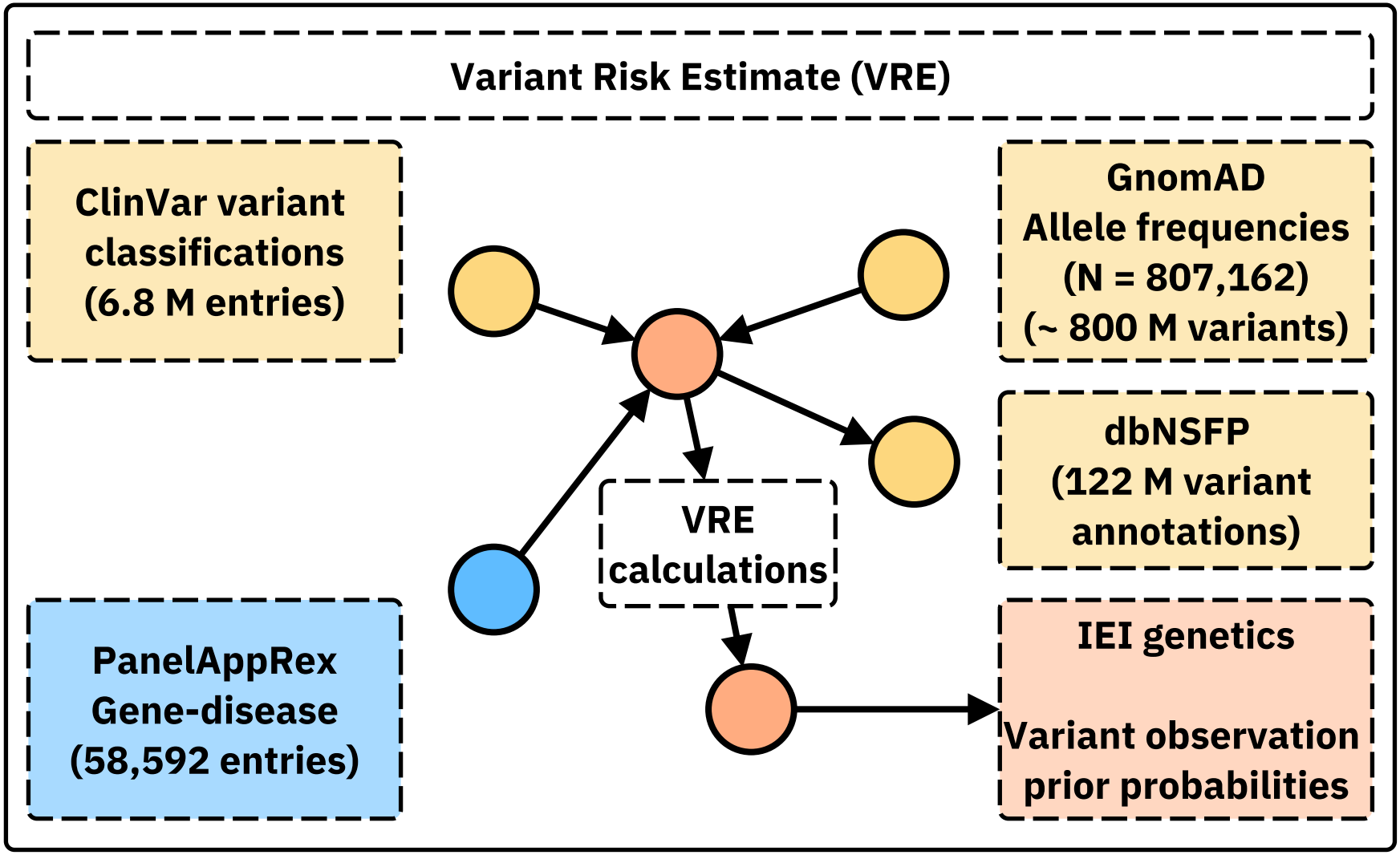
Variant Risk Estimate (VRE)
ClinVar variant classifications (6.8 M entries)
GnomAD Allele frequencies (N = 807,162) (~ 800 M variants)
dbNSFP (122 M variant annotations)
VRE calculations
PanelAppRex Gene-disease (58,592 entries)
IEI genetics
Variant observation prior probabilities