1073-05-98   **Eva Czabarka**, **Peter L Erdos**, **Virginia Johnson*** (`johnsonv@mailbox.sc.edu`) and
          Vincent Moulton. *Counting gene trees.*

Gene trees used in biology to describe the evolution of genetic material throughout different species. Internal nodes of the tree correspond to speciation or duplication events, and the leaves are labeled with the name of the species the gene comes from. Consequently, gene trees are leaf-labeled trees which ideally but not necessarily are rooted, the root is the only vertex that may have degree 2, and labels in the label set may be used multiple times or not at all (the latter corresponding to deletion events). Otter in 1949 has proved a formula on unlabeled trees that connects counts of rooted trees to corresponding counts of unrooted trees. We generalize this formula for semi-labeled graphs, and use this to provide ordinary generating functions for gene trees (binary or non-binary, rooted or unrooted) and leaf-labeled trees (where internal nodes may have degree 2 even if they are not the root) (Received July 28, 2011)

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