

ASSIGNMENT 3

- The goal is to familiarize with commonly used *in silico* statistical methods for inferring the nature of amino acid substitutions, whether they are “deleterious” or “neutral”, whether positive or purifying (negative) selection can be inferred.
- You should find some gene sequence, and analyse it by two software:
- **Sorting for intolerant from tolerant, SIFT**, <http://sift.jcvi.org/>
- **Selecton**, <http://selecton.tau.ac.il/>
- Course website includes references to these methods. You should look at them.
- Write a short report which shows that you have understood what you have done and what kind of differences the two methods include as methods, and as leading to (maybe) differing results
- **Note added 29. Nov: As too many practical problems have arised, you´ll find in course website today evening some suggestions for gene data and you don´t have to find the gene by yourself, just do the analyses.**