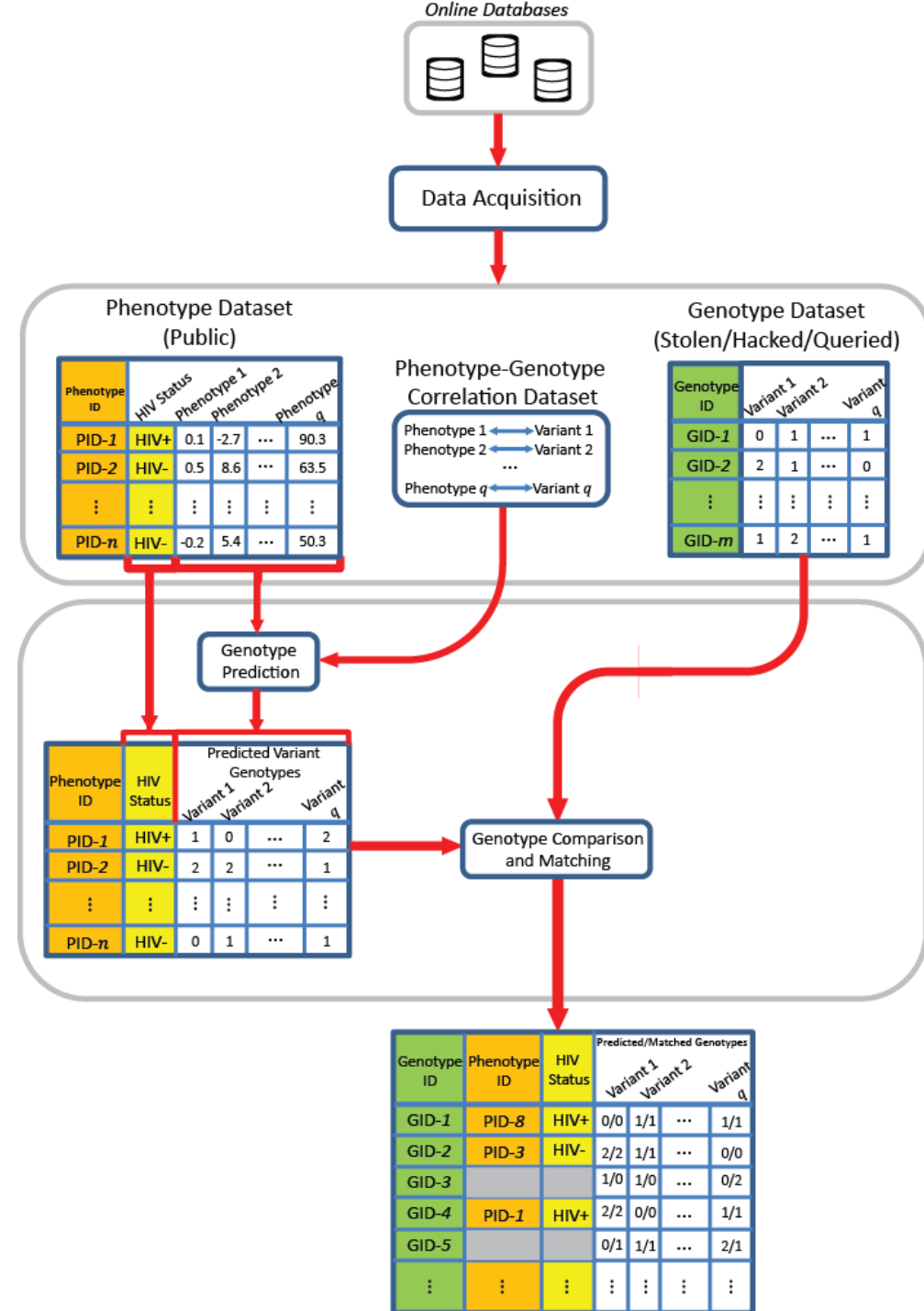
