

*O dentista infectou os seus pacientes com HIV ou não?*  
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## Background

In the spring of 1990, Kimberly Bergalis, a 22 year-old living in Fort Pierce, Florida, tested positive for HIV. This was surprising because she had no identifiable risk factors for contracting the virus. Epidemiological research focused on an invasive dental procedure performed by an HIV positive dentist, Dr David Acer, several years earlier. Searching the dentist's records revealed a number of other HIV positive patients, several of whom also had no known risk factors for contracting the virus. The Centers for Disease Control and Prevention (CDC) became involved and the case received a great deal of media attention due to the public's concern that HIV+ health care workers might be a threat to their patients. Multiple lawsuits were filed by these patients claiming the dentist infected them and they were now seeking damages (Donovan, p 1-2).

The case of the Florida AIDS dentist continues to fascinate many because it was unprecedented when first reported in 1990 by the CDC and it still remains unique today. No one has been able to put forth a likely mechanism for how the dentist infected his patients. It has been proposed that some of the patients had known risk factors for HIV and that others were not completely truthful about their medical, sexual and drug use histories. There is also possible evidence that potentially serious flaws in the phylogenetic analyses used by the CDC at that time concluded that the dentist and his patients had the same strain of HIV. (Barr, p. 2)

In this exercise we will look at how the analysis of viral evolution can be used to make biological and legal arguments about the transmission of the virus between individuals. Instead of looking for an identity match you will use the similarity between sequences to group strains of the virus and make inferences about their historical relationships. We now know that a population of HIV viruses within a person evolves quickly due to its rapid generation time and frequent mutations. (Donovan p. 1) The HIV virus can mutate within 24 hours and it is possible for a person to have several variations of HIV virus in his body at one time.

We will be using the same actual data that was collected and analyzed as part of the court proceedings. From this data we will look at the pattern of changes to see if these people shared the same virus source and we can then surmise whether the dentist did actually infect his patients.

As you try to establish whether there is evidence that the dentist was responsible for the HIV infection in his patients you will also explore:

- Characteristics of a nucleic acid sequence data
- How to align and compare multiple nucleic acid sequence data
- How to read a distance graph (unrooted tree) and make hypotheses about their evolutionary relationships

## Analysis

1. Use the sequences in the HIV.fas file.
2. Build a phylogenetic tree with a method at your choice.

Keeping in mind that the HIV virus evolves rapidly, it is unlikely that the viral sequences between individuals will be identical. However, using the assumption the genetically similar sequences are more closely related and possibly share a common ancestor, it is possible to make some inferences.

1. Write a brief summary of the argument you would make to a judge or jury regarding the claims from these patients that they received their HIV infections from the dentist. Refer directly to the data available in this exercise and be explicit about how you are interpreting it. Be careful not to overstate your conclusions.
2. What does the distance tree diagram tell you about the directionality of HIV transmission? What does it tell you about the likelihood of direct transmission between dentist and patient(s)? Does the language in the argument above reflect this understanding?
3. This exercise has been simplified dramatically by including only one sequence from each subject in the analysis. In fact, each of these individuals had a variable population of HIV in their bodies. How might information about the similarities and differences between HIV populations for each individual shape your argument?
4. Explain the importance of having local controls in your analysis. How are these sequences used to inform the case you make in the courtroom?