

# A Phylogenetic Analysis of the HIV-1 and HIV-2 Strains

## Initial Research Plan

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### Introduction / Rationale for Doing Project

HIV is a relatively new pandemic, responsible for causing AIDS and killing millions of people around the world. The two types of HIV known to cause AIDS, HIV-1 and HIV-2, have the same modes of transmission and clinical consequences. However, the two strains are very different in infection. HIV-2 is associated with lower viral loads and slower rates of CD4 decline, and as a result, HIV-1 is far more prevalent, accounting for a large proportion of AIDS cases.

Addressing these differences between the HIV-1 and HIV-2 strains using phylogenetic software may discover how and why these differences arise and how we can manipulate them to produce better treatments for HIV.

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### Hypothesis

By inspecting the genes of the HIV-1 and HIV-2 genome, it is hypothesized that, due to their many similarities in function, specific evolutionary relationships will be found between the two viruses and that these relationships can be expressed visually in the form of phylogenetic trees. It is expected that we will find how and why these differences arose and how they affect the virus's effectiveness.

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### Materials / Procedure

#### Materials

1. Modern computer with proper software downloaded and access to internet
2. A Nucleotide Database: [ncbi.nlm.nih.gov](http://ncbi.nlm.nih.gov) or [hiv.lanl.gov](http://hiv.lanl.gov)
3. Software
  - a. Download *KomodoEdit* (or any plain text editor), *Seaview*, *Mafft*, *Mesquite*, *BEAST*, *BEAUTi*, *Tree Annotator*, *Tracer*, *FigTree*

#### Procedure

1. Acquire all programs listed in "Materials".
2. Acquire data
  - a. Go to different nucleotide databases (e.g. [hiv.lanl.gov](http://hiv.lanl.gov), a database for HIV) and search for the necessary sequences.
  - b. Export a .fasta file with nucleotide sequences.
3. Aligning the File with *Seaview* / *Mafft*
  - a. Open the .fasta file in *Seaview*
  - b. Using the built-in alignment programs or *Mafft*, align the sequence
  - c. Optionally, you can manually adjust alignments with *Mesquite*

- d. Save aligned sequences in NEXUS format (.nex)
  4. Setting the Parameters for *BEAST*
    - a. Open the .nex file in *BEAUTi*
    - b. Separate the taxa into taxon sets depending on which sets are of interest
    - c. Set the dates of each taxa through “set tip dates” and setting them by hand
    - d. Click on Clock Models and change the Molecular Clock Model to a Strict Clock
    - e. Leave all else at the default settings unless you are willing to explore the other options that *BEAUTi* offers.
    - f. Click “Generate BEAST File” and an .xml file will be created.
  5. Input the .xml file into *BEAST* and click “Run”.
    - a. When *BEAST* is finished, it will produce a log file and a tree file in the same location as your .xml file
  6. Open the log file in *Tracer*
    - a. *Tracer* provides various graphs and quantities that can be used to explore *BEAST*'s output
  7. Open the tree file in *TreeAnnotator*
    - a. *TreeAnnotator* can be used to modify and annotate the tree file
  8. Open the tree file in *FigTree*
    - a. *FigTree* can view, color and change the trees as the user wishes
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## Data Collection and Analysis

With all of our data, we would first analyze how accurate it is, using some sort of guideline or another computer program. After confirming that our data is backed well, we would move to make some conclusions.

By inspecting the trees made, we can analyze the changes in the two viruses. We can note similarities, times and areas of divergence, and then relate these differences back to HIV-2's weaker infections in comparison to HIV-1's. We can repeat the procedure with a focus on other genes or proteins to get more data to use.

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## Bibliography

Baum, David. "Reading a Phylogenetic Tree: The Meaning of Monophyletic Groups." *Scitable*. NatureEducation, 2008. Web. 12 Oct. 2015.  
<<http://www.nature.com/scitable/topicpage/reading-a-phylogenetic-tree-the-meaning-of-41956>>. This article specializes in the reading and usage of an evolutionary tree, providing many illustrations to help detail the author's points. It goes over the different representations

of trees, and shows how although they look very different, they portray the same information.

Baum, David A., and Susan Offner. "Phylogenies and Tree Thinking." *American Biology Teacher* 70.4: 222-29. Print. This source provides an in-depth introduction to the concepts of phylogeny, going over basic definitions and terms while providing detailed examples with each topic. It is fairly accessible and goes into detail on mistakes that students make whilst analyzing trees, and how their use is more and more important in classrooms.

"Division of AIDS (DAIDS)." *National Institute of Allergy and Infectious Diseases*. Web. 12 Oct. 2015. <<http://www.niaid.nih.gov/about/organization/daids/Pages/default.aspx>>. This article provides basic information on the HIV virus, the HIV/AIDS epidemic, and what has been done so far to fight against it.

"Human Immunodeficiency Virus Type 2 (HIV-2)." *HIV Clinical Resource*. Web. 15 Nov. 2015. <<http://www.hivguidelines.org/clinical-guidelines/adults/human-immunodeficiency-virus-type-2-hiv-2/>>. This website provides an introduction to the HIV-2 subtype and talks about its history and effect on the human body. It also briefly discusses differences between it and the HIV-1 subtype as well as treatments for both viruses.

Nyamweya, Samuel, et al. "Comparing HIV-1 and HIV-2 Infection: Lessons for Viral Immunopathogenesis." *Wiley Online Library*. Web. 15 Nov. 2015. <<http://www.ncbi.nlm.nih.gov/pubmed/23444290>>. This article focuses on the differences between the HIV-1 and HIV-2 subtypes. It discusses differences in region, biochemistry, origin, and progression to AIDS. It also discusses how these differences could be used to better current treatment for HIV.

Thanukos, Anna. "Phylogenetic Systematics, a.k.a. Evolutionary Trees." *Understanding Evolution*. U of California Museum of Paleontology, 2006. Web. 12 Oct. 2015. <[http://evolution.berkeley.edu/evolibrary/article/phylogenetics\\_01](http://evolution.berkeley.edu/evolibrary/article/phylogenetics_01)>. This website provides further introductions into evolutionary trees, and defines various terms needed in the field. It also discusses the uses and applications of trees in modern-day biology.