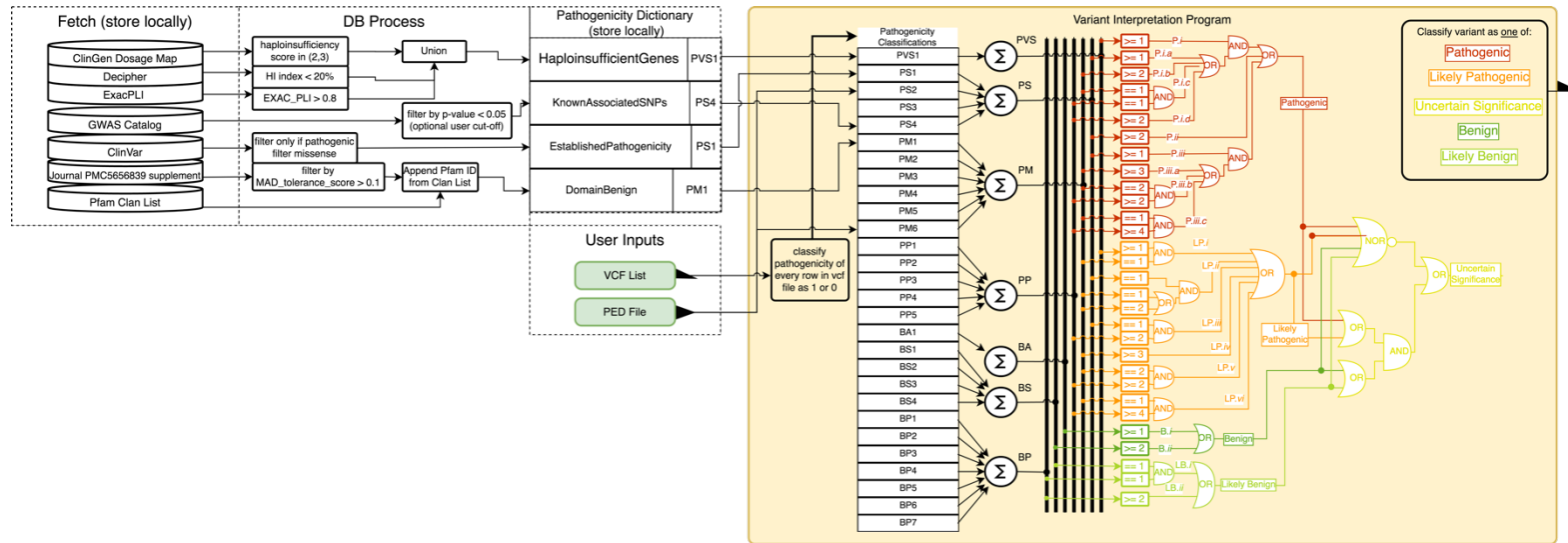




Supplementary Figure S3) Variant Interpretation Program (VIP) internal structure. External databases used for VIP are fetched and processed, with the output being stored in a MongoDB collection. In VIP, each database collection is associated with a specific ACMG classification, but not all classifications use these collections. Each row of the input VCF file is inputted to all classifications, flagging them as 1 or 0. Then, using the logic outlined in Table S2, the individual classifications are combined to provide the pathogenicity classification for each variant.