

The Decentralized FDA (dFDA) Protocol: Two-Stage Validation (RWE → Pragmatic Trials)

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Abstract

Only 1-10% of adverse drug events get reported to the FDA. Billions of people generate continuous health data through wearables (heart rate, sleep, activity, symptoms daily) while starting and stopping treatments. This data could detect treatment effects but remains unharvested.

A two-stage system solves the observational data problem. Stage 1 (\$0.100 (95% CI: \$0.030-\$1.00)/patient): aggregate millions of natural experiments, score causal confidence using Bradford Hill criteria via the Predictor Impact Score. Observational data finds signals cheaply but cannot prove causation. Stage 2 (\$929 (95% CI: \$97-\$3K)/patient): confirm top signals through pragmatic trials embedded in routine care. These are 44.1x (95% CI: 39.4x-89.1x) cheaper than traditional Phase III because they use existing clinical infrastructure, not specialized trial sites. This cost estimate is based on a meta-analysis of 108 pragmatic trials plus large-scale implementations like RECOVERY and ADAPTABLE.

Output: treatment rankings by effectiveness with validated effect sizes. Companies register treatments in minutes at zero cost. Patients generate outcome data worth \$41K (95% CI: \$20K-\$120K)/patient. The Predictor Impact Score operationalizes six Bradford Hill criteria using saturation functions, enabling automated causal signal detection from observational data at population scale. High PIS signals warrant experimental investigation; low PIS does not rule out true effects. This framework complements traditional RCTs. Stage 2 pragmatic trials are required to establish validated causal claims.

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1 Abstract

Current pharmacovigilance systems rely primarily on spontaneous adverse event reporting, which suffers from significant underreporting, lack of denominator data, and inability to quantify effect sizes. Meanwhile, the proliferation of wearable devices, health apps, and patient-reported outcomes has generated unprecedented volumes of longitudinal real-world data (RWD) that remain largely untapped for safety and efficacy signal detection.

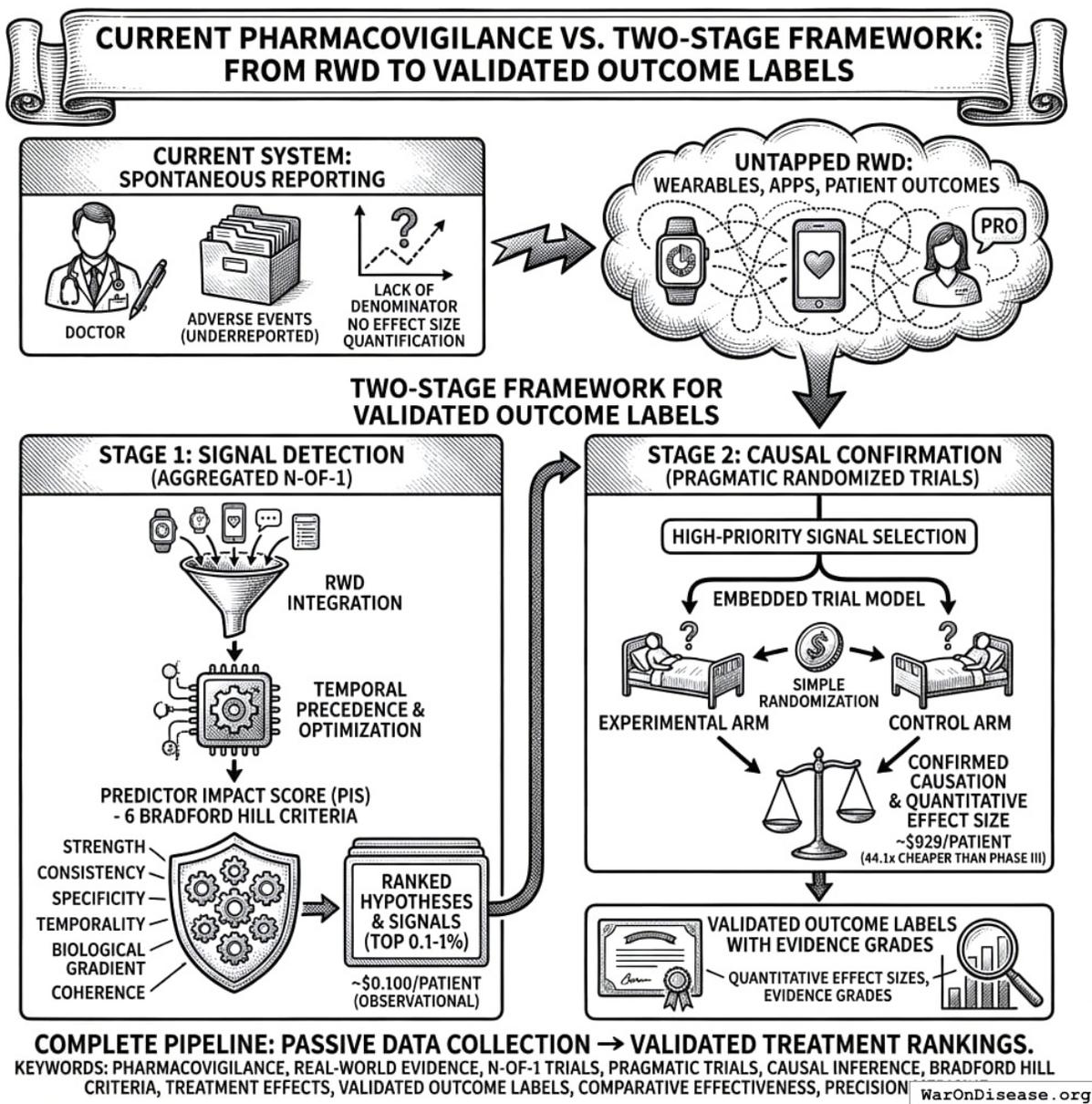


Figure 1: A two-stage methodological pipeline showing the transition from large-scale observational N-of-1 signal detection to causal confirmation via pragmatic randomized trials.

We present a comprehensive **two-stage framework** for generating **validated outcome labels** with quantitative effect sizes:

Stage 1 (Signal Detection): Aggregated N-of-1 observational analysis^{132,133} integrates data from millions of individual longitudinal natural experiments. The methodology applies temporal precedence analysis with automated hyperparameter optimization, addresses six of nine Bradford Hill causality criteria through a composite Predictor Impact Score (PIS), and produces ranked treatment-outcome hypotheses at ~\$0.100 (95% CI: \$0.030-\$1.00).

Stage 2 (Causal Confirmation): High-priority signals (top 0.1-1% by PIS) proceed to pragmatic

randomized trials following the embedded trial model validated across 108+ studies^{1,134}. Simple randomization embedded in routine care confirms causation at ~\$929 (95% CI: \$97-\$3K) (44.1x (95% CI: 39.4x-89.1x) cheaper than traditional Phase III trials) while eliminating confounding concerns inherent in observational data.

The complete methodology includes: (1) data collection from heterogeneous sources; (2) temporal alignment with onset delay optimization; (3) within-subject baseline/follow-up comparison; (4) Predictor Impact Score calculation operationalizing Bradford Hill criteria; (5) Trial Priority Score for signal-to-trial prioritization; (6) pragmatic trial protocols for causal confirmation; and (7) validated outcome label generation with evidence grades.

This two-stage design addresses the fundamental limitations of purely observational pharmacovigilance (confounding, self-selection, and inability to prove causation) while maintaining the scale and cost advantages of real-world data. The result is a complete pipeline from passive data collection to validated treatment rankings, presented as both scientific methodology and implementation blueprint for next-generation regulatory systems.

Keywords: pharmacovigilance, real-world evidence, N-of-1 trials, pragmatic trials, causal inference, Bradford Hill criteria, treatment effects, validated outcome labels, comparative effectiveness, precision medicine

2 System Overview: From Methodology to Implementation

This paper describes the statistical methodology powering a patient-facing system best understood as “**Consumer Reports for drugs**” - a searchable database where patients can look up any condition and see every treatment ranked by real-world effectiveness, with quantitative outcome labels showing exactly what happened to people who tried each option.

