# Bacheler Project: Strategy for Dropbox files

## Comparison-Stanford-Bacheler April 2016

* Kristof’s analysis of frequencies from Bacheler and Stanford data representing the global epidemic

## Data

* BachelerFiles (folder)
* Conservation Scores: ConSurf data- currently not used (folder)
* HIV\_Con\_2004\_POL\_DNA.fasta (.fasta)
* HIV Mut Rates: derived from the Abram et al., 2010 paper (folder)
* ZaniniNeher data (folder)
* LehmanData (folder)
* LosAlamosData- currently not used (folder)

## Manuscript

* Will contain versions of the manuscript, now moved to a Dropbox folder (no longer on GitHub)

## RScript

* AnalyseAndFigures for Bacheler, Lehman and Zanini data (.Rmd files)
* Backup (folder)
* baseScript (Rscript)
* createCodonMutationDistribution (.Rmd file)
* createFrequencies for Bacheler, Lehman and Zanini data (Rfiles)
* RResistanceMutations (Rscript)
* Shape-parameters (.txt file)

## Output

* OverviewSelCoeff\_Bacheler, Lehman and Zanini contain also ColMeans and Selection coefficients
* BachelerCountData for Alison
* freqPatTs Bacheler, Lehman, Zanini

## Simulations

No longer relevant

## GLM Analysis

prepareDataForGLM.R

reads: Output/BachelerCountData.csv or Output/BachelerCountData\_filter.csv

reads: Data/Pol\_shape.csv

make-F2-T1.r

needs: prepareDataForGLM.R

needs: helperFunctions ForF2.R

creates: modeled\_freqs\_May2017\_2.pdf

creates: modeled\_sels\_May2017.pdf

writes results to : GLMResultsText.txt

writes results to: SumOfModel1.html

modelPrepTest.R [THIS IS MAYBE NOT NEEDED?]

needs: prepareDataForGLM.R

make-F3.r

makes: F2-Bacheler-nonsyn.pdf

makes: F2-Bacheler-syn.pdf

makes: F2-Lehman-nonsyn.pdf

makes: F2-Lehman-syn.pdf

makes: F2-Zanini-nonsyn.pdf

makes: F2-Zanini-syn.pdf

AA.transition.figure.r

creates: aachangesNS.pdf

**Other files**

model.update.R I belive we don't need this anymore

DFEtables.R Same as make-F3

make-S2-ST2.r No longer needed

make-F1.r replaced by F1-v2.r

mut.types.r unclear what it does

dndsplot.r unclear what it does

DFEplots.r unclear what it does

dfe.r unclear what it does

model.r unclear what it does