Comparison of Markov and Discrete Event Simulation Models for HIV-Disease

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Objective

To compare the output data from a Markov model and a Discrete Event Simulation (DES) model in order to determine which model is more realistic for a specific disease process.

Methods

Using a previously published Markov model, the output data was compared with the output of an identical DES model. The models were run on a coeditor for each regimen on costs and QALYs (Quality-Adjusted Life Years). The final model was compared with a previously published Markov model.

The model is not limited to a single process, but can with ease contain many sub-processes. In our case, we use a sub-process that allows for transitions between the CD4+ T-cell count and HIV-1 RNA levels (viral load, VL) every 3 months.

In addition, the output data allows for the user to see the relationship between two sub-models. This can help the user understand the outcomes of the model and make changes to the model accordingly. The output data can then be compared with previous studies to see if the outcomes are consistent.

Results

Comparison of DES model to Markov model (Figure 7)

The results of both models are used to evaluate the outcomes of the DES model. The results are then compared with the results of the Markov model. The results show that the DES model is more accurate in predicting the outcomes of the disease.

Conclusions

Due to the limitations of the Markov model, researchers end up using a combination of simulation software that can overestimate a patient’s progression from a subclinical condition to a more advanced stage of disease. Discrete Event Simulations are more effective in predicting the outcomes of individual patients and are not subject to the limitations of the Markov model. This provides a probabilistic sensitivity analysis, which is something that cannot be performed with a Markov model.

References


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