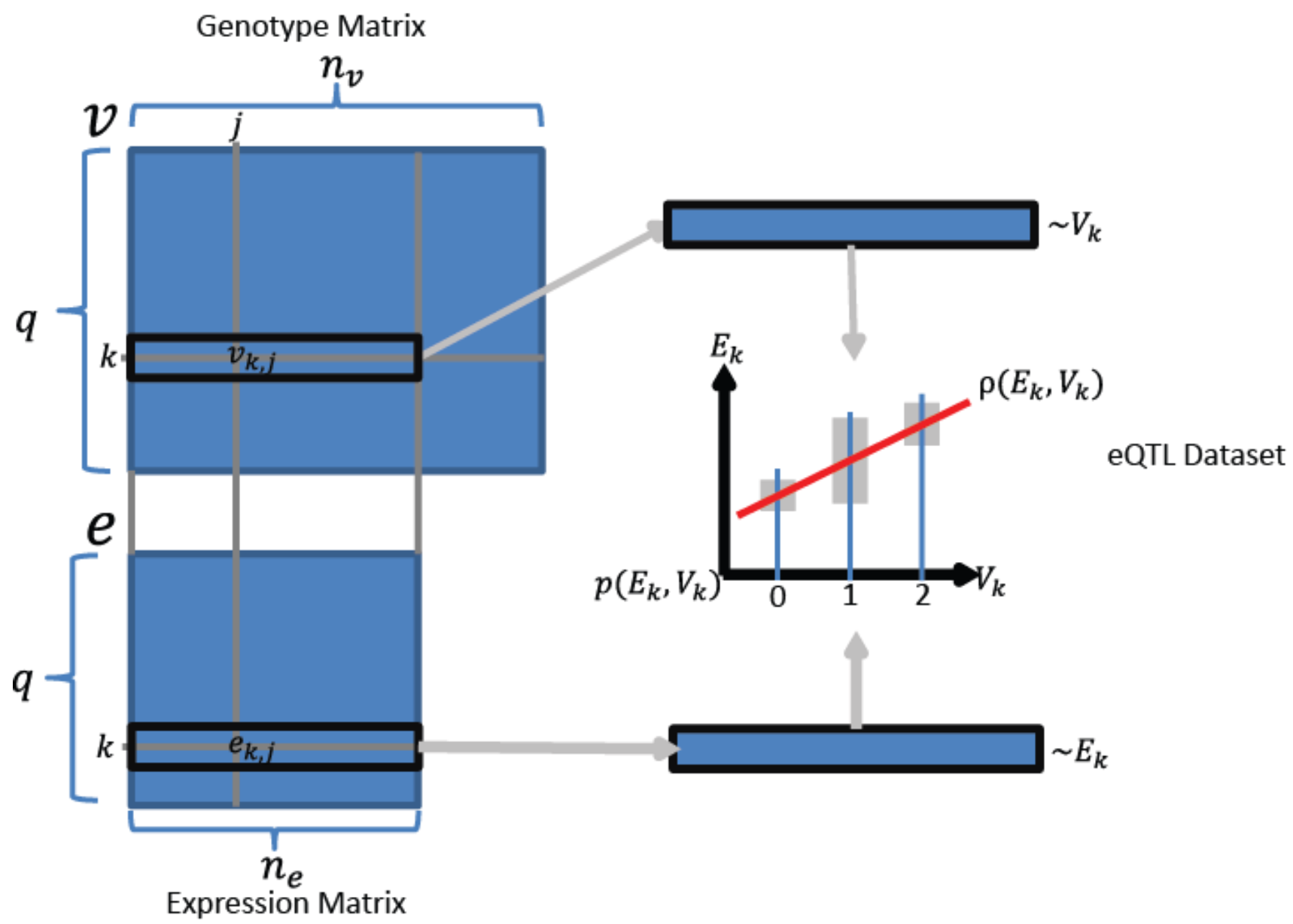