SYSTEM OVERVIEW: FROM METHODOLOGY TO IMPLEMENTATION

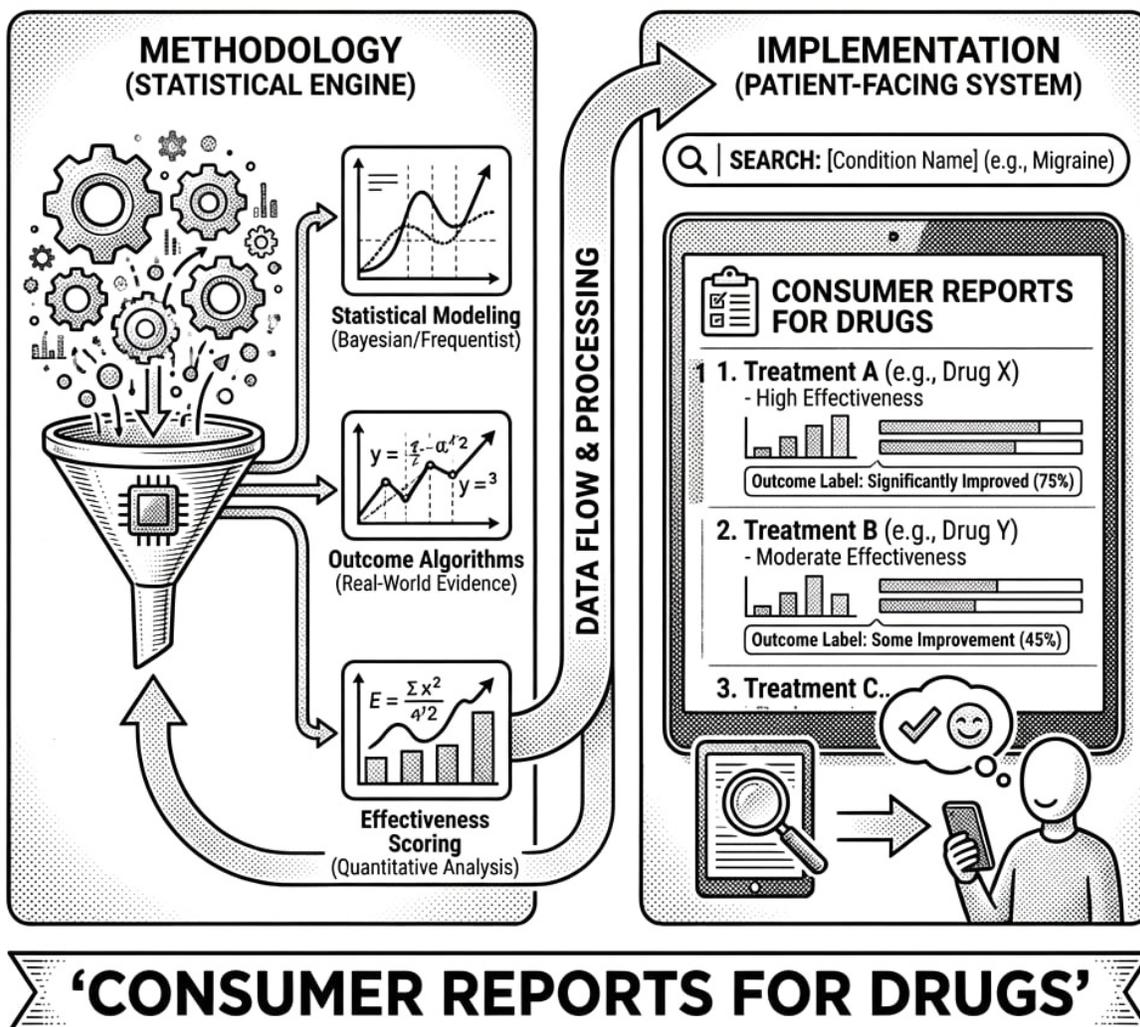


Figure 2: A conceptual diagram showing the flow from raw data and statistical methodology to a user-facing searchable database that ranks drug effectiveness based on real-world outcomes.

2.1 What Patients See

When a patient searches for their condition, they see:

- 1. Treatment Rankings:** Every option (FDA-approved drugs, supplements, lifestyle interventions, experimental treatments) ranked by effect size from real patient data
- 2. Outcome Labels:** “Nutrition facts for drugs” showing percent improvement, side effect rates, and sample sizes - not marketing claims
- 3. Trial Access:** One-click enrollment in available trials, from home, via any device
- 4. Personalized Predictions:** Based on their health data, which treatments work best for

people like them

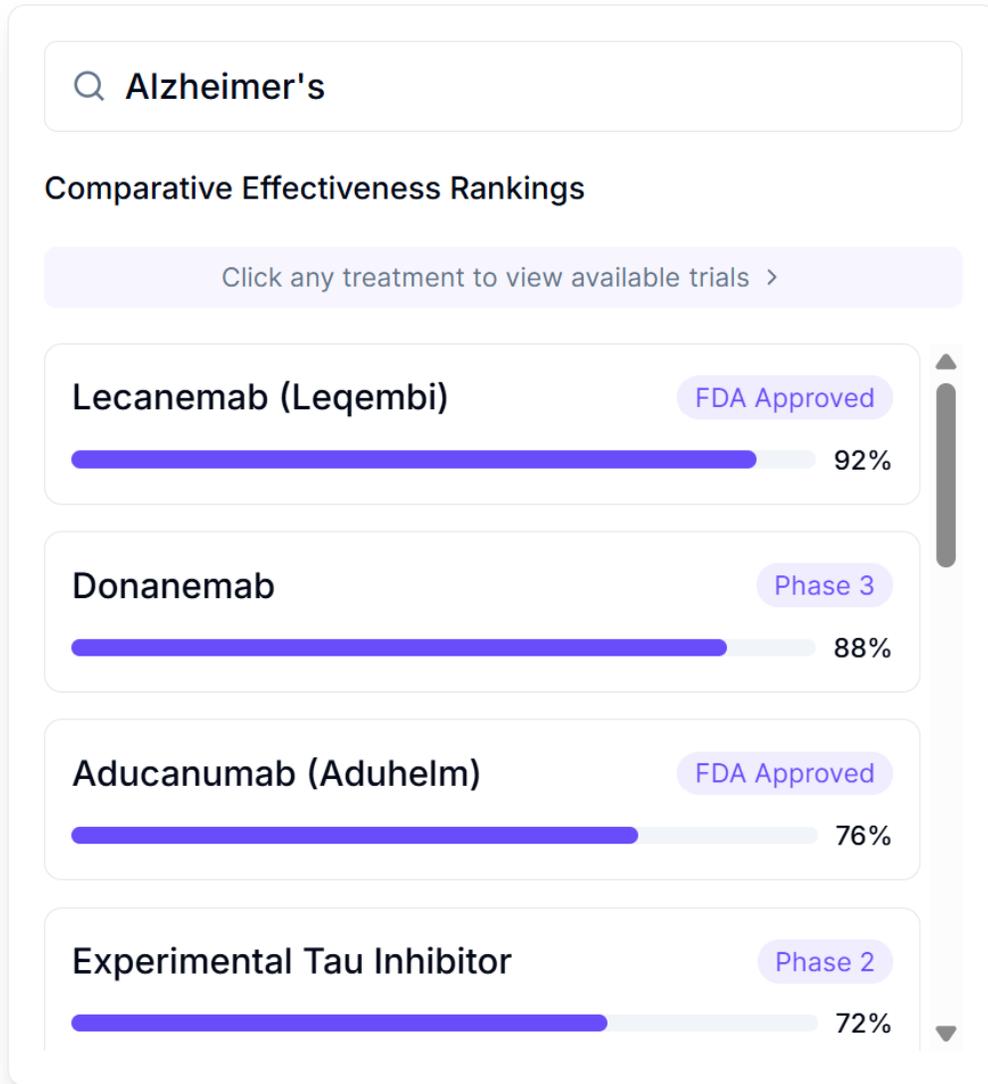


Figure 3: Treatment Rankings Example - Patients see all treatments ranked by real-world effectiveness for their condition

