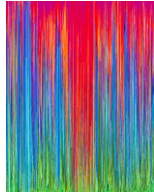


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Cover photo: A new method called topology weighting provides a visual summary of evolutionary relationships across the genome. This figure summarizes the relationships among 18 individual *Heliconius* butterflies from five distinct populations across a one million base-pair region of their genome. Each color represents a different tree of relationships among the populations. The strong excess of reddish colors in the middle of the region is due to an adaptive introgression event, in which a beneficial wing patterning allele from one species was acquired by another through hybridization, making these two species more closely related in this part of the genome than in other parts. Topology weighting could be used to explore the genomes of other species for similar signals. See [Martin and Van Belleghem](#), pp. 429–438. Image courtesy of Simon Martin.

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