

Split genome into LD blocks



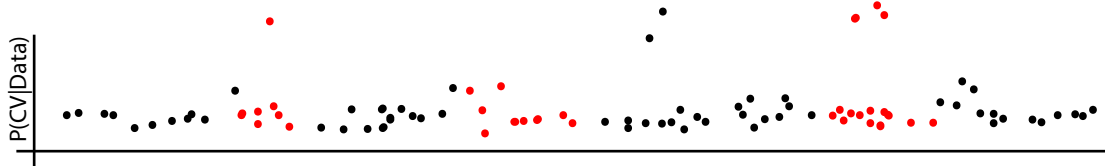
Chr1-22

Compute posterior prob. for variants to be causal for a given LD block using Wakefield's method for Query (PID) and **target disease**



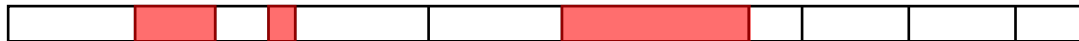
**Target
Disease**

Label blocks based on $\text{sum}(P(CV|Data)) > 0.95$



Compute Wilcoxon (**W**) statistic for **red** vs black

Use circularised permutation to compute $\text{Var}(W_{h_0})$ to allow for underlying LD block structure.



Compute Wilcoxon statistic for **red** vs black



Compute Wilcoxon statistic for **red** vs black