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**D. Schleuter, M. Daufresne, F. Massol, and C. Argillier. 2010. A user's guide to functional diversity indices. *Ecology* 80:469–484.**

## Appendix C: One-dimensional functional divergence ( $FD_s$ )

Functional divergence measures the clustering of species along the trait axis and is often approached through the weighted variance of trait values. However, it can also be expressed through the relative range of trait distribution.  $FD_s$  is a new index specifically designed to compute divergence based on the span of trait distribution (calculated as the range between the lower quartile  $Q_1$  and the upper quartile  $Q_3$ ). The advantage of  $FD_s$  in contrast to the variance is that it is *always* low when species traits are clustered (be it at the edges or in the centre, Fig. C1). The broader the distribution within the range, the higher  $FD_s$  gets.

The recipe to compute  $FD_s$  is as follows. First, each species' mean trait value  $X_{ts}$  (in a given community) is replicated  $A_s$  times ( $A_s$  is species  $s$  abundance in the community):

$$Y_t = \left[ \underbrace{X_{ts}, X_{ts}, \dots, X_{ts}}_{\times A_s} \right] \quad (C.1)$$

Example:

When  $A_{s_1} = 3$ ,  $A_{s_2} = 5$  and  $A_{s_3} = 2$ , we get:

$$Y_t = [X_{t1}, X_{t1}, X_{t1}, X_{t2}, X_{t2}, X_{t2}, X_{t2}, X_{t2}, X_{t3}, X_{t3}]$$

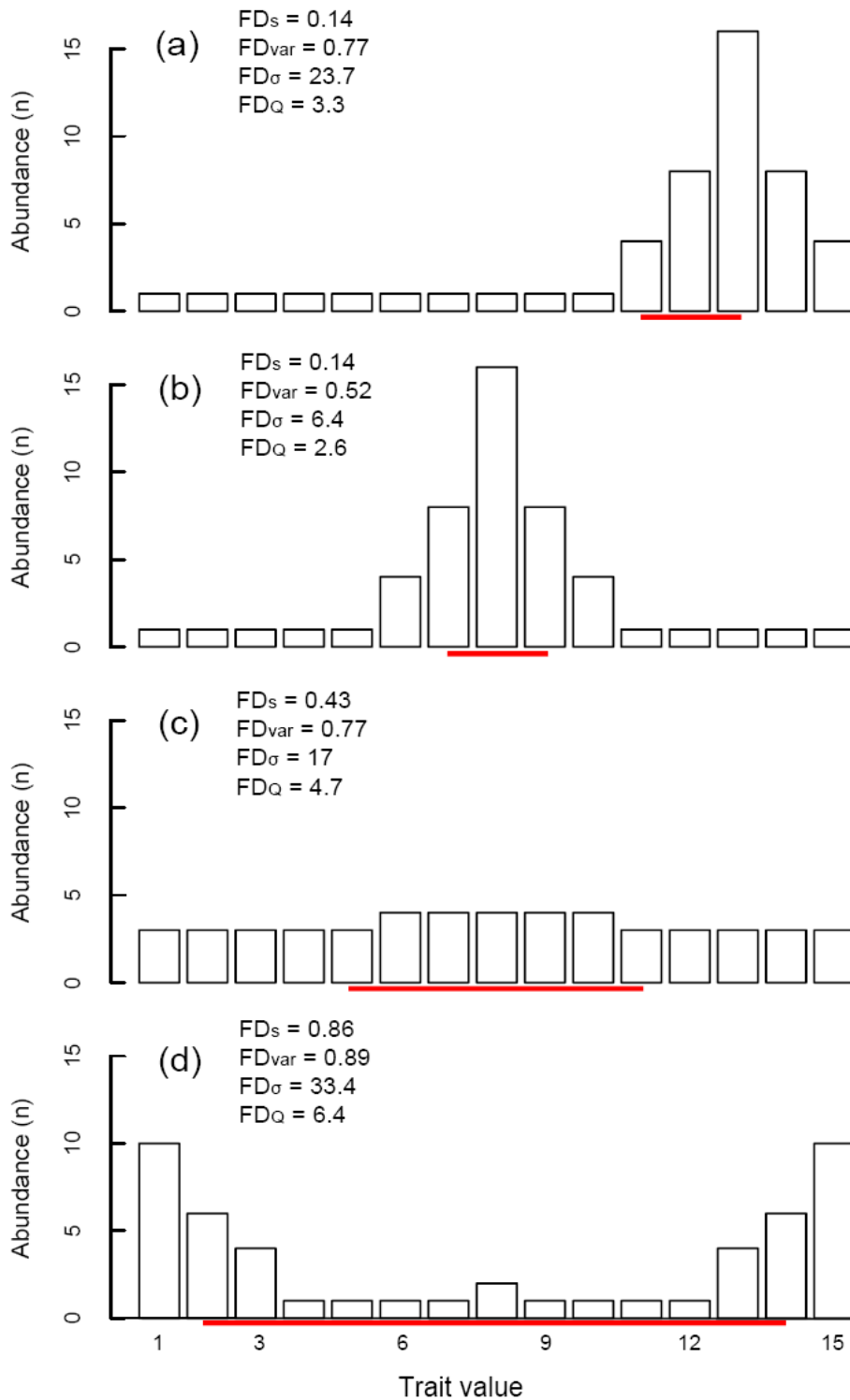
In a second step, the  $z^{\text{th}}$  percentiles (here  $Q_1$  and  $Q_3$ , corresponding respectively to the lower and upper 25% of the replicated  $X_{ts}$ ) of the vector  $Y_t$  are calculated:

$$P_t = Q_1(Y_t) - Q_3(Y_t) \quad (C.2)$$

In the last step,  $P_t$  is divided by the overall trait range of the community:

$$FD_s = \frac{P_t}{\max_{s \in S_c}(X_{ts}) - \min_{s \in S_c}(X_{ts})} \quad (C.3)$$

overall range



**Fig. C1** – 50 individuals, who are distributed into 15 species with different trait values between 1 and 15. In each graph the distributional center of trait values (second and third quartiles) is underlined in red. For each example, all one-dimensional functional divergence values are given. a) one cluster, centered at the right edge; b) one cluster centered in the middle (c) no cluster, distribution close to uniform (d) two clusters at both edges of the trait axis.