

# Prediction of the effect of single aminoacid protein variants using deep mutational scanning data

University of Bologna — Master Thesis in Bioinformatics

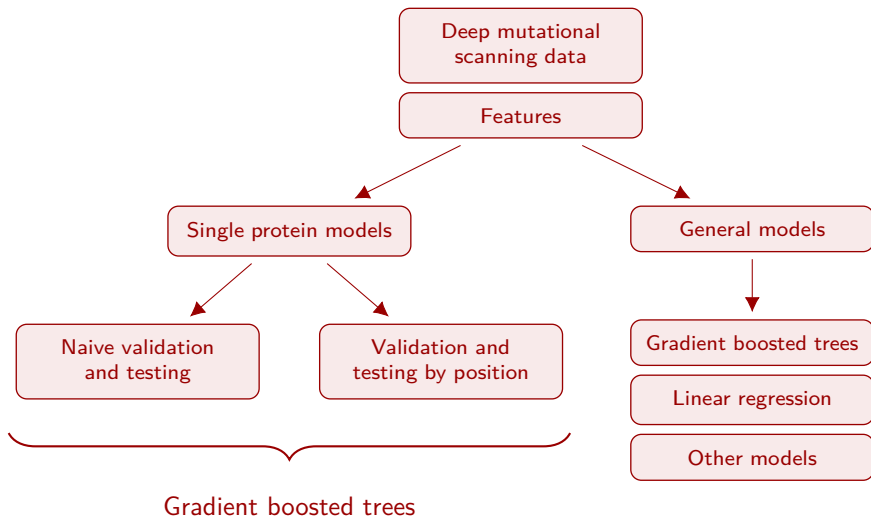
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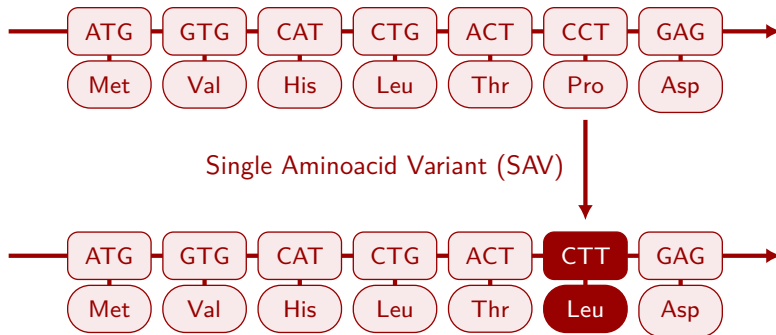
July 19, 2021

# Structure of the project

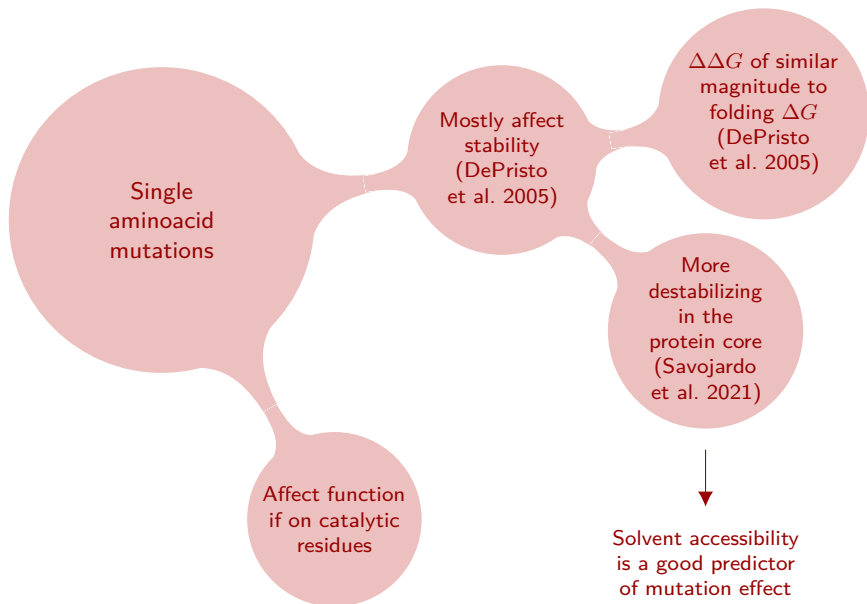


# Single aminoacid variants

In this work I focused exclusively on point missense mutations. Nonsense mutations, indels, and mutations in non-coding regions were not considered.



# Effect of single aminoacid mutations in proteins



# Deep mutational scanning

High-throughput technique for obtaining fitness information on a large number of mutations.