Attack based on quantifications and eQTLs

- One can still perform an attack if he/she has access to quantifications.





- Amount of individual characterizing Information (ICI) in a set of n variants:
 - Analogy: Count how many rare genotypes there are in the set.

$$\begin{array}{c}
 \text{Sum individual characterizing} \\
 \text{information from all variants} \\
 \hline
 \bullet \text{ICI}(\underbrace{\{V_1 = g_1\}}_{\substack{\text{Variant 1} \\ \text{Genotype}}}, \underbrace{\{V_2 = g_2\}}_{\substack{\text{Variant 2} \\ \text{Genotype}}}, \dots, \underbrace{\{V_n = g_n\}}_{\substack{\text{Variant } n \\ \text{Genotype}}}) = \sum_{k=1}^n \underbrace{-\log(p(V_k = g_k))}_{\substack{\text{Convert the genotype} \\ \text{frequency to number of bits} \\ \text{that can be used to characterize} \\ \text{individual}}}
 \end{array}$$

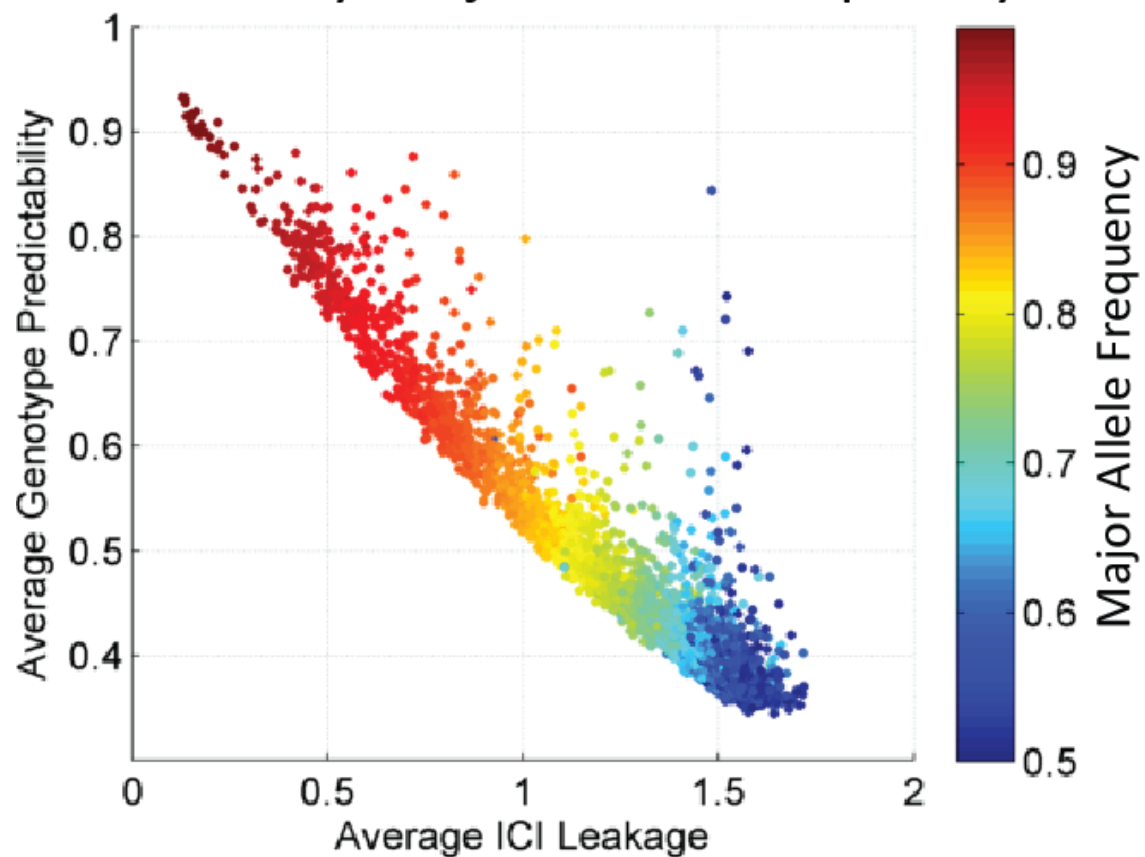
$$(g_i \in \{0,1,2\})$$

- Predictability of genotypes given expression levels (π):
 - How well can we estimate the genotypes given expression levels?
 - Given that the k th gene's expression level is $e_{k,j}$, how much randomness is left in the genotype?
 - Convert the randomness into a metric of predictability

$$\pi(V_k | E_k = e_{k,j}) = \underbrace{\exp(-1 \times \overbrace{H(V_k | E_k = e_{k,j})}^{\text{Randomness left in } V_k \text{ given } E_k = e_{k,j}})}_{\text{Convert the entropy to average probability}}$$

[[Replace w. Equations]]

Colors by Major Allele Frequency



Colors by Absolute Correlation

