

Supplementary Material for How AlphaFold shaped the structural coverage of the human transmembrane proteome

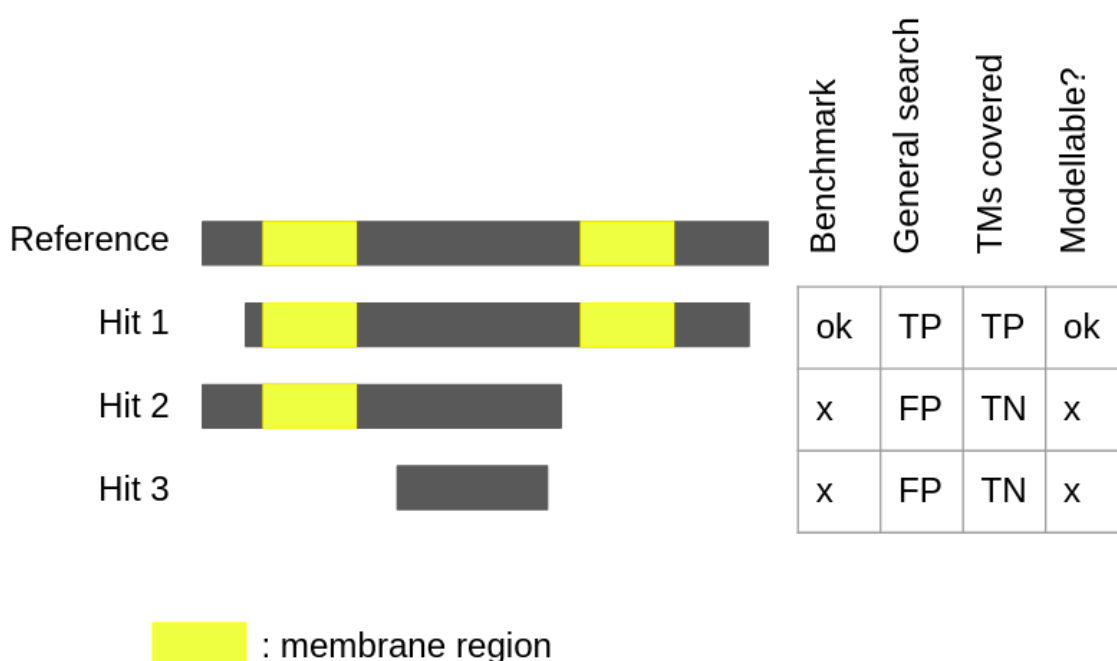
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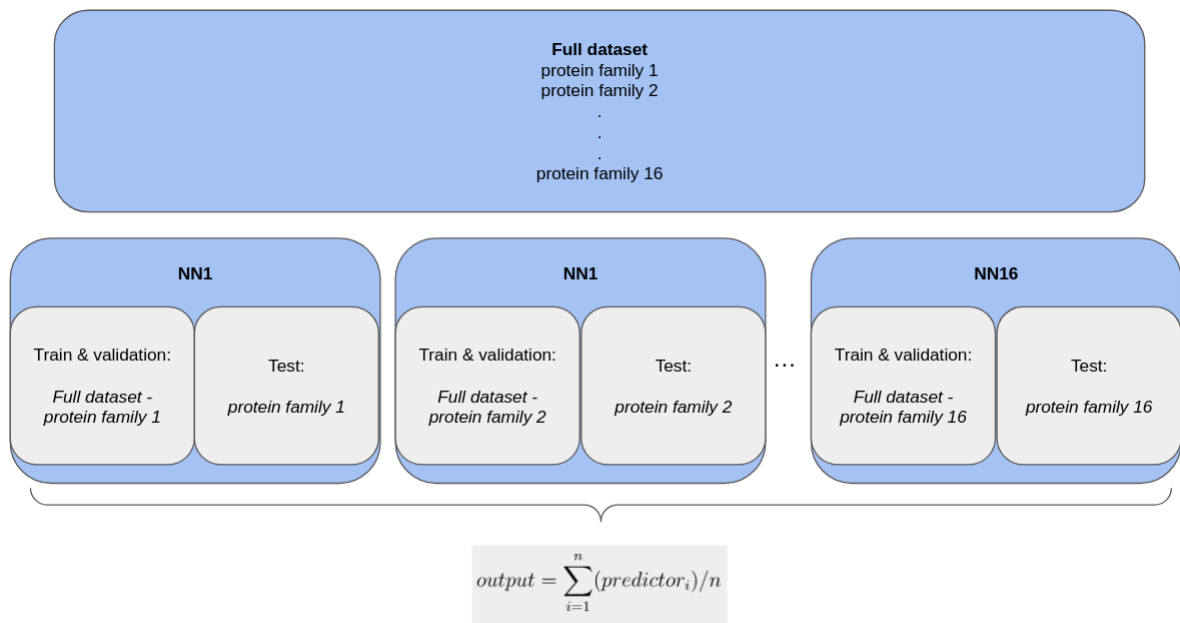
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Supplementary Figure 1: Logic of how homology searching results were handled. In the benchmark set we only accepted pairs of proteins where all TM regions overlapped. In general search, all kinds of hits were accepted. In the next search we required TMs to be covered, which eliminates Hit2/Hit3. If someone would like to model the structure of the TM domain, only hit 1 can be used as a reference (for homology modeling).



Supplementary Figure 2: Schematic graph of data processing in NNSearch