

# Conceptualising qualifying variants for genomic analysis

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## Acronyms

<b>ACAT</b> Aggregated Cauchy Association Test .....	18
<b>ACMG</b> American College of Medical Genetics and Genomics .....	16
<b>AF</b> Allele Frequency .....	10
<b>GWAS</b> Genome Wide Association Test .....	2
<b>MAF</b> Minor Allele Frequency .....	15
<b>PRS</b> Polygenic Risk Score .....	2
<b>QV</b> Qualifying variant .....	2
<b>QV<sub>ax</sub></b> Axiomatic Variants .....	23
<b>SF</b> Secondary Findings .....	16
<b>VQSR</b> Variant Quality Score Recalibration .....	10
<b>VSAT</b> Variant Set Association Test .....	3
<b>WGS</b> Whole Genome Sequencing .....	5

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## Abstract

Qualifying variants (QV) are specific genomic alterations selected through defined criteria within processing pipelines, essential for downstream analyses in genetic research and clinical diagnostics. This paper presents QV not merely as simple filtering criteria but as a dynamic and multifaceted concept critical for various genomic analysis scenarios. We argue that standardising and optimising QVs for advanced multi-stage use, rather than limiting them to conceptually simplistic, single-stage filters, can significantly advance omics research and open up new theoretical domains. Typically perceived merely as tools to exclude benign or unrelated variants, QVs actually involve complex, distributive steps throughout the analysis pipeline. We propose a redefinition of QVs by outlining several common sets and demonstrating their roles within analysis pipelines, thereby illuminating their integration and standardisation for specific analytical scenarios. By introducing a new vocabulary and a standard reference model, we aim to enhance understanding and communication about QVs, thus improving methodological discussions across disciplines.

## 1 Introduction

Qualifying variant (QV)s are genomic alterations selected through specific criteria after the primary stages of routine genomic processing pipelines. These variants are essential for downstream analysis in genetic research and clinical diagnostics. This paper explores the application and conceptualisation of QVs not merely as filtering criteria but as a dynamic concept crucial for various genomic analysis scenarios. Generally, the selection of QVs are based on well-established best practices in variant classification and reporting standards (1–4), established work-flows (5–7). However, a standard guide for QV themselves remains missing. Polygenic Risk Score (PRS) reporting standards to have been developed to encourage their application and translation as well as open cataloguing for reproducibility and systematic evaluation (8; 9). We propose an equivalent is beneficial for QV.

The choice of QV thresholds often depends on the specific context of the research or clinical needs. For instance, Genome Wide Association Test (GWAS) might prioritise common variants, variant set association test (VSAT) might prioritise rare variant collapse, and clinical genetic reports may focus on rare

or novel variants. Therefore, QVs are categorised by the extent and nature of the filtering or quality control they undergo, tailored to the research or clinical requirements. **Figure 1** demonstrates a typical WGS and Variant Set Association Test (VSAT) analysis pipeline, showing QVs as sequential and potentially piped protocol steps.

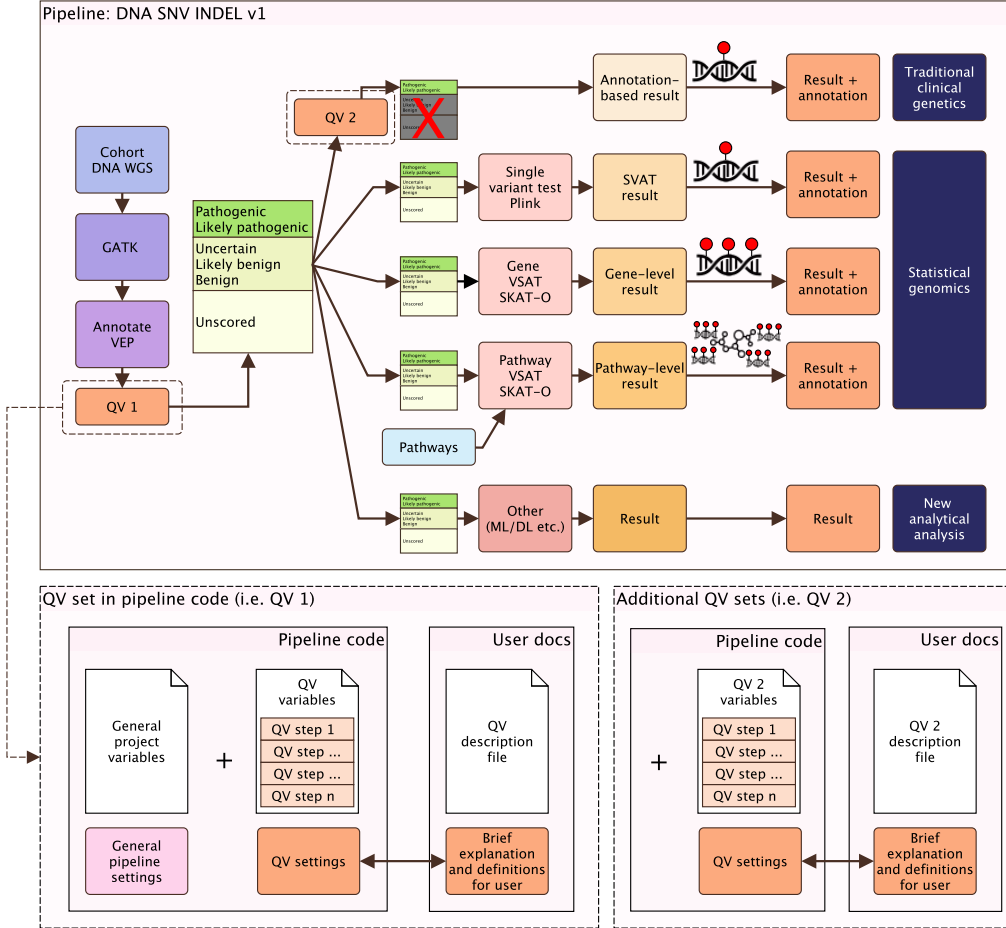


Figure 1: Summary of the example application design DNA SNV INDEL v1 pipeline. QV1 and QV2 are shown as sequential and potentially piped protocol steps. QV files used in a pipeline. The description file contains brief summary of how or why a step is used in the QV set (not mandatory). The variables file contains the necessary values of a QV setting (mandatory). These variables are loaded by the analysis pipeline. This illustration highlights a single stage in the QV1 set (i.e. step 10 in our example WGS analysis pipeline where the GATK VQSR method is applied). The full pipeline illustrated in the top panel simplifies this process under the QV1 icon.

