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David Sankoff* (sankoff@uottawa.ca). *Fractionation after whole genome doubling.*

A basic tool for studying the polyploidization history of a genome, especially in plants, is the distribution of duplicate gene similarities in syntenically aligned regions of a genome. This distribution can usually be decomposed into two or more components identifiable by peaks, or local maxima, each representing a different polyploidization event. The distributions may be generated by means of a discrete time branching process, followed by a sequence divergence model. The branching process, as well as the inference of fractionation rates based on it, requires knowledge of the ploidy level of each event, which cannot be directly inferred from the pair similarity distribution. We have developed a way of inferring the ploidy of up to three successive WGD and/or WGT events by estimating the time of origin of each of the similarities in triples of genes. This may be generalized to a larger number of events and to higher ploidies. (Received August 25, 2019)