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Q: Combinatorial logic over the structure of a parse tree We say a parse tree for a natural language sentence  $s$  is an "ancestry tree", if every leaf  $u$  of the tree is labeled with a grammatical head  $w$  of some  $w \in \mathcal{W}(s)$ , and the labels are ordered such that the first is  $w$  and the last  $w$ , and each node is labeled with the set of labels of its children. In this situation, the order of the children of a node is defined by the order of the leaves in the ancestral path connecting the parent node with the first leaf. Given a parse tree  $T$ , with  $|\mathcal{W}(s)|=n$ , and a leaf  $u$ , how can we decide whether  $u$  is the last leaf of  $T$ ? A: This problem can be solved by counting unique paths in the parse tree. Since any grammatical sentence  $s$  has exactly  $n$  words, a parse tree will have  $n$  nodes (and no further nodes). Let  $L_u$  be the set of labels on the path from  $u$  to the root of the tree, with  $u \in \mathcal{W}(s)$ . Note that  $|L_u| \leq n-1$ , since there is at least one leaf in  $L_u$ , and  $|L_u| \geq n-1$ , since there are no leaves in  $L_u$ . If  $|L_u|=n-1$ , then  $u$  is the last leaf in the tree. This problem is discussed in "Algorithms for Parsing Sentences into a Dependency Tree", which appears in the proceedings of the 6th International Conference on Artificial Intelligence and Statistics (AISTATS'06). Modulation of the proliferation of mouse, rat and human mast cells by the dietary fatty acids. Dietary fatty acids, possibly through their impact on the microflora of the intestine, may exert influence on the function of cells of the immune system. The effect of fatty acids on the proliferation of mast cells (MC) is of particular interest since these cells may play a key role in the pathogenesis of allergy. The aim of the present study was to examine the effects of fatty acids on the proliferation of mouse, rat and human MC (hMC) in 82157476af

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