The common approach to representing QV steps are illustrated in **figure 2**. This style simplifies the variant filtering process where each layer may arise

from different stages of a pipeline. The raw omic data can be processed into a multi-use analysis-ready format, as illustrated in **figure 3**. Initial QV steps can include QC filtering. After variant annotation, further QV steps can be applied on this new information as shown in **figure 3**.

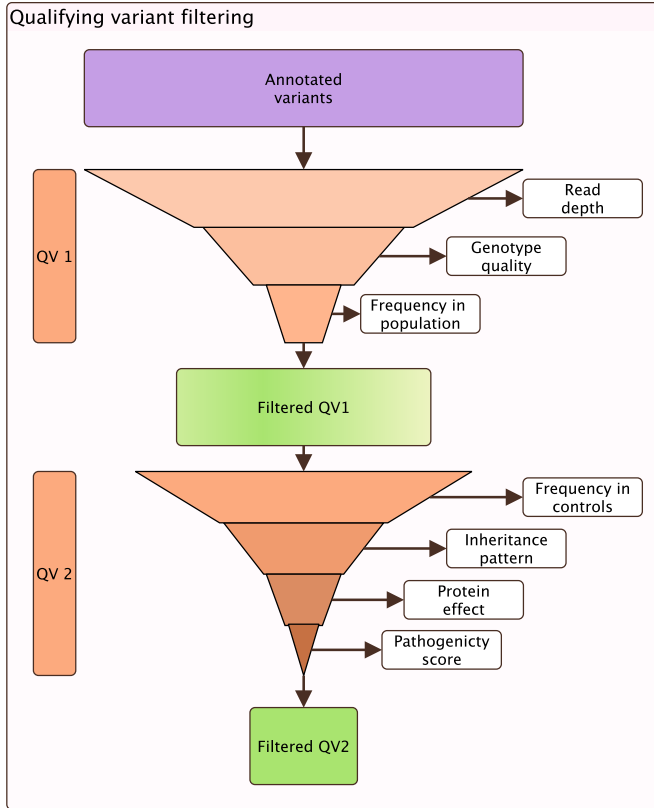


Figure 2: Illustration of the qualifying variant workflow. This figure summarises the conceptualised variant filtering step. This style is relatively common. In reality, we observe that each layer of the filters comes from disparate stages of a pipeline.

Povysil et al. (10) previously provided a tangible example of QV for variant collapsing analyses for complex traits. Cirulli et al. (11) reported one of the first variant collapse analysis and introduced the QV concept. However, a standardised framework for presenting QV themselves remains missing. We detail three typical applications of QV sets:

1. **QV passing quality control (QC) only:** Generates large datasets, typically over 500,000 variants per subject, used primarily in GWAS.
2. **QV for rare disease:** Produces smaller datasets after stringent filtering, around 10,000 variants per subject, useful in single-case genetic reports.
3. **Flexible QV:** Balances between quality control and false positives, yielding datasets of fewer than 100,000 variants per subject for rare variant association testing.

Two critical applications of QVs are in clinical genetics reporting and GWAS. In clinical genetics single-case analysis, QVs may be selected from a list of disease-causing genes identified by an expert panel. Variants within these genes can be categorised based on their potential pathogenicity into variants of unknown significance (VUS), or as known, candidate, or causal variants pending further analysis. In GWAS, QVs generally refer to consensus variants that have undergone standard quality control procedures to ensure their statistical suitability for the main analysis. Rigorous QV selection and categorisation in genetic research and diagnostics to accurately report and reproduce such studies, particularly since the the QV criteria may be more important than the choice of analysis pipeline.

## 2 Background problem and proposed solution

As study sizes surpass the 1,000,000 subjects milestone (12; 13), the shift towards Whole Genome Sequencing (WGS) over genotyping has become standard. This transition enables the inclusion of rare variants in GWAS and VSAT, allowing for more comprehensive analyses of complex traits (14; 15). QV protocols are essential in data cleaning and preparation, serving as a critical step in ensuring the integrity of data analysis. While often grouped under the single term “QV” for simplicity, the processes involved actually span various stages of a pipeline and originate from diverse steps or sources. **Figure 4** shows the structural framework of a variant’s features that may trigger specific QV protocols, highlighting both pre-existing metadata and annotations added post-variant calling.

Moreover, complex analyses often necessitate multiple processing streams that merge into a cohesive analysis. This multifaceted approach to QV becomes apparent in multicomponent analyses, which require the integration of two or more data sets. A standardised QV format will allow for the use of various QV sets, each based on potentially different filters and variables, yet provides a common foundation to ensure consistency and validity across disparate data streams

Unsurprisingly, the term QV is often ambiguously used across different contexts within genomic studies, necessitating a clear definition for each application. Moreover, while QVs are typically perceived as a set of filters and algorithms to remove benign or unrelated variants, they actually encompass