2.2 What Companies See

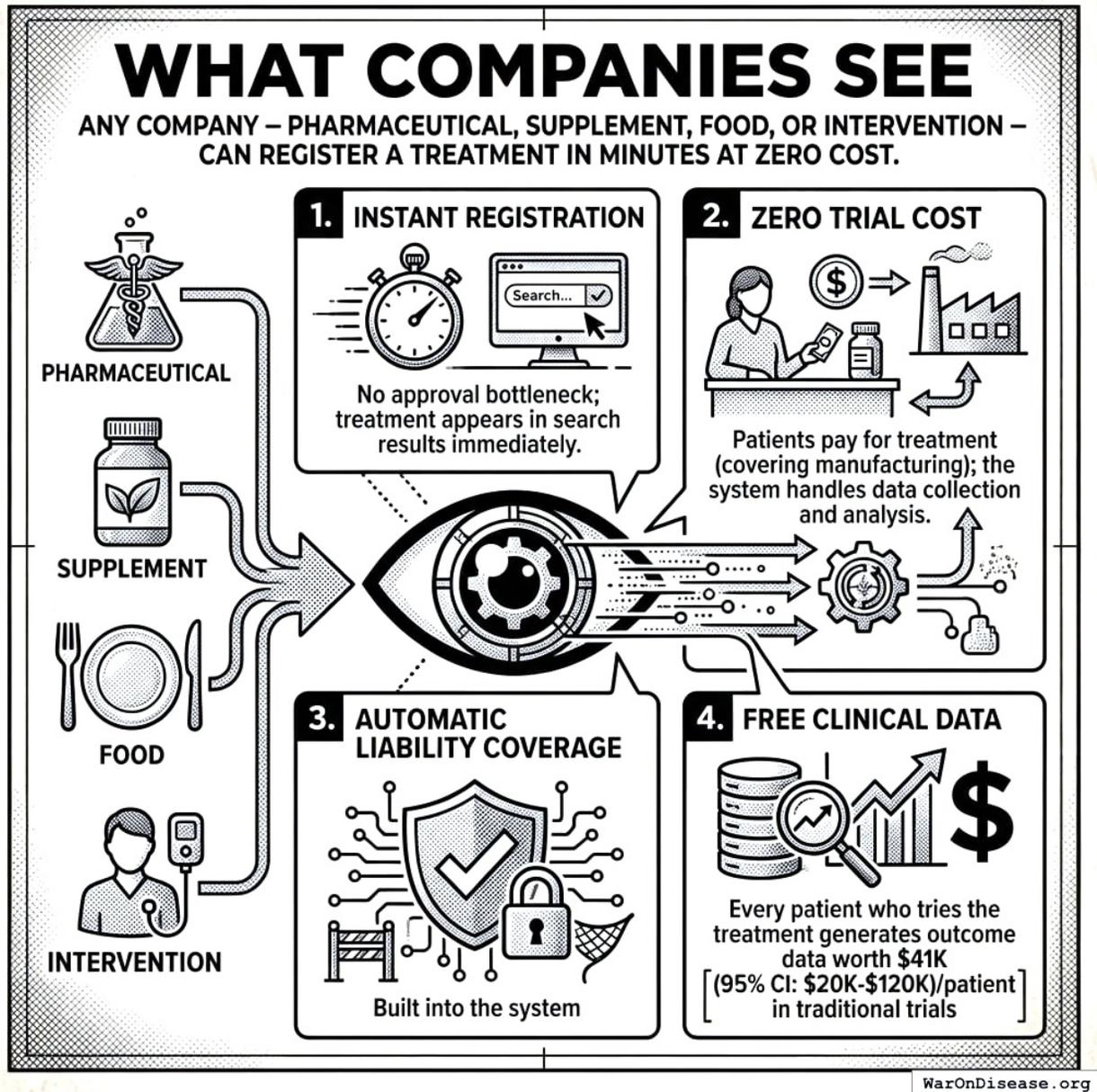


Figure 4: A workflow diagram showing the streamlined process for companies, from instant registration to the generation of high-value clinical data through patient-funded treatments.

Any company - pharmaceutical, supplement, food, or intervention - can register a treatment in minutes at zero cost:

1. **Instant Registration:** No approval bottleneck; treatment appears in search results immediately
2. **Zero Trial Cost:** Patients pay for treatment (covering manufacturing); the system handles data collection and analysis
3. **Automatic Liability Coverage:** Built into the system

4. **Free Clinical Data:** Every patient who tries the treatment generates outcome data worth \$41K (95% CI: \$20K-\$120K)/patient in traditional trials

2.3 Where This Methodology Fits

The **Predictor Impact Score (PIS)** described in this paper is the engine that powers treatment rankings. It transforms raw patient data into the ranked, quantified outcome labels that patients and clinicians use to make decisions. The two-stage pipeline ensures that:

- **Stage 1** (this methodology) generates treatment rankings from millions of real-world observations at ~\$0.100 (95% CI: \$0.030-\$1.00)/patient
- **Stage 2** (pragmatic trials) confirms causation for high-priority signals at ~\$929 (95% CI: \$97-\$3K)/patient

The result is a self-improving system where every patient's experience helps the next patient make better decisions, transforming the current bottleneck of 1.90 million patients/year (95% CI: 1.50 million patients/year-2.30 million patients/year) annual trial participants into a system where anyone can contribute to medical knowledge.

