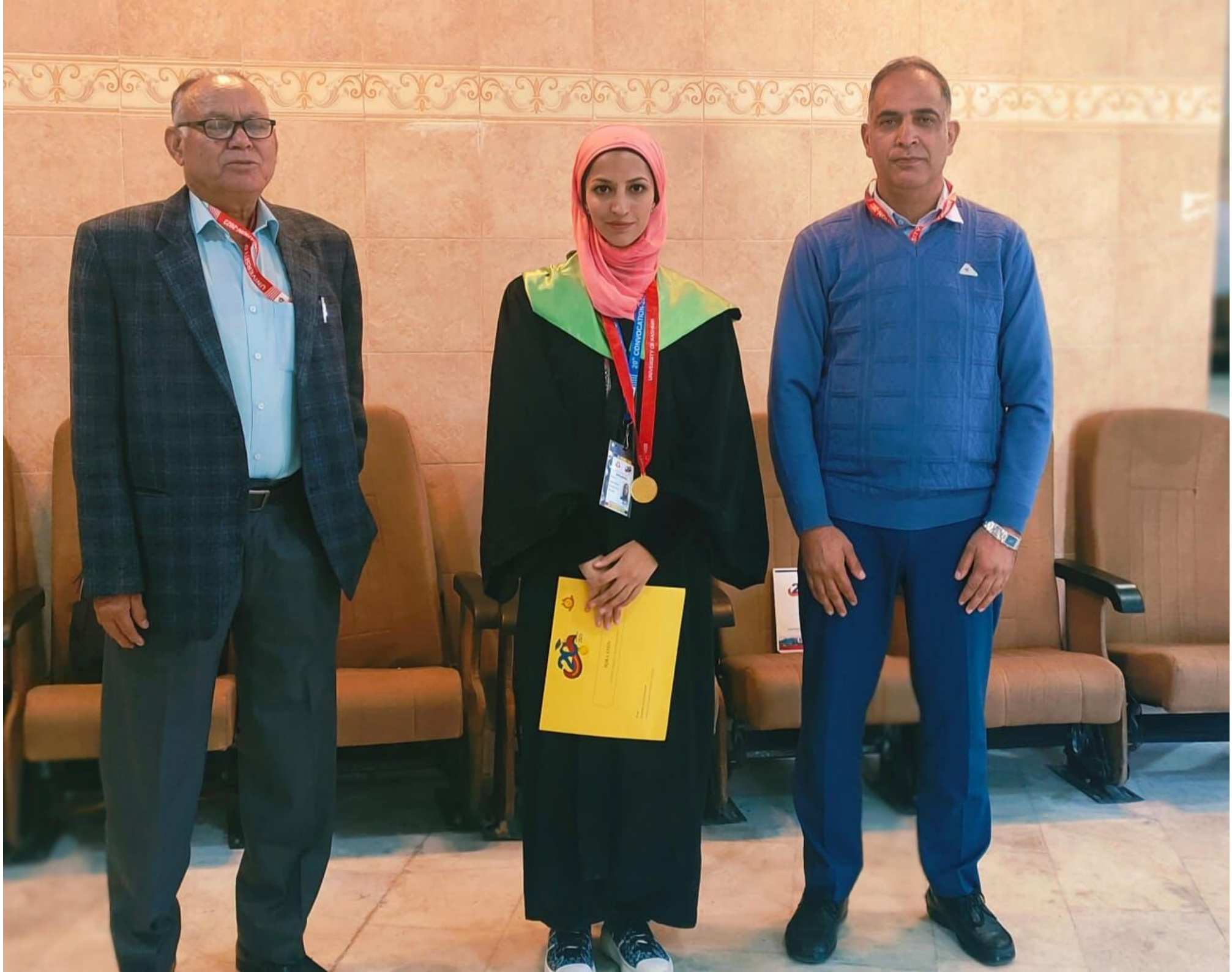

UNDERSTANDING OF OFFICIAL
STATISTICS AND STATISTICAL SYSTEM
By
lenovo


Problem of Identification of Associated Genes
The association of a gene with a particular trait is determined through the analysis of genetic variation, often referred to as variant or SNP (Single Nucleotide Polymorphism) data. Variants can be categorized into common and rare variants based on their allele frequency (HH, Hh, hh).
Common Variants: These are genetic variants with relatively higher frequencies in the population. Common variants are typically captured in large-scale genetic studies and often have modest effects on traits. They are more amenable to detection using traditional association tests due to their frequency.
Rare Variants: Rare variants, on the other hand, have low frequencies in the population. They are less common and are often poorly captured by traditional tests. However, rare variants can have significant individual effects on traits and diseases




WINNER


STATISTICS
STATISTICS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