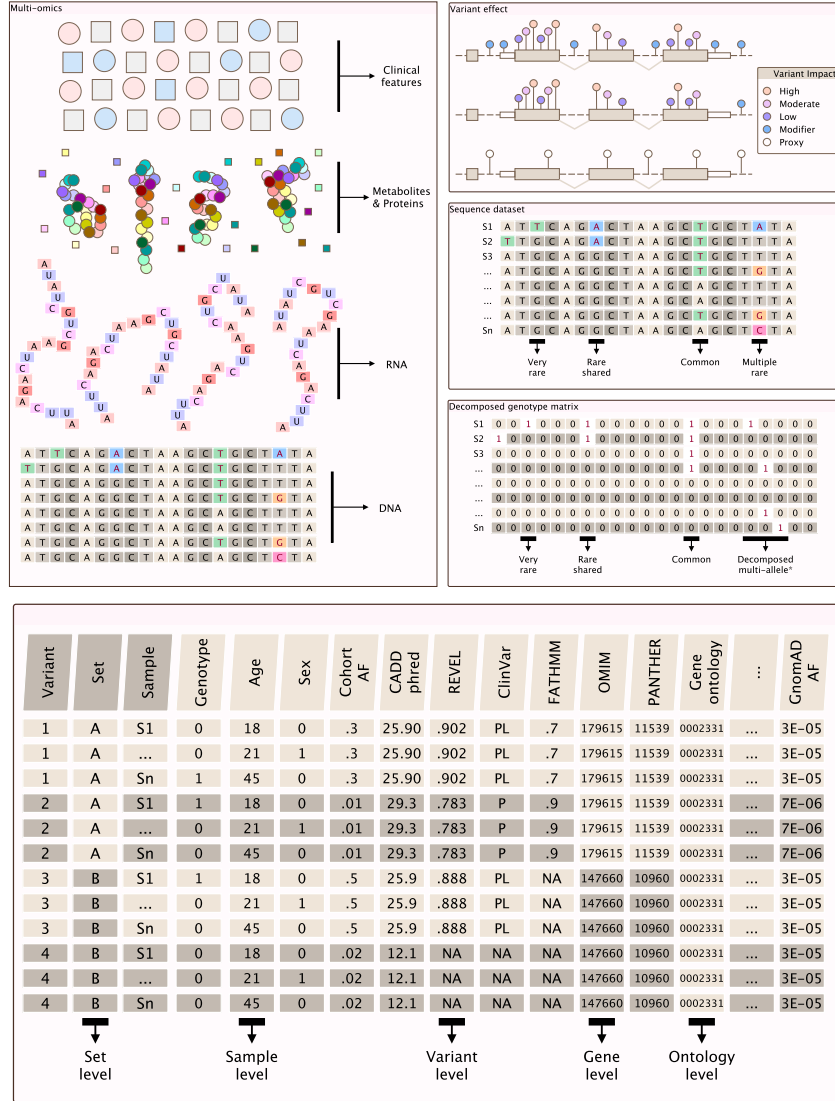


Figure 3: Top: From raw omics to data matrix. We focus on DNA variants in QV but the same concept applies to other datasets. Bottom: The initial variant detection pipeline generally requires QC and filtering rules that are the first QV steps. Once complete, annotation of variants can follow. Further QV steps can be run based on these new annotations.

many complex steps distributed throughout the entire analysis pipeline, and not necessarily confined to a single step. This dispersion of QV steps challenges the conventional view and highlights the need for a flexible definition that not only encompasses their common uses but also acknowledges their implementation across multiple stages of genomic analysis.

The complex, multi-step nature of QVs often goes unrecognised by those outside the field of bioinformatics. This makes it challenging to share knowl-

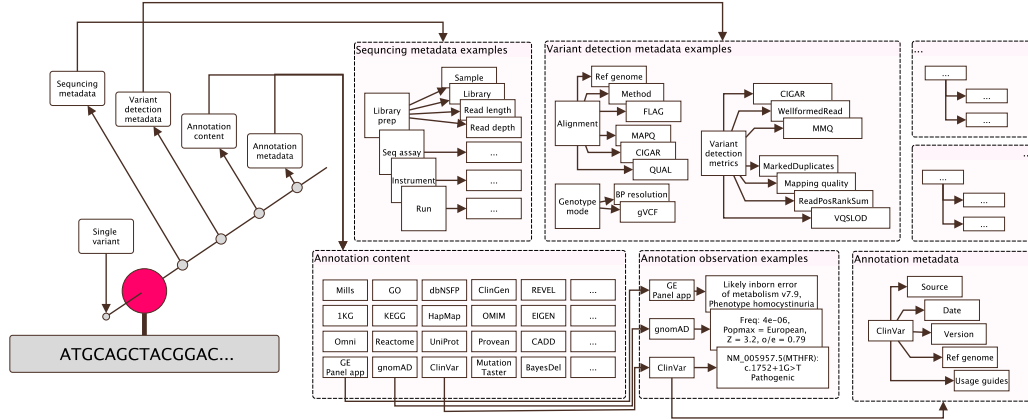


Figure 4: This illustration shows the structural framework of an annotated variant in relation to the features used for qualification. For every individual variant, a number of features are capable of triggering QV protocols. The diagram highlights a select group of these features, showcasing both pre-existing metadata established before data generation and annotations applied after variant calling.

edge across disciplines for more advanced tasks and underscoring the importance of a clear and comprehensive understanding of QV protocols.

By introducing a new vocabulary and a standard reference model for QVs, we aim to clarify the concept and improve the communication and methodological discussions around QVs. We therefore define and exemplify several common sets of QVs, illustrating their potential configurations and roles within analysis pipelines:

1. We demonstrate the theoretical pipelining of QV sets.
2. We outline how standardised QV sets can be established for specific analytical scenarios.
3. We highlight that QVs are integral throughout the analysis pipeline, not merely as an end-stage addition but as essential components distributed across the process.

## 3 Advanced applications and case study

### 3.1 How and why QV are used

Here we provide an in-depth look at specific scenarios where QVs have inadvertently been crucial, such as in GWAS, WGS, and clinical genetics. We note that application of QVs would be appropriate in large-scale studies and rare disease research, such as sophisticated risk models that integrate clinical and genomic data, which enhance predictive accuracy in large, well-defined cohorts (16–18). Likewise, QV protocols can aid reproducibility across studies, especially in isolated or specific populations. This includes the analysis of complex signals within well-defined cohorts which can significantly aid rare disease studies (19).

### 3.2 Example application of qualifying variants in WGS analysis

Several QV protocols can be piped together to create increasingly filtered datasets to match the needs at a certain stage of analysis. It is also typical that different analyses from QVs sets are used and the final results from each step are merged to cover multiple scenarios. For example, a complex analysis pipeline might use all of QV SNV/INDEL + QV CNV + QV structural variation + QV rare disease known + QV statistical association QC, merged for a thorough multi-part analysis to reach the final combination of (1) newly identified cohort-level genes associated with disease with (2) single case-level known disease-causing results.

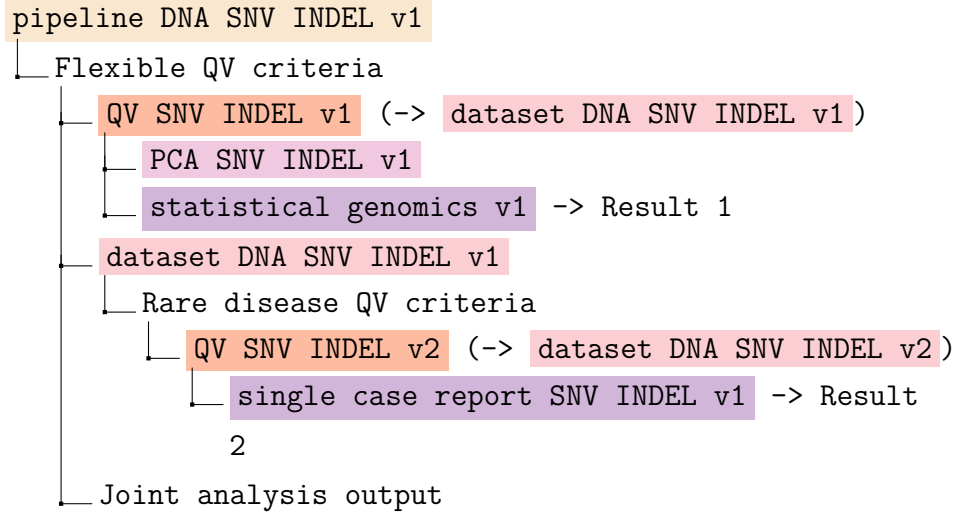
We propose an example focusing on a SNV/INDEL pipeline using two QV sets named QV SNV INDEL v1 and QV SNV INDEL v2. The QV sets are illustrated in box 1 and would be described in an analysis pipeline as follows:

