

# Predictions of Future HIV Infection by Subtype and Circulating Recombinant Form.

Brown B.J.<sup>1</sup> and Zhang L.<sup>2</sup>

*Department of Mathematics, National University of Singapore  
Science Drive 2, Singapore 117543*

## ABSTRACT SUMMARY

Twenty three million people have died as a result of the onset of acquired immunodeficiency syndrome, better known as AIDS, caused by the HIV virus. This tells us that AIDS is one of the worst diseases in existence. Sub-Saharan Africa had a total of 25 million HIV infections in 2000 and 29 million infections in 2002. Globally, the world contained a total of 36 million HIV infections in 2000 and 42 million in 2002 [6]. The subtypes causing HIV infections in Sub-Saharan Africa will be the most common subtypes of HIV that cause HIV infection throughout the globe in the future since these subtypes account for 70 percent of global infections.

Phylogenetic analysis of HIV-1 strains has revealed that they could be divided into groups due to their high genetic diversity. Group M infections cause greater than 95 percent of infections across the globe [5]. Group M is especially genetically diverse thus it is broken into subtypes including A, B, C, D, E, F, G, H, I, and J. There are also circulating recombinant forms which are the combinations of these subtypes. Some of the recombinants include types AE, AG, AB, DF, BC, CD, AE, GJ, and others [5].

The different subtypes are generally geographically distinct with Sub Saharan Africa containing all known HIV-1 subtypes [5]. The HIV subtypes are associated with specific modes of HIV infection and transmission rates. Subtype B is associated with homosexual intercourse and intravenous drug use, whereas subtypes A, E, and C are associated with heterosexual transmission [1]. This finding coupled with the fact that subtype A has increased from 28 percent to nearly 35 percent of all cases is significant since it suggests that AIDS is being transmitted more through heterosexual sexual contact. Also, according to some studies, subtype A is most transmissible [7]. This leads us to believe that subtype A infections will continue to increase at a high rate in the future and possibly cause the majority of HIV infections within ten years.

All the data for comparing numbers of total worldwide HIV infection was obtained from the UNAIDS 2000 and 2002 reports on the epidemic [6]. Subtype data for the year 2000 was obtained from an article on global HIV subtypes [4]. The subtype data for the year 2002 was obtained from the Los Alamos National Laboratory [2]. The sample sizes for the 2000 and 2002 data on HIV subtypes can be viewed to show the accuracy of each years subtype approximations by region (table 1). Significant changes are viewed when considering the proportion of HIV infections caused by each subtype between the years 2000 and 2002 (figure 1).

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<sup>1</sup> Student

<sup>2</sup> Assistant Professor

Table 1. Sample sizes for HIV subtypes in the various regions around the world for the years 2000 and 2002.

<u>Region</u>	<u>Year 2000</u>	<u>Year 2002</u>
Southern Africa	744	430
West Africa	1,921	293
East Africa	1,969	498
Ethiopia	40	164
Central Africa	536	900
North Africa/Middle East	25	114
Western Europe	967	5,956
Eastern Europe and Central Asia	536	514
East Asia and Pacific	84	902
Southeast Asia	640	612
South Asia(excluding India)	52	142
Latin America and Caribbean	933	800
North America	57	8,668
Worldwide	8,504	19,993

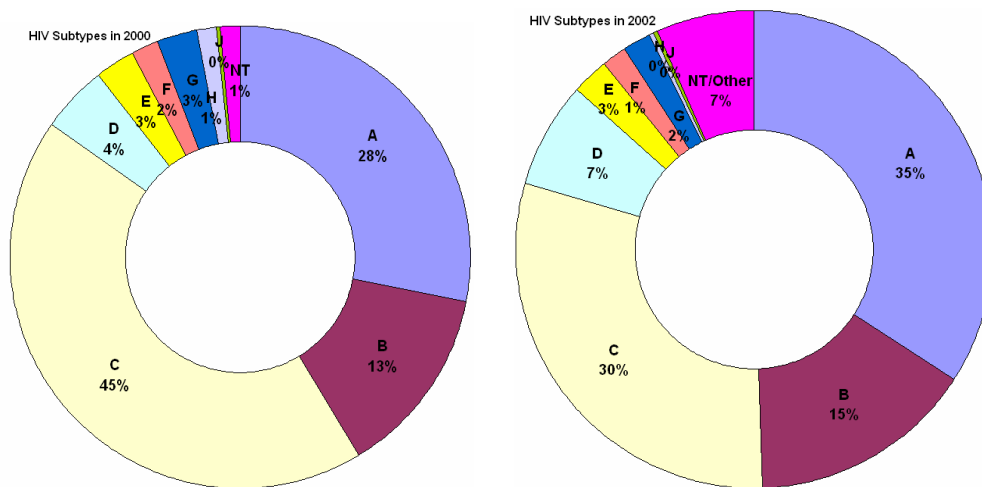


Figure 1. A comparison of the proportion of HIV infection by subtypes in 2000 (left) and 2002 (right).

We can observe that the two subtypes which caused the majority of HIV infection in 2000 and 2002 are subtypes C and A. It is significant to note that that subtype A HIV infections increased and subtype C HIV infections decreased as a proportion of the total infections within this period. This tells us that the growing problem of HIV will most likely depend more on subtype A infections, rather than subtype C.