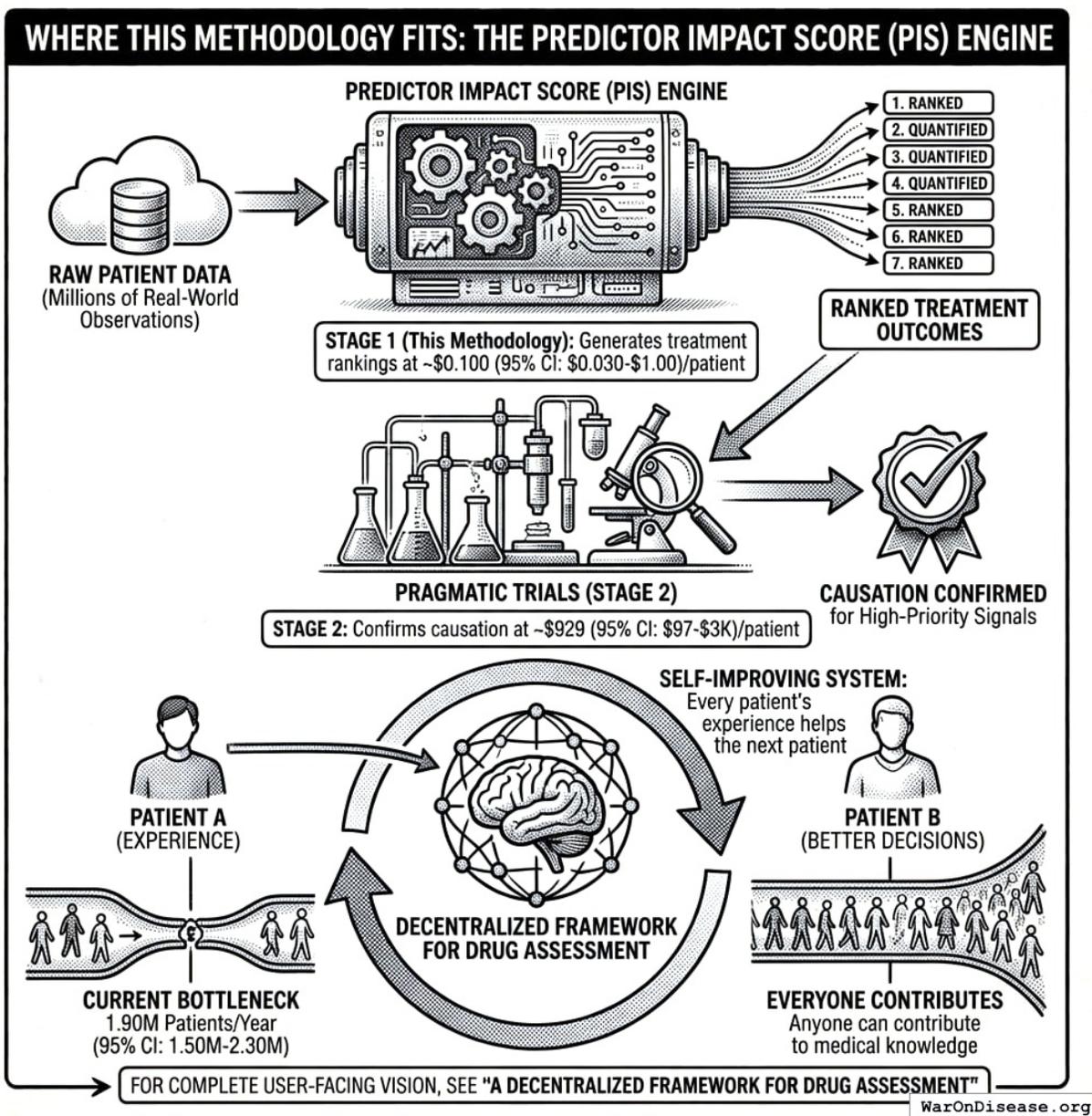


Figure 5: The two-stage Predictor Impact Score pipeline illustrating the flow from low-cost real-world data analysis to high-priority pragmatic trials.

For the complete user-facing vision, see [A Decentralized Framework for Drug Assessment](#).

3 Introduction

3.1 The Human Cost of the Current System

Every year, 55.0 million deaths/year (95% CI: 46.6 million deaths/year-63.2 million deaths/year) people die from diseases for which treatments exist or could exist. The tragedy is not that we lack medical knowledge. It's that our system for generating and validating that knowledge operates at a

fraction of its potential capacity.

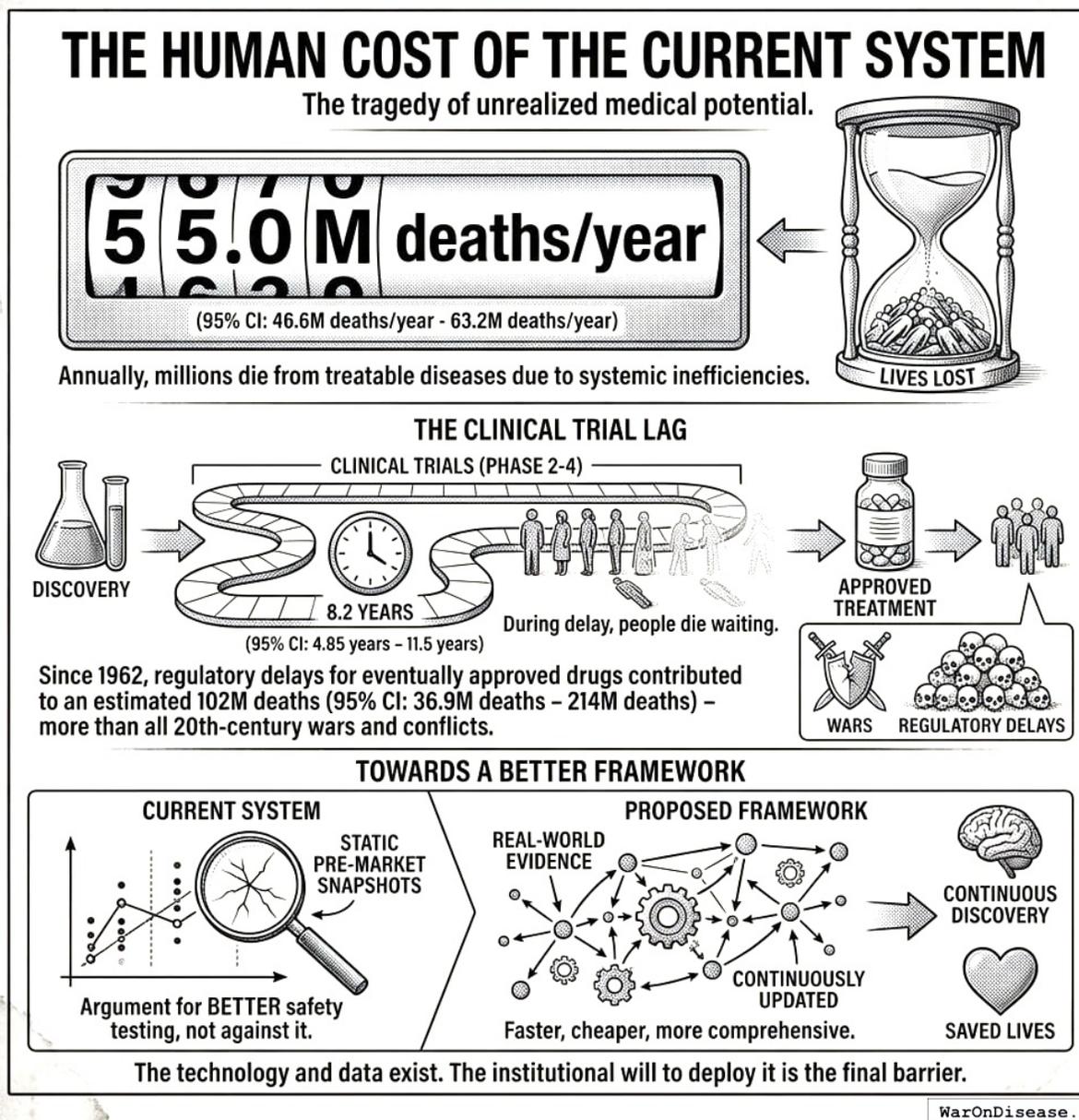


Figure 6: A visualization of the 8.2-year clinical trial delay and its cumulative human cost, comparing the 102 million preventable deaths to the scale of 20th-century war casualties.

Consider: a treatment that could save lives today takes an average of 8.2 years (95% CI: 4.85 years-11.5 years) to complete Phase 2-4 clinical trials after initial discovery. During this delay, people die waiting. Since 1962, regulatory testing delays for drugs that were eventually approved have contributed to an estimated 102 million deaths (95% CI: 36.9 million deaths-214 million deaths) preventable deaths, more than all wars and conflicts of the 20th century combined.

This is not an argument against safety testing. It is an argument for *better* safety testing: faster, cheaper, more comprehensive, and continuously updated with real-world evidence rather than static

pre-market snapshots.

The framework presented here could eliminate this efficacy lag for existing treatments while simultaneously enabling continuous discovery of new therapeutic relationships. The technology exists. The data exists. What remains is the institutional will to deploy it.