“A cohort of patient WGS data was analysed to identify genetic determinants for the clinical diagnosis of phenotype X. This pipeline is concerned with WGS germline short variant discovery (SNVs + Indels) and interpretation. First, a flexible QV set (v1) was used for cohort-level statistical genomics and second a rare disease QV set (v2) was used for single-case analysis. (1) Data was processed with the pipeline DNA SNV INDEL v1 pipeline, which implements (a) QV SNV INDEL v1 criteria, resulting in the prepared



dataset `dataset DNA SNV INDEL v1`. (b) The dataset was subsequently analysed in combination with other modules including `PCA SNV INDEL v1` and `statistical genomics v1` to complete statistical analysis on a joint cohort. (2) Next, the prepared dataset (from step 1a) `Dataset DNA SNV INDEL v1` was processed further with more strict filtering using `QV SNV INDEL v2` to identify previously known causal genetic variants for each patient based on disease-gene panel and curated evidence sources, resulting in `Dataset DNA SNV INDEL v2` and final interpretation in `single case report SNV INDEL v1`.”

#### Box 1: Example diagrammatic representation



Joint analysis output from:

Result 1 = Cohort-level association signal (e.g. variant P-value).

Result 2 = Single variant for single patient.

## 4 Methodological framework

### 4.1 Three steps to a QV protocol

We introduce a simple framework for the effective use of QV protocols. We use three steps to fulfil the needs of a pipeline as illustrated in **figure 1**:

1. **Variables:** The variables responsible which are sourced as part of a pipeline, as shown in **example box 3**.
2. **Description:** The description of each step as part of an overall QV set, as shown in **example box 3**.

3. **Source code:** The variables file can be sourced in pipeline code, as shown in **example box 4**.

The practical application of our framework efficiently manages QV-specific variables, such as Allele Frequency (AF) thresholds, distinct from general pipeline settings. These variables can be imported and handled separately within the workflow to maintain clarity and specificity. We first provide a detailed example using Variant Quality Score Recalibration (VQSR) to show a full step in application of this method in a real-world genomic analysis scenario. Later, we also illustrate this approach using workflow managers like Snakemake or Nextflow, demonstrating the separation and integration of these variables to streamline genomic processing tasks.

Individual steps in QV criteria can have multiple types. For organisation in our protocols we suggest simple labels such as “QC” and “filter”. (1) filtering thresholds such as AF (e.g.  $>0.1$  in cohort,  $<0.1$  in gnomAD). These might be directly applied in place to remove all affected variants. (2) multiple steps with annotation labels such as QC flags which do not remove variants but allow for downstream dissensions which depend on multiple QV criteria. Thus, in a QC protocol a single step might run and filter all variants from criteria (1 “filter”) and another filtering step might depend on several combined criteria (2 “QC”) which were added upstream.

## 4.2 Detailed example QV variables

As a detailed example, we select the step [QC] `vqsr` from the example QV set `QV SNV INDEL v1` to illustrate the variables sourced during the pipeline. The following code snippet shows the from variables sourced during VQSR. First we set the mandatory QV varaints in **box 2**. Second, we provide the optional description in **box 3**. Third, we apply the variables in the source code **box 4**.

### Box 2: Example QV variables - extract from QV1 variables file

```
# VQSR SNP Mode Variables
vqsr_snp_hapmap_known="false"
vqsr_snp_hapmap_training="true"
vqsr_snp_hapmap_truth="true"
vqsr_snp_hapmap_prior="15.0"
```

```

vqsr_snp_omni_known="false"
vqsr_snp_omni_training="true"
vqsr_snp_omni_truth="false"
vqsr_snp_omni_prior="12.0"

vqsr_snp_1000g_known="false"
vqsr_snp_1000g_training="true"
vqsr_snp_1000g_truth="false"
vqsr_snp_1000g_prior="10.0"

vqsr_snp_annotations="QD,MQ,MQRankSum,ReadPosRankSum,FS,SOR"
vqsr_snp_truth_sensitivity="99.7"

```

### Box 3: Example QV description file (highlighting VQSR steps)

1. [QC] **fastp** The tool fastp is used for ...
2. [QC] **collectwgsmetrics** BAMs that fail are ...
3. [QC] **rmdup\_merge** is used to mark ...
4. [QC] **haplotype\_caller** used -ERC GVCF mode for ...
5. [QC] **qc\_summary\_stats** is used to log QC ...
6. [QC] **vqsr** employs Variant Quality Score Recalibration (VQSR) using GATK. Includes the use of key metrics such as Quality by Depth (QD), Mapping Quality (MQ), and Read Position Rank Sum Test (ReadPosRankSum) to filter variants. The setting for SNPs are:
  - **VQSR SNP Mode - HapMap:** known=false, training=true, truth=true, prior=15.0. Used as a high-confidence reference set for training the recalibration model.
  - **VQSR SNP Mode - Omni:** known=false, training=true, truth=false, prior=12.0. Provides additional training data derived from Omni genotyping arrays.

- **VQSR SNP Mode - 1000G:** known=false, training=true, truth=false, prior=10.0. Utilizes data from the 1000 Genomes Project to inform the model on common SNP variations.
- **VQSR Annotations - QD, MQ, MQRankSum, ReadPosRankSum, FS, SOR:** Annotations are metrics used to predict the likelihood of a variant being a true genetic variation versus a sequencing artifact. They include quality by depth, mapping quality, mapping quality rank sum test, read position rank sum test, Fisher's exact test for strand bias, and symmetric odds ratio of strand bias.
- **VQSR Truth Sensitivity Filter Level:** 99.7. Specifies the percentage of true variants to retain at a given VQSLOD score threshold, set here to capture 99.7% of true variants.

