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Mathematical Modeling of HCV

We present a mathematical model which describes the development of HCV, and its resistant variants, in a patient. We assume that, apart from the variants that are already in the patient's blood stream, it requires only one more mutation at a specific nucleotide for an HCV virus to become resistant to the antiviral drug being administered, i.e for $S_{u,0}$ (virus, together with all its variants, present when the treatment starts) to change into $S_{u,1}$, virus which is resistant to the drug (telaprevir). We assume that, in the presence of drug pressure, it is easier for $S_{u,0}$ to change to $S_{u,1}$ than the other way around, so that we assume that the probability of $S_{u,1}$ changing to $S_{u,0}$ is much smaller than the one of $S_{u,0}$ changing to $S_{u,1}$. We also assume that $S_{u,0}$ changes to $S_{u,1}$ after one more mutation at a given nucleotide. The Model will say that there are exactly two outcomes of treatment: either the patient has a REBOUND of virus or SVR, sustained viral recovery. The model will also say a protease inhibitor, like telaprevir, has profound effect on treatment.