3.2 The Pharmacovigilance Gap

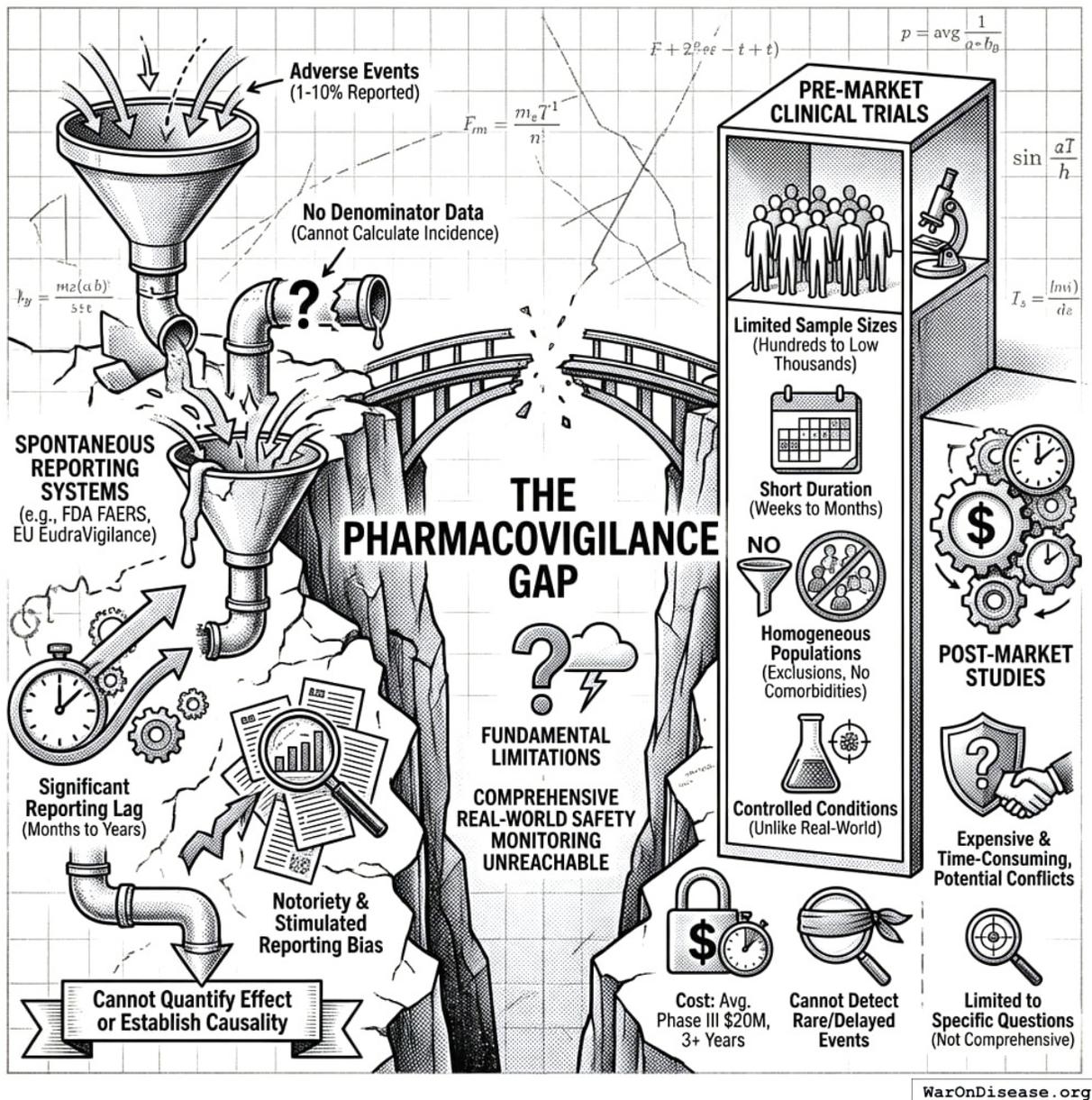


Figure 7: A comparison of the three primary pharmacovigilance methods highlighting their respective limitations in scale, speed, cost, and data quality.

Modern pharmacovigilance (the science of detecting, assessing, and preventing adverse effects of pharmaceutical products) faces fundamental limitations:

Spontaneous Reporting Systems (e.g., FDA FAERS, EU EudraVigilance):

- Estimated 1-10% of adverse events are reported¹³⁵
- No denominator data (cannot calculate incidence rates)
- Cannot quantify effect sizes or establish causality
- Significant reporting lag (months to years)
- Subject to stimulated reporting and notoriety bias

Pre-Market Clinical Trials:

- Limited sample sizes (typically hundreds to low thousands)
- Short duration (weeks to months)
- Homogeneous populations (exclusion criteria eliminate comorbidities)
- Controlled conditions unlike real-world use
- Cannot detect rare or delayed adverse events
- Cost: Average Phase III trial costs \$20M and takes 3+ years⁷³

Post-Market Studies:

- Expensive and time-consuming
- Often industry-sponsored with potential conflicts
- Limited to specific questions rather than comprehensive monitoring

3.3 The Real-World Data Opportunity

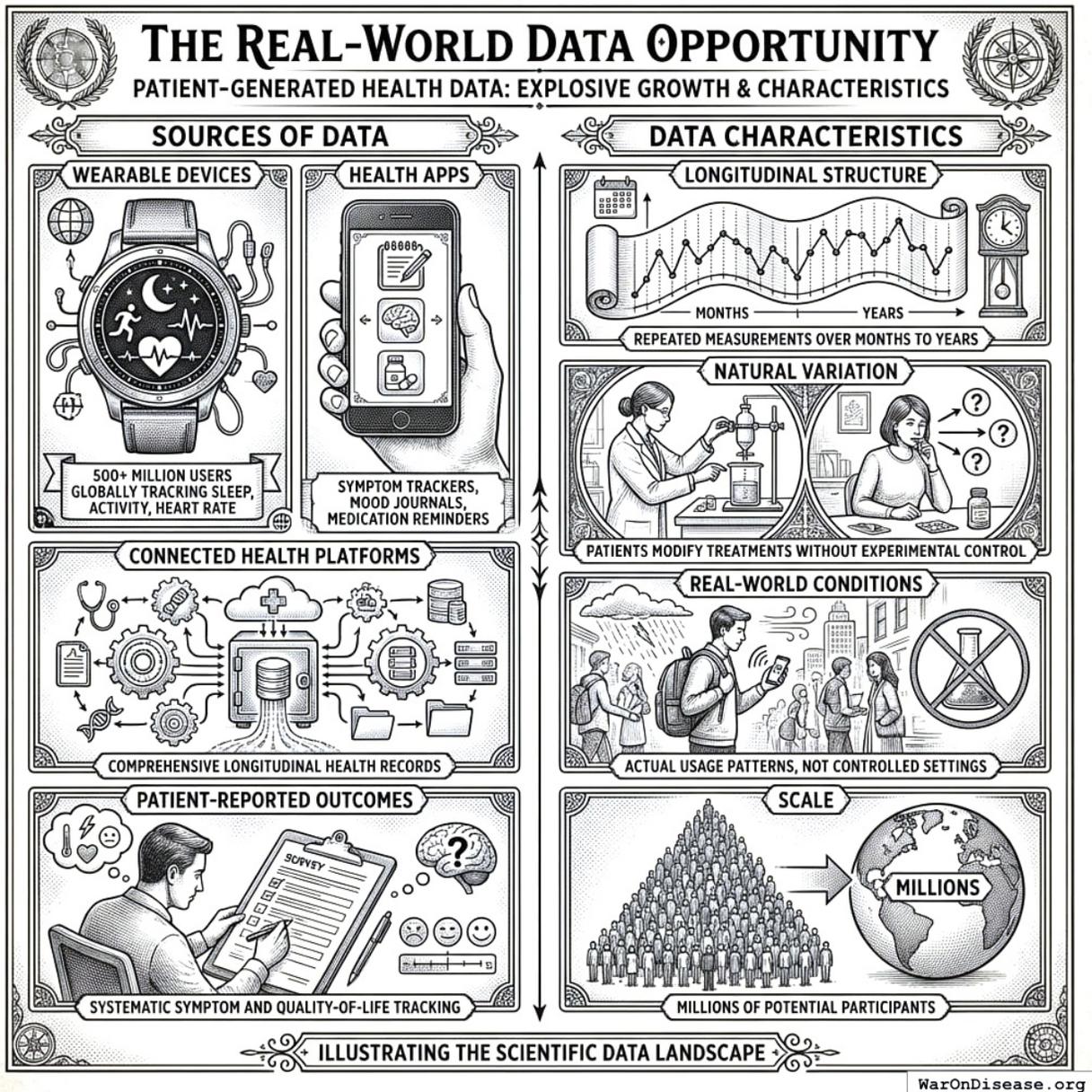


Figure 8: A visual summary of the patient-generated health data ecosystem, showcasing various sources like wearables and apps alongside key data characteristics such as scale and longitudinal structure.