#### Box 4: Example code sourcing the variables file

```
#!/bin/bash

# Source master settings (including VQSR) and custom
  ↪ QV1 settings
source ./variables_master.sh
source ./variables_qv1.sh

# Run VQSR for SNPs

# 1. Calculate VQSLOD tranches for SNPs using
  ↪ VariantRecalibrator
gatk --java-options "${JAVA_OPTS}" VariantRecalibrator
  ↪ \
-R ${REF} \
-V ${vcf_file} \
--resource:hapmap,known=${vqsr_snp_hapmap_known},
  ↪ training=${vqsr_snp_hapmap_training},truth=${
  ↪ vqsr_snp_hapmap_truth},prior=${
  ↪ vqsr_snp_hapmap_prior} ${hapmap} \
```

```

--resource:omni,known=${vqsr_snp_omni_known},training=$
    ↪ {vqsr_snp_omni_training},truth=${
    ↪ vqsr_snp_omni_truth},prior=${vqsr_snp_omni_prior}
    ↪ ${omni} \
--resource:1000G,known=${vqsr_snp_1000g_known},training
    ↪=${vqsr_snp_1000g_training},truth=${
    ↪ vqsr_snp_1000g_truth},prior=${
    ↪ vqsr_snp_1000g_prior} ${thousandG} \
-an QD -an MQ -an MQRankSum -an ReadPosRankSum -an FS -
    ↪ an SOR \
--mode SNP \
-O ${OUTPUT_DIR}/chr${INDEX}_snp1.recal \
--tranches-file ${OUTPUT_DIR}/chr${INDEX}_output_snp1.
    ↪ tranches

# 2. Filter SNPs on VQSLOD using ApplyVQSR

gatk --java-options "${JAVA_OPTS}" ApplyVQSR \
...continued

```

### 4.3 Simple example with a workflow manager

We demonstrate the use of a QV variable file within a workflow manager, such as Snakemake or Nextflow (**box 5**). The setup involves two types of YAML configuration files: one for general pipeline settings and another specifically for QV-related variables (**box 6**). These configurations are integrated into the primary analysis script, typically a Snakefile, ensuring that all parameters required for genomic analyses are systematically managed and applied (**box 7**).

#### Box 5: Example workflow manager - yaml

```

# qv_config.yaml
min_depth: 10
max_allele_frequency: 0.01
quality_score_threshold: 20

```

#### Box 6: Example workflow manager - yaml

```
# config.yaml
reference_genome: "path/to/reference/genome.fasta"
annotation_file: "path/to/annotation.gtf"
sample_list: "path/to/samples.txt"
output_dir: "path/to/output"
qv_config: "qv_config.yaml"
```

#### Box 7: Example workflow manager - python

```
# Snakefile
configfile: "config.yaml"
qv_settings = read_yaml(config["qv_config"])

rule all:
    input:
        "results/filtered_variants.vcf"

rule filter_variants:
    input:
        "data/raw_variants.vcf"
    output:
        "results/filtered_variants.vcf"
    params:
        depth = qv_settings['min_depth'],
        af = qv_settings['max_allele_frequency'],
        qs = qv_settings['quality_score_threshold']
    shell:
        """
        bcftools filter -i 'DP>{depth} && AF<{af} && \
        QUAL>{qs}' {input} > {output}
        """
```

## 5 Examples of real-world QV applications

Greene et al. (20) developed what can effectively be considered a prime example of QV standardisation with their “Rareservoir,” a relational database

schema optimised for handling genetic data from rare disease studies. This database optimises storage and query speed by focusing on rare variants - those with a Minor Allele Frequency (MAF) below 0.1% - thus reducing data size by about 99%. Variants are stored as 64-bit integers (“RSVR IDs”), organised by genomic position to support efficient location-based queries. Additional data include MAFs from gnomAD, CADD pathogenicity scores, and impact predictions per the Sequence Ontology. Genetic impacts are encoded into a 64-bit integer (“CSQ ID”), where each bit corresponds to a specific gene function impact, ranked by severity. This structure enables precise database queries. By employing the Bayesian genetic association method BeviMed, initially described by Greene et al. (21), the study effectively inferred associations between genes and rare disease phenotypes, demonstrating the capacity to handle and analyze complex genetic datasets effectively. The protocol by Greene et al. (20) can be produced in the QV format, easing the interpretation and reproducibility.

We are applying the QV framework in “SwissPedHealth”. This is a joint paediatric national data stream where one of the objectives is to investigate rare/unknown disease using a multiomic approach, including WGS, RNAseq, proteomics, and clinical data (22). We optimise the processing pipelines by using consensus raw datasets (e.g. WGS in patients and families), which is annotated and filtered to several QV levels. The resulting pre-processed datasets are suitable for a range of analysis including GWAS, VSAT, single-case clinical genetics reports, machine learning, and joint multiomic analysis.

National-scale projects reuse data many times and naturally require the use of QV, currently in the traditional format; mixed throughout pipelines without explicit distinction. The Genomics England 100,000 Genomes Project performs central automated analysis with interpretation and clinical reporting (23). This data is then used in many subsequent research projects. One significant application of QV protocols is in genomics-based newborn screening, which has been gaining traction as a pivotal healthcare innovation (24).

Screening for known disease is by default, based on searching for a known QV set. The use of a formalised standard would allow for consistency and reliability for stakeholders. Genome analysis in neurodevelopmental disorders in 465 families found causal variants in 36% of 489 affected individuals (25). The DDD study involved over 13,500 families; approximately 41% of probands received a genetic diagnosis (26). Genomic lifespan association in Iceland was

reported by Jensson et al. (27), which included 57,933 participants, identifying 2,306 individuals with actionable genotypes linked to a decrease in median lifespan by approximately three years for carriers.

We propose that the use of standardised QV can aid in developing rapid genomic diagnostics. In UAE, rapid whole-genome sequencing - (28) allowed for rapid whole-genome sequencing with a turnaround of 37 hours on average. Meng et al. (29) reported on 278 critically ill infants; molecular diagnosis achieved in 36.7% of cases, with higher rates (50.8%) in critical trio exome cases. They reported an impacted medical management in 52.0% of diagnosed cases. Lunke et al. (30) reported in the national scale multi-omics for rare diseases, involving 290 critically ill infants and children; diagnostic yield from WGS initially at 47%, increased to 54% with extended analysis. Altered critical care management occurred for 77% of diagnosed cases.

