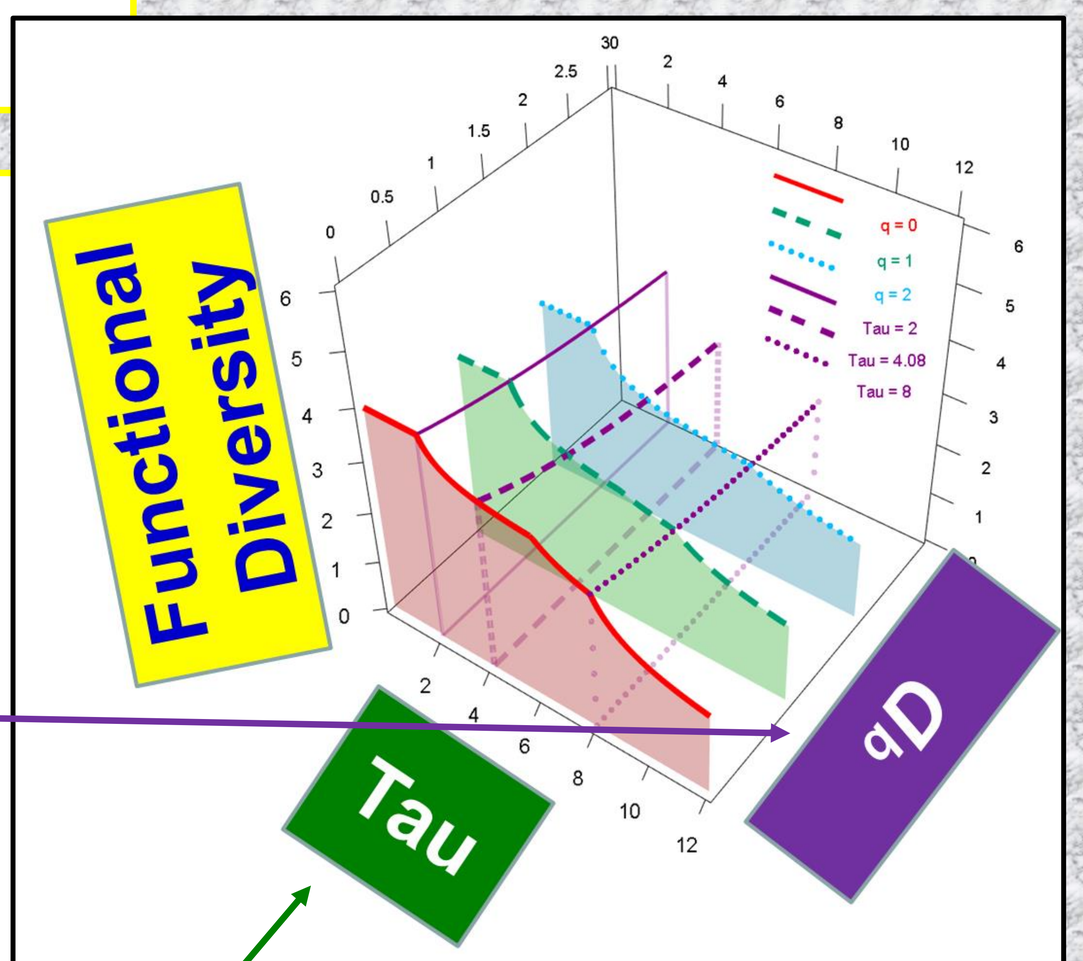
p_i = Proportion *("Frequency") of allele "i"*

Function: tau-profile (novel):
(low τ emphasizes finer distinctions Chao et al '19)

.- d_{ij} functional distance (expression level, base pairs…)

d_{ij}	Seq 1	Seq 2	Seq 3	Seq 4
Seq 1	0	2	8	8
Seq 2	-	0	8	8
Seq 3		-	0	6
Seq 4			-	0

.- Tau-cutoff: if $d_{ij} \geq \tau$, variants treated as functionally distinct
.- Use all possible τ-cutoffs, to give τ-profile



3 **3**

Profile shows *effective* numbers of molecular variants that are:
- *equally*-frequent

AND
- *equally*-functionally distinct

Best discrimination:
- usually with q=1 & mean Tau.

No Counterintuitive effects

Hierarchy possible:
- Within location (α)
- Between locations (β)
- Over all locations (γ)….

Video, Software, Refs….
- Chao et '19 ***Ecol. Monogr.*** 10.1002/ecm.1343
- Sherwin et '17. ***Trends Ecol. Evol.*** 32: 948 (with video)
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