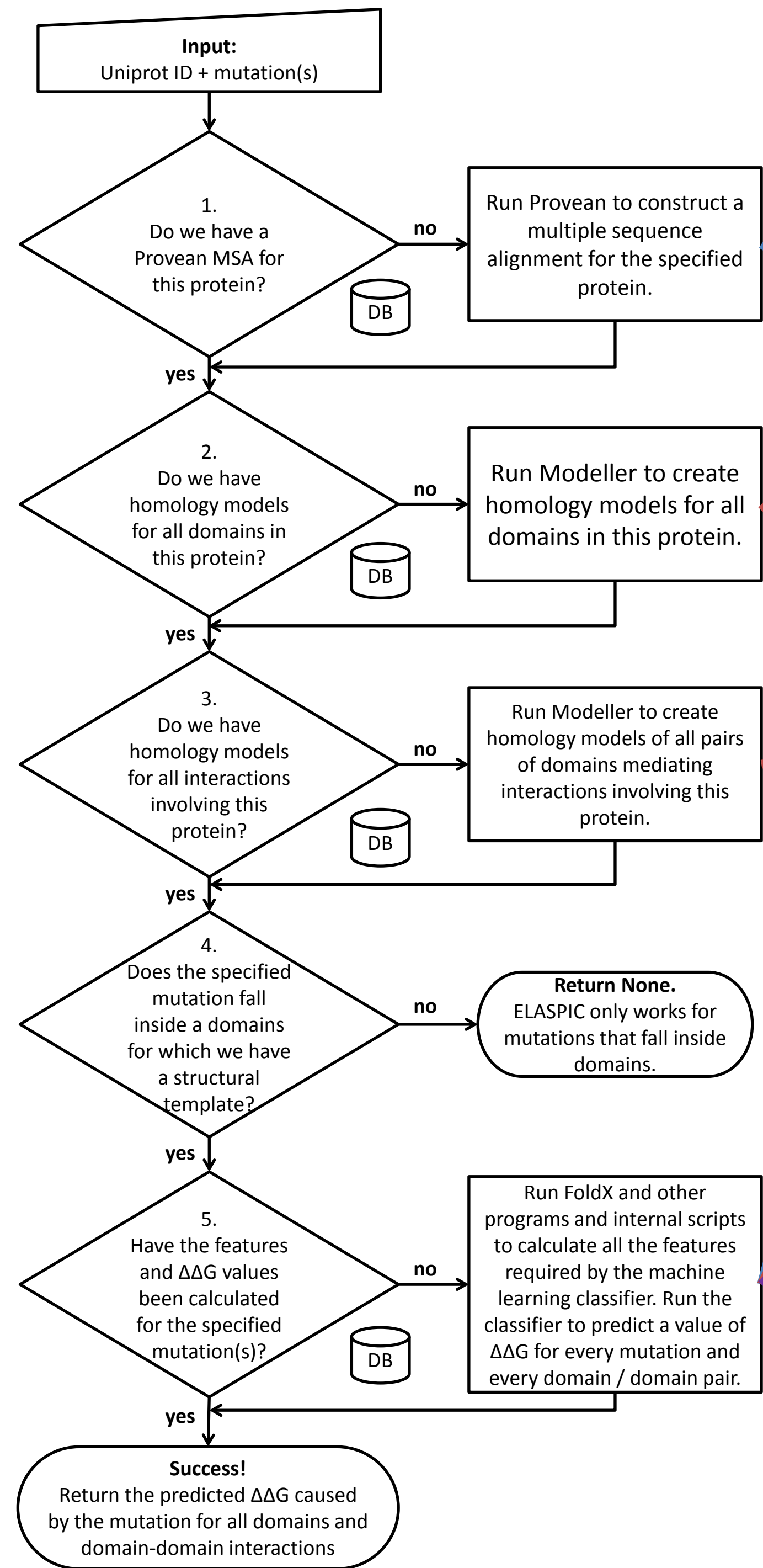


Database Pipeline



ELASPIC internals

elaspic_sequence.py
Input: fasta file with domain sequence
Output: proven supporting set
.mutate(mutation): to compute sequence-based features of a mutation.

elaspic_model.py
Input: fasta file with target sequences, pdb file of the template
Output: Homology model + model properties
.mutate(mutation): to compute sequence-based features of a mutation.

elaspic_predictor.py
Input: DataFrame of all features, with one mutation per row (as if pulled out from the database)
Output: $\Delta\Delta G$ predictions

Standalone Pipeline