The past decade has seen explosive growth in patient-generated health data:

- **Wearable devices:** 500+ million users globally tracking sleep, activity, heart rate¹³⁶
- **Health apps:** Symptom trackers, mood journals, medication reminders
- **Connected health platforms:** Comprehensive longitudinal health records
- **Patient-reported outcomes:** Systematic symptom and quality-of-life tracking

This data is characterized by:

- **Longitudinal structure:** Repeated measurements over months to years
- **Natural variation:** Patients modify treatments without experimental control
- **Real-world conditions:** Actual usage patterns, not controlled settings
- **Scale:** Millions of potential participants

3.4 Our Contribution

We present a framework that transforms real-world health data into actionable pharmacovigilance intelligence:

1. **Quantitative Outcome Labels:** For each treatment, generate effect sizes (percent change from baseline) for all measured outcomes
2. **Treatment Rankings:** Rank treatments by efficacy and safety within therapeutic categories
3. **Automated Signal Detection:** Identify safety concerns (negative correlations) and efficacy signals (positive correlations)
4. **Bradford Hill Integration:** Composite scoring that operationalizes causal inference criteria^{137,138}
5. **Scalable Implementation:** Analyze millions of treatment-outcome pairs automatically

This is not a replacement for RCTs but a complement, providing continuous, population-scale monitoring that can:

- Generate hypotheses for experimental validation
- Detect signals missed by spontaneous reporting
- Quantify effects that RCTs can only describe qualitatively
- Enable personalized benefit-risk assessment

Multiple meta-analyses demonstrate that well-designed observational studies produce effect sizes concordant with randomized controlled trials, supporting the validity of real-world evidence for hypothesis generation:

4 Data Collection and Integration

4.1 Data Sources

Our data integration protocol specifies how data flows from multiple sources, each contributing different variable types:

Source Category	Examples	Data Types
Wearables	Fitbit, Apple Watch, Oura Ring, Garmin	Sleep, steps, heart rate, HRV
Health Apps	Symptom trackers, mood journals	Symptoms, mood, energy, pain
Medication Trackers	Medisafe, MyTherapy	Drug intake, dosage, timing
Diet Trackers	MyFitnessPal, Cronometer	Foods, nutrients, calories
Lab Integrations	Quest, LabCorp APIs	Biomarkers, blood tests

Source Category	Examples	Data Types
EHR Connections	FHIR-enabled systems	Diagnoses, prescriptions, vitals
Manual Entry	Custom tracking	Any user-defined variable
Environmental	Weather APIs, air quality	Temperature, humidity, pollution

4.2 Variable Ontology

Variables are organized into semantic categories that inform default processing parameters:

Category	Examples	Onset Delay	Duration	Filling
Treatments	Drugs, supplements	30 min	24 hours	Zero
Foods	Diet, beverages	30 min	10 days	Zero
Symptoms	Pain, fatigue, nausea	0	24 hours	None
Emotions	Mood, anxiety, depression	0	24 hours	None
Vital Signs	Blood pressure, glucose	0	24 hours	None
Sleep	Duration, quality, latency	0	24 hours	None
Physical Activity	Steps, exercise, calories burned	0	24 hours	None
Environment	Weather, air quality, allergens	0	24 hours	None
Physique	Weight, body fat, measurements	0	7 days	None

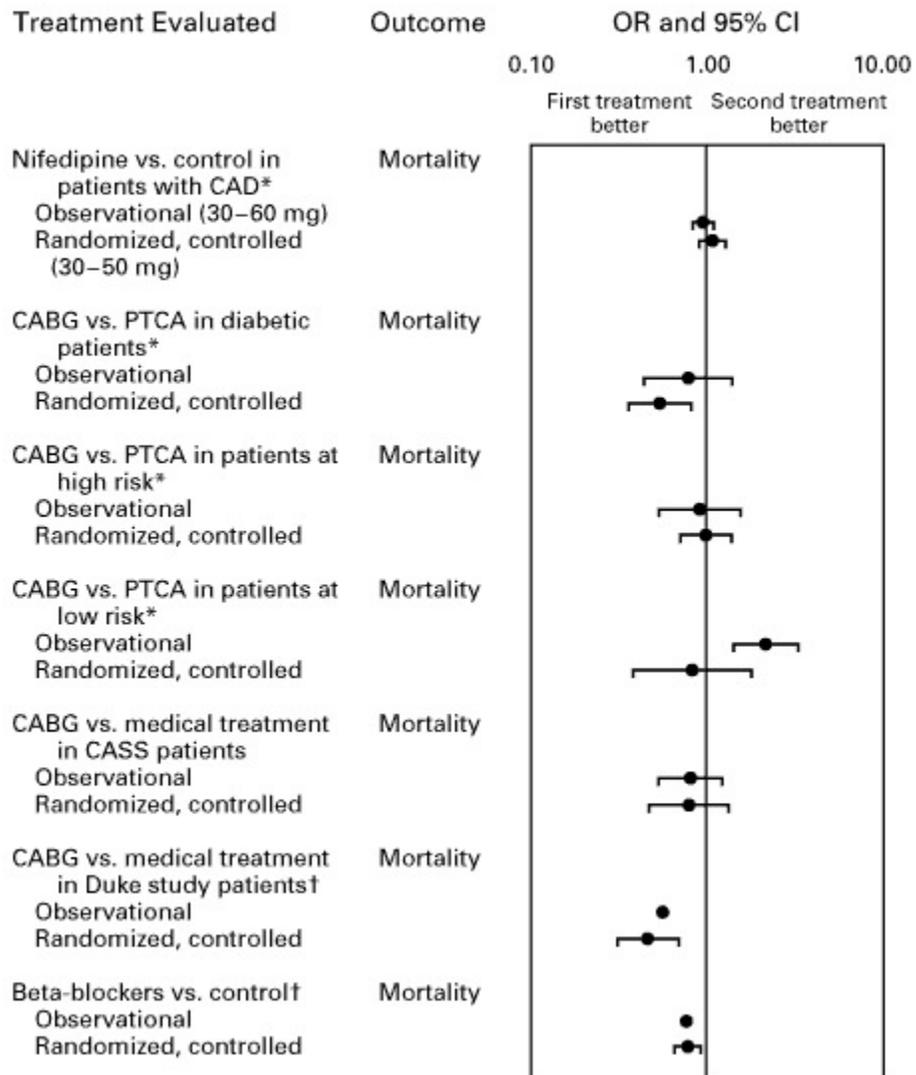


Figure 9: Effect sizes from observational studies vs. randomized trials show strong concordance for mortality outcomes

