

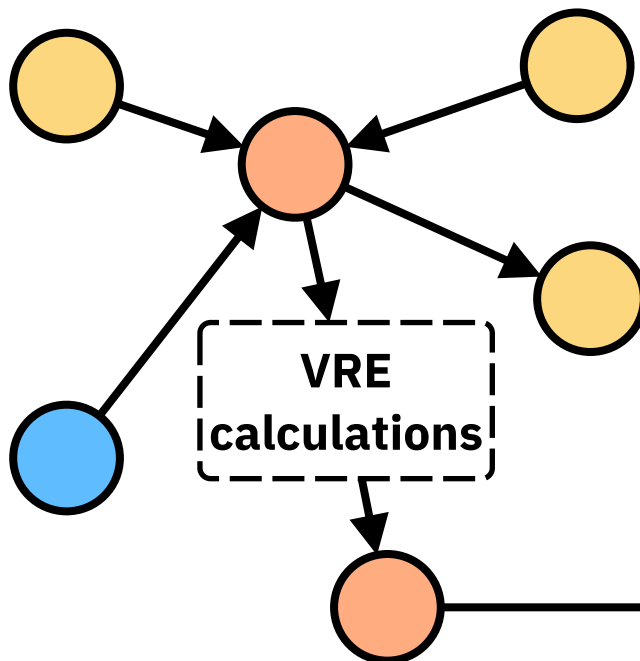
Variant Risk Estimate (VRE)

**ClinVar variant
classifications
(6.8 M entries)**

**GnomAD
Allele frequencies
(N = 807,162)
(800 M variants)**

**dbNSFP
(122 M variant
annotations)**

**PanelAppRex
Gene-disease
(58,592 entries)**



**VRE
calculations**

**IEI genetics
Variant observation
prior probabilities**