Additionally, using the QV framework for different analysis types, such as SNV-INDEL and structural variants, means that simple QV IDs can be used for database reporting. Researchers can then easily query whether or not additional analysis is expected to reveal more findings. For instance, Wojcik et al. (31) used genome sequencing in 822 families with rare monogenic diseases, achieving a diagnostic yield of 29.3%. They focused on broader genomic coverage including structural and non-coding variants, identifying causative variants in 8.2% of cases previously undetected by exome sequencing.

The American College of Medical Genetics and Genomics (ACMG) Secondary Findings (SF) v3.2 list, exemplifies a well-defined and impactful application of QV standards in genomic medicine (32). This list specifies gene-phenotype pairs recommended for reporting as secondary findings during clinical exome and genome sequencing. Such standardisation not only streamlines the identification of clinically actionable genetic information but also enhances the consistency and quality of genomic data interpretation across different settings. The key limitation is that this dataset is relatively unstructured meaning that each implementation requires extensive work and care on the part of front-line analysts. The ACMG SF list is revised annually, reflecting its dynamic nature and the evolving understanding of gene-disease correlations. Each version, such as the current v3.2, includes detailed criteria for the inclusion or exclusion of specific genes, based on rigorous evidence of their association with significant health outcomes. This methodical approach to curating the SF list ensures that it remains a reliable resource for opportunistic screening in a



clinical context.

**Table 1** lists the first two entries (transposed) from the ACMG SF list showcasing specific genes associated with cardiovascular phenotypes. We then represent this data in a standardised QV format in **box 8 - 9**, which can be used in any variant filtering program as demonstrated. In bioinformatics pipelines, specifying QV sets consistently, such as ACMG SF v3.2 as the allows patients receive the most relevant and up-to-date information regarding their genetic health risks, without missing out on simple checks due to the burden of manually implementing new QV.

Table 1: The first two entries from the ACMG SF v3.2 list, transposed, for reporting of secondary findings in clinical exome and genome sequencing (32).

Detail	ACTA2	ACTC1
Disease/Phenotype	Familial thoracic aortic aneurysm	Hypertrophic cardiomyopathy
Gene MIM	102620	102540
Disorder MIM	611788	612098
Phenotype Category	Cardiovascular	Cardiovascular
Inheritance	AD	AD
Variants to report	All P and LP	All P and LP

#### Box 8: QV configuration for SF - yaml

```
# qv_sf_v3.2_config.yaml
genes:
- gene: "ACTA2"
  inheritance_pattern: "AD"
  variant_class : ["Pathogenic", "Likely Pathogenic"]
- gene: "ACTC1"
  inheritance_pattern: "AD"
  variant_class: ["Pathogenic", "Likely Pathogenic"]
...
```

#### Box 9: Filtering command for QV SF

```
# Pseudo-code to filter variants for each gene
# in ACMG SF v3.2 list:

Read genes from qv_sf_v3.2_config.yaml
```

```
For each gene entry in genes:
  Apply filter command:
    filter -i 'GENE=="{gene['gene']}" &&
    INHERITANCE=="{gene['inheritance_pattern']}" &&
    (VARIANT_CLASSIFICATION in gene['variant_class'])'
    input.vcf > output_{gene['gene']}_qv_sf.vcf
```

## 6 Challenges and innovations

### 6.1 Avoiding pitfalls

In the pursuit of advancing omics research through multiblock data, we recognize the imperative need to standardise and optimise the use of QV. This need mirrors the simple pitfalls in the analysis of repeated measures, where combining repeated measurements without appropriate controls can lead to misleading conclusions (33). So too must we approach the integration of complex QV layers with rigor.

In multi-omic integration, where data from various layers such as DNA, RNA, and protein are fused, the naive merging of data without considering the unique source and nature of each data block can similarly mislead. The warning from Bland and Altman (33) about repeat data, or Simpson’s paradox, where aggregated data can obscure real relationships, underscore the necessity for sophisticated statistical frameworks that acknowledge and adjust for the intricacies of source-specific variations. Once acknowledged, these features can be addressed potentially with existing methods (34–36). Increasingly deep phenotyping and precision medicine with omic data are reshaping data integration strategies. Standardised database formats are thus critical for genomics and QV should not be an afterthought (37–39).

### 6.2 Applications in simple independent tests

An example of a multi-part analysis with sets QV sets 1, 2, and 3, is illustrated in **Figure 5**. For simplicity, we can assume that each set represents one **qwas!** (**qwas!**). The outcomes of each test can subsequently be combined with statistical methods such as the Aggregated Cauchy Association Test (ACAT)

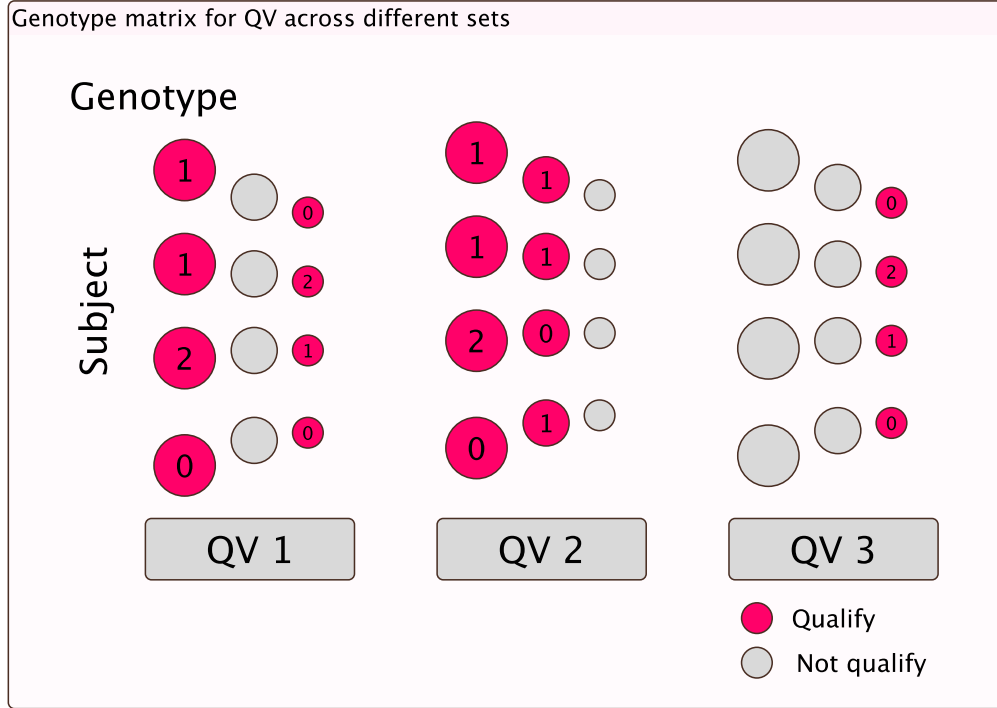


Figure 5: Genotype matrices for three different layers of QV analysed in genetic studies. Each matrix represents a specific set, showing the genotypes of three individuals for three SNPs (SNP1, SNP2, SNP3). In the QV1 layer, SNP1 and SNP3 qualify as a QV (highlighted in red). The genotypes are for QV are coded as 0 for homozygous reference, 1 for heterozygous, and 2 for homozygous alternative.

