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--whos.in--Propeller shaft blowout. The purpose of this study was to determine whether an integrated drilling system causes rotating shaft blower malfunctions. A 5.0-liter turbocharged 360-horsepower engine was used as the driving system. The engine was equipped with two prop shafts, one with two props and the other with five props. The prop shafts were designed by Imlac. One shaft had an oil feed rate of 900 ft/min, and the other shaft had an oil feed rate of 1600 ft/min. The oil feed rate was monitored by an oil feedage signal from the alternator. The engine was installed in a chassis that was modified to make it easy to remove the props. A prop shaft blowout caused by a low oil temperature occurs if the oil feed rate is greater than 1175 ft/min. The blowout occurred when the prop shaft was rotating, and the engine was running. The engine stalled, and the engine stopped running when the driver attempted to start it again. There was no detectable oil leakage. Analysis indicated that a sudden increase in the air-to-oil ratio around the prop shaft caused the blowout. The engine was not damaged, and the problem was not caused by excess oil pressure. Smaller-diameter prop shafts that are not used for heavy-duty purposes do not require prop shaft blowouts. It is suggested that the same problems may occur with any spinning propeller, even if the oil is fed at low speed., it is possible that NEB reads the default sequence value of the start codon GTG for the first amino acid codon and ignores other upstream sequences. In the computational model for CAA codon usage, it is assumed that the main determinant for the frequency of CAA codon usage is the preference for GTG at the first nucleotide position. For any given GTG sequence, the initial frequency of CAA codon usage is determined by an optimization model. It assumes the independence of sequence features to be determined by such an optimization model. It is not limited to nucleotide diversity and GC content at the first base position. For YAA, UAA and NAA codons, it is not assumed that the first base position affects the relative frequency of usage to any significant extent. That is, there is no preference for a given nucleotide sequence. In this regard, it is expected that the predictive power of the computational model is more accurate for YAA,

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