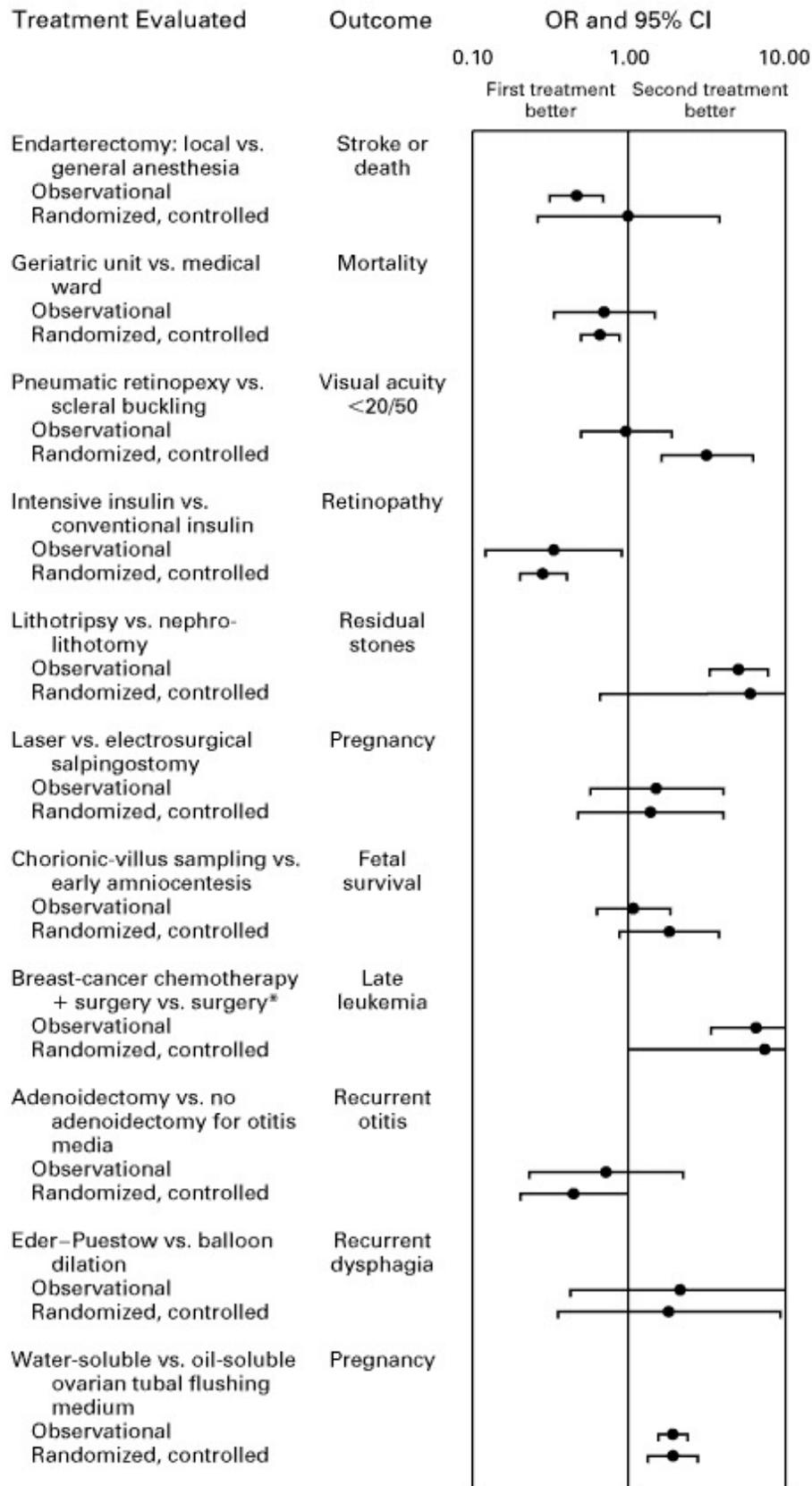


Figure 10: Across multiple clinical domains, observational and randomized effect sizes track closely

4.3 Measurement Structure

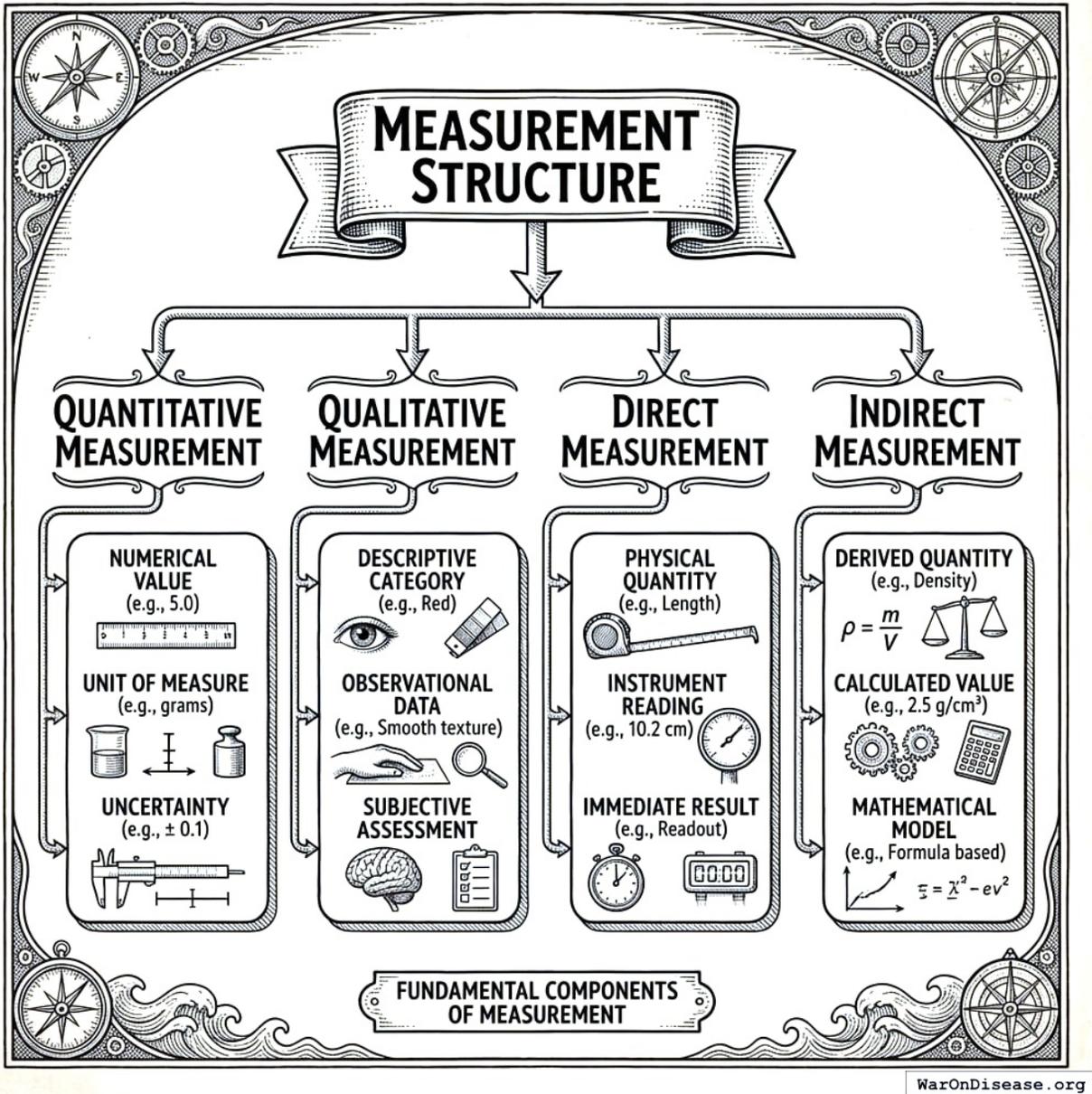


Figure 11: A relational diagram showing how a Measurement object acts as a central hub connecting participant, variable, unit, and source identifiers.

Each measurement includes:

```
Measurement {
    variable_id: int           // Reference to variable definition
    user_id: int              // Anonymized participant identifier
    value: float              // Numeric measurement value
    unit_id: int              // Standardized unit reference
    start_time: timestamp    // When measurement was taken
```

```
    source_id: int           // Data source for provenance
    note: string (optional) // User annotation
}
```

4.4 Unit Standardization

The measurement standardization protocol converts all measurements to standardized units for cross-source compatibility:

- Weights → kilograms
- Distances → meters
- Temperatures → Celsius
- Dosages → milligrams
- Durations → seconds
- Percentages → 0-100 scale
- Ratings → 1-5 scale (normalized)

5 Mathematical Framework

The short version: We track what people take (treatments, supplements, foods) and how they feel (symptoms, mood, energy) over time. Then we look for patterns: “When people take more of X, does Y get better or worse?” We account for the fact that treatments take time to work (onset delay) and their effects fade (duration of action). The math below makes this rigorous.

MATHEMATICAL FRAMEWORK: TRACKING & PATTERN ANALYSIS

The short version: We track what people take... and how they feel...
Then we look for **patterns**... We account for... **onset delay**... and... **duration of action**.