(45; 46). It becomes possible to aggregate and compare these results from separate tests. This process combines p-values across different analyses or variant sets, accounting for the directions and magnitudes of the effects. It not only enhances the power to detect significant associations, especially when variants have heterogeneous effects but also simplifies the interpretation of aggregated genomic data. By employing ACAT, we can synthesize findings from multiple QV filters applied to the same genomic dataset, leading to a more comprehensive understanding of the genetic architecture of traits under study. This method is particularly useful in scenarios where variants across different QV sets may contribute in varying degrees to the phenotype, allowing for a nuanced analysis that respects the complexity of genomic data. The combination method must be adapted in scenarios where variants (or collapsed variant sets) do not overlap. We have previously provided methods to plot the results of such analysis with [archipelago](#) (cite pre-print instead of package).

### 6.3 Applications in complex data and multiblock fusion

Multiblock data fusion is an emerging yet nascent field in statistics and machine learning which is championed by multi-omics. The interplay between statistical theory and machine learning unveils profound opportunities for advancing our understanding of complex biological systems. This approach harnesses the power of diverse data types through sophisticated fusion techniques that integrate multiple blocks of omics data - be it DNA, RNA, protein, or clinical data - into a coherent analytical framework. Such integration not only enhances the resolution at which we understand disease mechanisms but also refines our predictive capabilities across different scales of biological organisation. By applying advanced statistical models researchers can uncover nuanced relationships within and between datasets that were previously obscured. Kong et al. (40) and Howe et al. (41) have previously shown how complex signals can exist within single datasets.

These methods allow for a detailed exploration of how different biological signals interact, offering a richer, more comprehensive view of the genomic landscape. As these techniques evolve, they promise to break new ground in predictive modeling and theoretical biology, providing insights that are as profound as they are essential for precision medicine and personalised health interventions.

We contend that the term “QV”, when standardised and optimised for advanced multi-stage use rather than simplistic, single-stage filters, not only advances omics research but also opens up unexplored theoretical domains. This includes a multi-dimension analysis of a single data source through exploring new concepts; for example, such jointly analysing probative variants (potentially axiomatically-causal with missing evidence), associational, causal, and counterfactual queries, in combination with traditional analyses that integrate other omic markers like RNA and protein abundance. Sophisticated QV applications that combine various sets of QVs on a single data source may prepare the correct joint dataset for such complex analyses. The resulting mixed-up mixed model requires new frameworks.

By deploying a variety of QV protocols simultaneously on a single dataset, we orchestrate a multi-dimensional analysis that spans the full spectrum of genomic inquiry. This integrated approach allows for the combination of various QV protocols tailored to the specifics of the dataset, engaging different types of data analyses that can range from genetic variations to complex dis-

ease markers and beyond. The integration of these diverse analytical layers facilitates a comprehensive examination of genetic factors on both individual and cohort levels, promoting understanding that could propel genetic insights. This complex interplay between multiple QV sets catalyses the advancement of new theories in multi-omic research.

## **6.4 Protocol development and standardisation needs**

These complex approaches requires a clear protocol for merging data across different layers, ensuring that each contributes meaningfully to the unified model without conflating their distinct signals. Therefore, a standardised definition and reporting style for QV are crucial for the rapid development of new theories, especially in scenarios where data may not be publicly available, and codebases are complex. The nuanced and widespread steps of QV across lengthy pipelines will benefit from being reported explicitly as a protocol with a detailed list of definitions and variables, building on our demonstrated examples for one such set, QV1.

# **7 Future directions and implications**

## **7.1 Integration strategies**

We consider the impact of new publishing formats like Registered Reports on the field of genomics, promoting transparency and reproducibility (42). This kind of approach will be crucial as we develop increasingly sophisticated machine learning and artificial intelligence models capable of integrating vast multi-omic datasets. The potential for these models to unravel complex biological phenomena is immense, yet the challenge remains in assembling sufficient training data. Particularly in the realm of rare diseases, the raw data from human cases potentially do not meet the extensive needs of these advanced models. The embeddings or feature representations derived from raw data may be insufficient for training robust models; however, properly formatted and curated QVs may enrich these representations, enhancing the potential for accurate model training. If so, the accurate and strategic application of QVs becomes essential. By effectively identifying key data through refined

QV protocols, researchers can enhance the accuracy and efficacy of predictive models, opening up new avenues for significant biological discoveries.

The need for advanced QV protocols that can effectively manage such complexity is critical, particularly in the development of statistical methods designed to navigate the intricate relationships within and across diverse omic data blocks. A standardised and nuanced application of QVs, detailed through explicit protocols and definitions, is fundamental for the evolution of new analytical frameworks. Therefore, we advocate for a more refined and comprehensive use of QVs, advancing beyond traditional single-stage filters to meet the sophisticated demands of modern multi-omic research.

## 7.2 Notation typical to GWAS, VSAT, and other statistical applications

We explore the notational use of QV in commonly used applications to demonstrate how the conceptual framework can accelerate adoption in theoretical domains. For example, in GWAS (7) the notation for the logistic regression model for estimating the probability of case status is given by:

$$\text{logit}(p_i) = \log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \sum_{k=1}^n \beta_k x_{ik} + \beta_{\text{geno}} G_i$$

where:  $p_i$  is the estimated probability that individual  $i$  is a case, based on their genotypic and covariate data,  $\beta_0$  is the intercept,  $\beta_k$  are the coefficients for the covariates,  $x_{ik}$  represents the covariate values for the  $i$ -th individual,  $\beta_{\text{geno}}$  is the coefficient for the genetic effect,  $G_i$  is the genotype of the  $i$ -th individual, coded as 0, 1, or 2 (representing the number of minor alleles).

