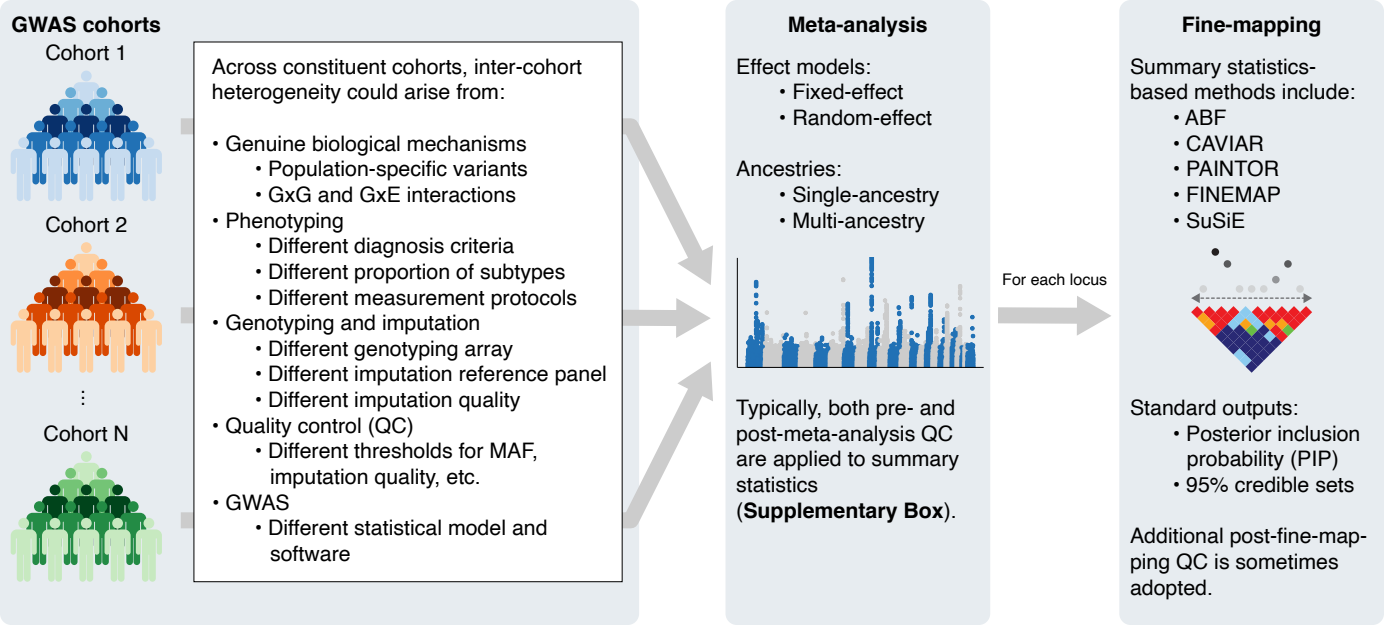
GWAS cohorts
Cohort 1
Cohort 2
Cohort N
Across constituent cohorts, inter-cohort heterogeneity could arise from:
• Genuine biological mechanisms
• Population-specific variants
• GxG and GxE interactions
• Phenotyping
• Different diagnosis criteria
• Different proportion of subtypes
• Different measurement protocols
• Genotyping and imputation
• Different genotyping array
• Different imputation reference panel
• Different imputation quality
• Quality control (QC)
• Different thresholds for MAF, imputation quality, etc.
• GWAS
• Different statistical model and software
Meta-analysis
Effect models:
• Fixed-effect
• Random-effect
Ancestries:
• Single-ancestry
• Multi-ancestry
Typically, both pre- and post-meta-analysis QC are applied to summary statistics (Supplementary Box).
For each locus
Fine-mapping
Summary statistics-based methods include:
• ABF
• CAVIAR
• PAINTOR
• FINEMAP
• SuSiE
Standard outputs:
• Posterior inclusion probability (PIP)
• 95% credible sets
Additional post-fine-mapping QC is sometimes adopted.