We used three software programs to create exponential growth projections of HIV infections, and proportion of HIV subtypes, namely Matlab, Biota, and Populus. Using the ratio of change in total infections between 2000 and 2002 for each subtype and region, we acquired rates that we used to predict future HIV infections with results differing from UNAIDS for 2002 by less than one percent. Predicting HIV infection globally and within Sub-Saharan Africa results in an average of 57 million projected HIV infections for Sub Saharan Africa by 2010 and 81 million globally by 2010. In both cases, the number of HIV infections doubled. We also predicted HIV infections by

subtype from 2002 to 2010. Subtypes A, B, C, and D caused the majority of infections (figure 2). Our time step is organized in periods of one year each starting from 2000 and ending in 2010. The figure illustrates that subtype D seems to be at the root of a future HIV problem. Subtype D has a greater rate of increase of infection at the onset of the program with an 87.53 percent increase over 2 years compared to subtype A with an increase of 41.8 percent. The increase in subtype A is particularly likely since it is more easily transmissible and currently causes the majority of HIV infections worldwide. Infection by subtypes E, F, G, H, and I/J seem to be stabilized in terms of their rate of increase and their relationship to the dramatic increase of subtypes A, B, and D. The recombinants had also increased a great deal in the time period between 2000 and 2002, up 400 percent. In 2000, there were 480,541 recorded cases of recombinant HIV infections while in 2002 there were 2,829,630 cases [4]. This change is most likely due to the emergence of new subtypes that were not included in the subtypes counted in 2000.

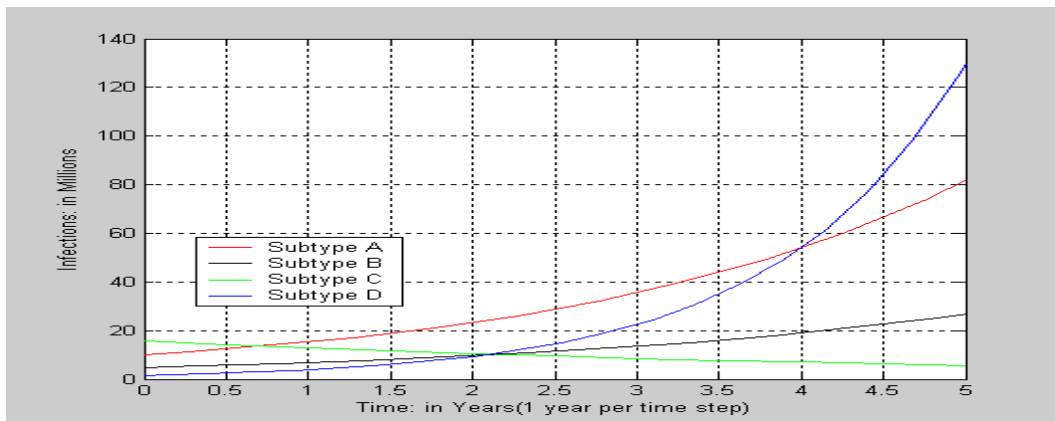


Figure 2. Future subtype approximations for A, B, C, D.

Next, we created a linear growth model for the subtypes using the same base case and change in cases of infection over two years as in the exponential model, but without the exponential term. Utilizing this model, we projected how many HIV infections will occur in the future if all trends for HIV infection growth continue to increase exactly as they did between 2000 and 2002 for each subtype and geographical region in 2010.

The linear and exponential models showed similar trends, but in comparison to the exponential models, the linear model results in a low number of predicted HIV infections for 2010. Another difference is that the exponential models yield subtype D as the major subtype causing infection, while the linear model predicts subtype A to cause the majority of infections. Nevertheless, due to the epidemiology of HIV-1 subtype A, coupled with the fact that it is more easily transmitted than subtype D, it is likely that subtype A will cause the majority of HIV infections in 2010.

The numerical data produced show that all 4 programs give similar output for the change in HIV infections by subtype and region. In order to validate the results obtained using our models, we compared our results with those of the United States National Intelligence Council and the XIV International AIDS Conference whom predicted 80 million and 87 million infections respectively by 2010 [3][9]. These numbers are comparable to our predictions using the various models (figure 3).

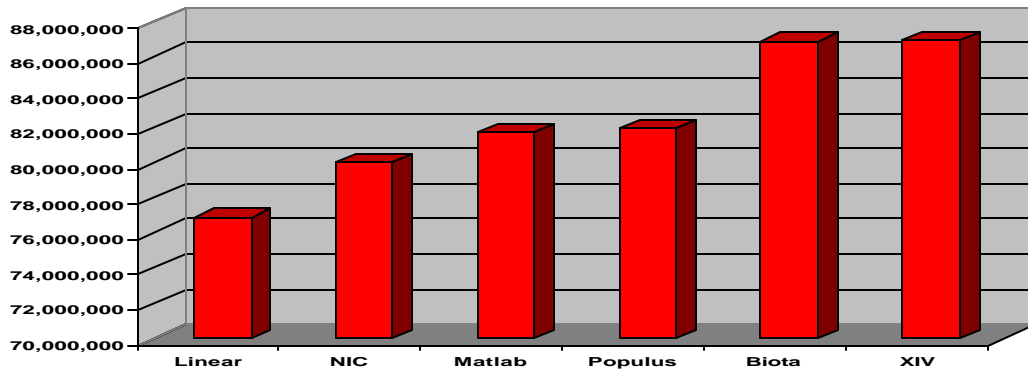


Figure 3. A comparison of projections of total HIV infections in 2010. NIC is the National Intelligence Council and XIV is the Barcelona 2002 International AIDS Conference.

There are also similarities in predictions with respect to regional infections. In our models, Sub-Saharan Africa controls not only the current trend but also the future spread of HIV infections, with a projected 58 million infections by 2010. The National Intelligence Council makes a similar prediction. They estimate that Nigeria and Ethiopia, two of the world's most populous countries, are two of the countries which will cause most of the HIV infections in 2010 [3]. These countries lie within Sub-Saharan Africa. Comparing our results on future global HIV infection and infection in Sub-Saharan Africa with other sources, we found that simple exponential and linear models can be used for a complex purpose.

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