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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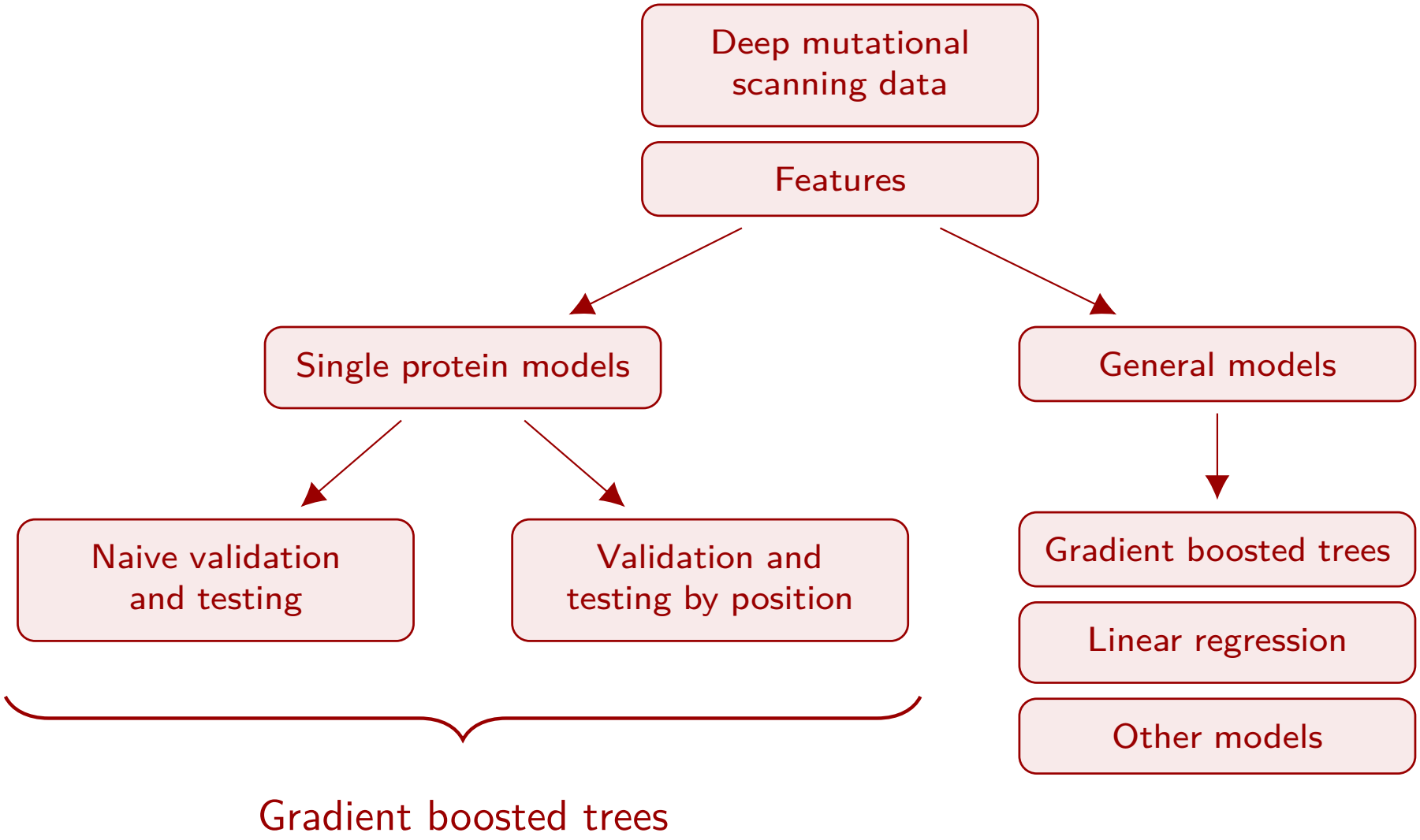
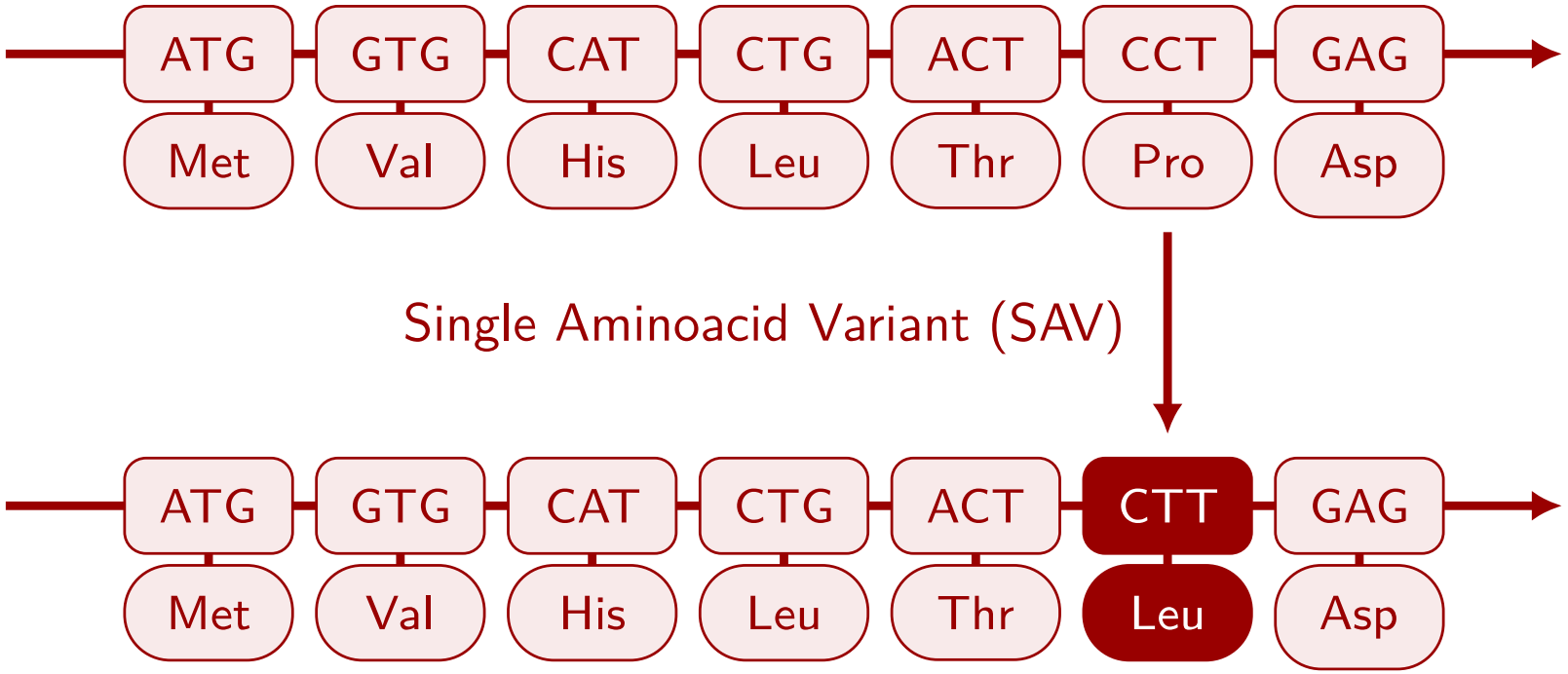
Structure of the project



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.