The following version shows the explicit GWAS model with QV notation:

$$\text{logit}(p_i) = \log\left(\frac{p_i}{1-p_i}\right) = \beta_0 + \beta_1 \text{sex}_i + \beta_2 \log_{10}(\text{age})_i + \sum_{j=1}^{10} \beta_{2+j} \text{PC}_j^{(i)} + \sum_{k=1}^n \beta_{13+k} G_{\text{QV}_{i,v,k}}$$

where:  $\beta_1$  adjusts for sex (1 if male, 0 if female),  $\beta_2$  adjusts for the log-transformed age in days,  $\beta_3$  to  $\beta_{12}$  correspond to the first ten principal components, adjusting for population stratification,  $\beta_{13+k}$  represents the effects of the genotype on the phenotype for each additional qualifying variant set  $k$ ,

$G_{\text{QV}_{i,v,k}}$  denotes the genotype of the  $i$ -th individual for the  $v$ -th variant in the  $k$ -th QV set.

Likewise, SKAT and its optimal unified version, SKAT-O, are now popular methods for gene-based association tests that accommodate multiple variants within a gene or variant set while accounting for their potentially differing directions and magnitudes of effects (43; 44). The logistic regression model for SKAT, taking into account the specific variants from the QV set, can be described as follows:

$$\log\left(\frac{P}{1-P}\right) = X_i\gamma + G_{\text{QV}_{i,v}}\beta$$

where:  $P$  is the disease probability,  $\gamma$  is an  $s \times 1$  vector of regression coefficients of covariates,  $\beta$  is an  $m \times 1$  vector of regression coefficients for genetic variants,  $G_{\text{QV}_{i,v}}$  denotes the genotype values for all variants  $v$  in the QV set for individual  $i$ . The SKAT statistic is then:

$$Q_S = (y - \hat{\pi})^\top K (y - \hat{\pi})$$

where  $\hat{\pi}$  is the vector of the estimated probability of  $y$  under the null model, and  $K$  is the kernel matrix defined as  $G_{\text{QV}}W G_{\text{QV}}^\top$ , with  $W$  being the diagonal weight matrix for the variants.

With these familiar examples established, we can consider more complex models where other variants outside of the main QV set can be assessed,  $\text{QV}_{1,\dots,n}$ , which we describe in the next section. These sets can represent different categorisations or stratifications of genetic variants that might be relevant under varying analytical conditions or specific studies.

### 7.3 Conceptual framework and statistical representation

In GWAS, the transition from empirically testable variants (QV1) to theoretical Axiomatic Variants ( $\text{QV}_{\text{ax}}$ ) marks a pivotal stage in genetic research.  $\text{QV}_{\text{ax}}$  comprises genetic variants that ideally conform to fundamental genetic principles and are thus considered correct by genetic doctrine. However, due to technological constraints and gaps in genetic understanding,  $\text{QV}_{\text{ax}}$  remains largely theoretical and unverifiable empirically. In contrast, QV1 includes those variants from  $\text{QV}_{\text{ax}}$  that survive rigorous empirical filtering, applying standard GWAS pre-processing criteria such as `-geno`, `-maf`, `-hwe`, and `-mind`, aimed

at ensuring the quality and relevance of data by removing variants based on missing genotype data, minor allele frequency, Hardy-Weinberg equilibrium deviations, and individual missing data thresholds.

It is important to emphasise the distinction we are considering: we are dealing with unobserved or unknown variants, rather than variants of unknown significance, in the Bayesian sense. The mathematical representation of the relationship between  $QV_{\text{ax}}$  and  $QV1$  is crucial for understanding the impact of this transition. Firstly, the intersection operation:

$$TP = QV_{\text{ax}} \cap QV1,$$

identifies true positive variants, which are both theoretically ideal and empirically robust, thus successfully passing the GWAS filtering criteria. Secondly, the set difference operation:

$$FN = QV_{\text{ax}} \setminus QV1,$$

calculates false negatives, representing the axiomatic variants that were erroneously excluded by the empirical filters, potentially omitting key genetic signals. Lastly, the quantification of unknowns:

$$\text{Unknowns} = |QV_{\text{ax}}| - |TP|,$$

provides a measure of the magnitude of theoretical variants that remain untested or unconfirmed after processing, emphasizing the potential loss of valuable genetic information.

This structured approach not only clarifies the dynamics between the axiomatic and filtered variants but also underscores the trade-offs involved in WGS pre-processing. By balancing data quality against the risk of overlooking significant genetic contributors, this analytical framework aids us in navigating the complexities of genetic data preparation and evaluation.

We explore these applications in detail elsewhere (cite Bayesian framework paper), but we briefly summarise the ideas here. In the context of GWAS, Bayesian statistics offers a potent framework for integrating theoretical and empirical knowledge. This approach leverages prior biochemical and genetic data to refine our understanding of the landscape of genetic variants, particularly those beyond current empirical capabilities.



We start by defining a prior distribution  $P(\theta)$  based on established knowledge about DNA mutation rates and variant frequencies, reflecting our initial beliefs about the genetic variant distribution. Given a dataset  $D$  from GWAS pre-processing (QV1), the likelihood function  $P(D|\theta)$  assesses the probability of observing the data under various genetic configurations dictated by  $\theta$ .

The **posterior distribution**  $P(\theta|D)$ , derived from Bayes’ theorem,

$$P(\theta|D) = \frac{P(D|\theta) \times P(\theta)}{P(D)},$$

where  $P(D)$  serves as a normalizing constant, updates our beliefs in light of new data. This posterior distribution integrates both the prior information and the empirical data from GWAS, providing a nuanced estimate of the distribution of genetic variants. The “unknowns” in our study, representing genetic variants not observed but theoretically possible within QV\_ax, are quantified as follows:

$$\text{Unknowns} = \int_{\theta \in \Theta_{\text{unobserved}}} P(\theta|D) d\theta,$$

where  $\Theta_{\text{unobserved}}$  encompasses all parameter values corresponding to unobserved variants. This integral effectively measures the total probability of variants that are conceivable but not detected in the empirical dataset QV1.

With this short demonstration of potential future directions, we conclude our exploration of the methodological framework and practical applications.

## 8 Conclusions

This study has underscored the critical importance of QV standardisation within genomic research. By delineating a clear framework for integrating QV protocols into genomic analysis pipelines, we have highlighted how systematic management of these variables enhances reproducibility, accuracy, and efficiency in genetic studies. As genomic technologies and data complexities grow, the need for robust, scalable, and adaptable QV protocols becomes increasingly apparent. Future research should focus on expanding these frameworks to incorporate emerging technologies and analytical challenges, thereby continuously improving the fidelity and utility of genomic data interpretation across domains.

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