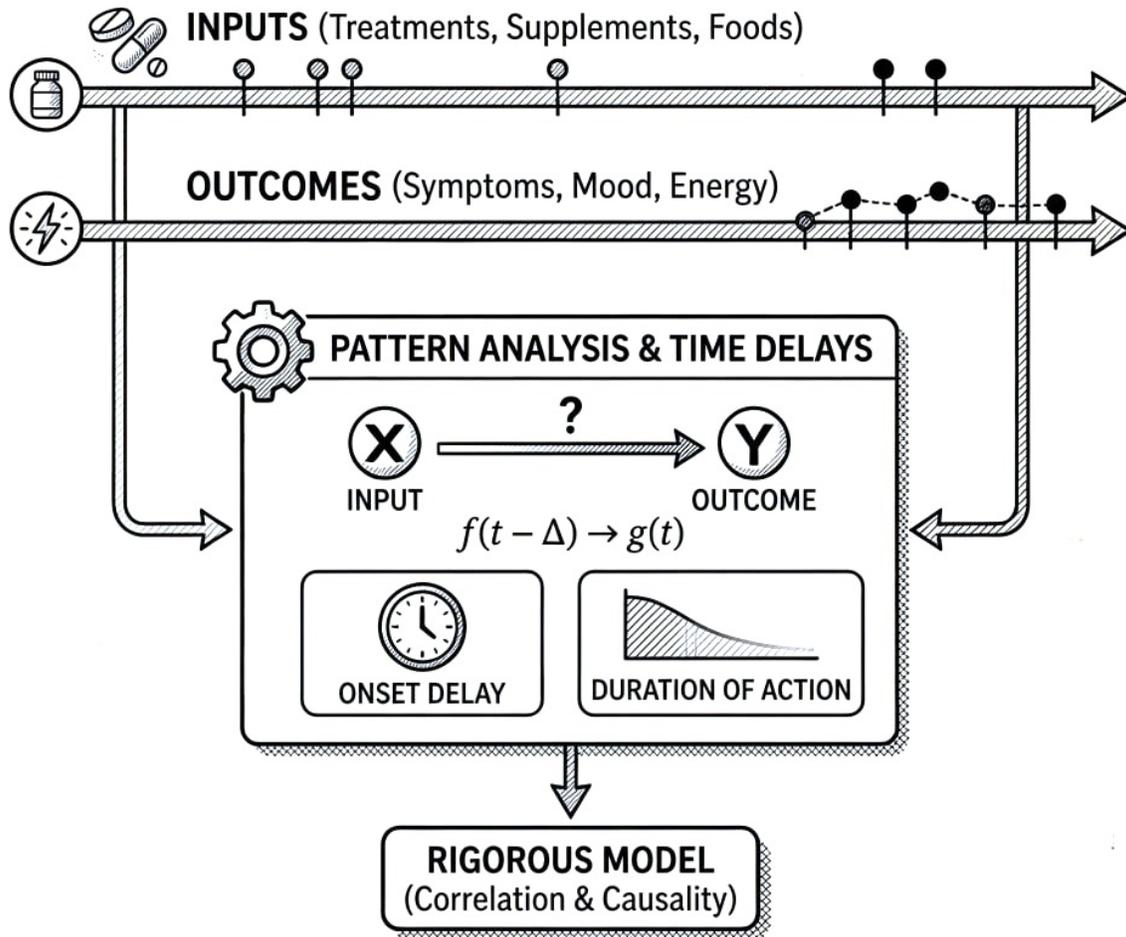


Figure 12: A conceptual diagram showing the relationship between a treatment dose and its impact on symptoms over time, highlighting the onset delay and duration of action.

5.1 Data Structure

For each participant $i \in \{1, \dots, N\}$, we observe time series of predictor variable P (e.g., treatment) and outcome variable O (e.g., symptom):

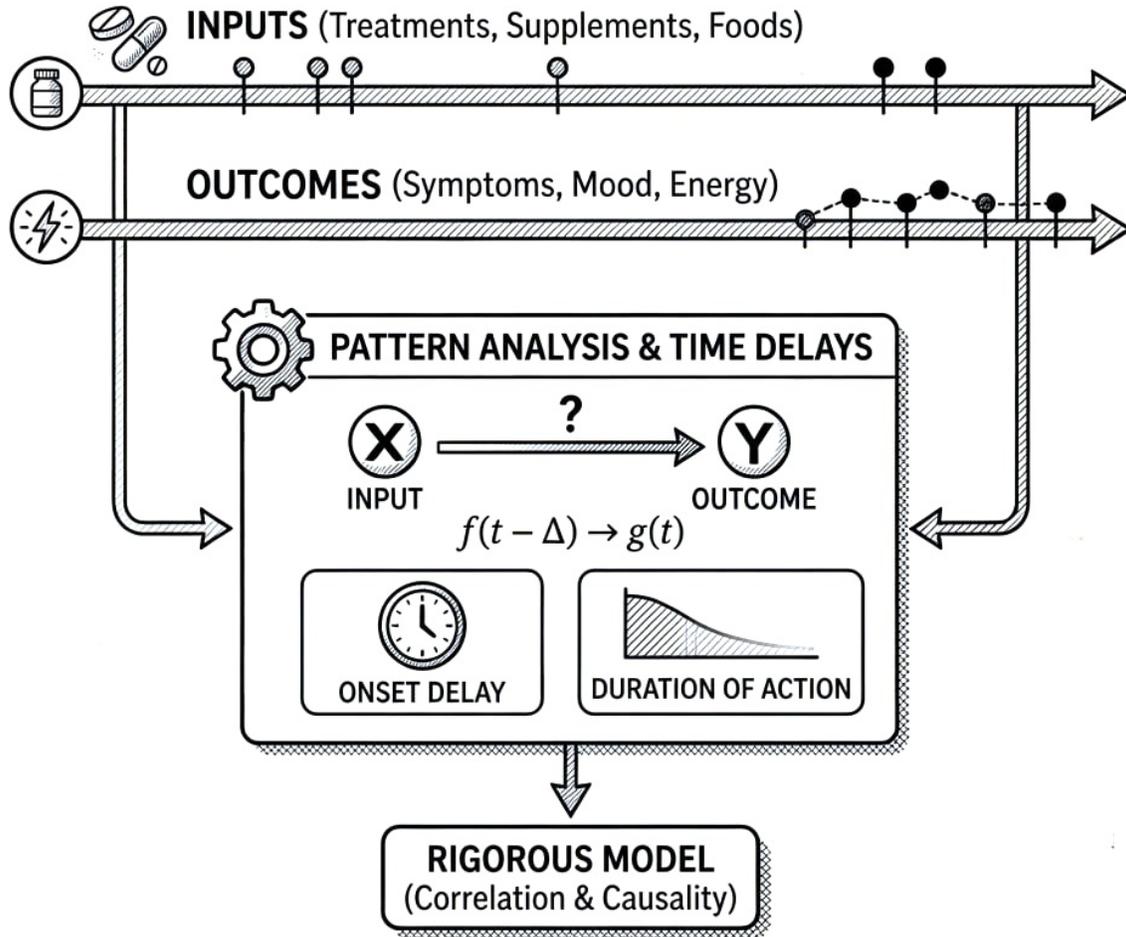
$$P_i = \{(t_{i,1}^P, p_{i,1}), (t_{i,2}^P, p_{i,2}), \dots, (t_{i,n_i}^P, p_{i,n_i})\}$$

$$O_i = \{(t_{i,1}^O, o_{i,1}), (t_{i,2}^O, o_{i,2}), \dots, (t_{i,m_i}^O, o_{i,m_i})\}$$

where t denotes timestamp, p denotes predictor measurements, and o denotes outcome measurements. Critically, timestamps need not be aligned. The temporal alignment protocol handles asynchronous, irregular sampling.

MATHEMATICAL FRAMEWORK: TRACKING & PATTERN ANALYSIS

The short version: We track what people take... and how they feel...
Then we look for **patterns**... We account for... **onset delay**... and... **duration of action**.



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Figure 13: Temporal alignment diagram illustrating how a single predictor measurement at time t creates an outcome window $W(t)$ defined by onset delay (Δ) and duration of action (τ) .

5.2 Temporal Alignment

5.2.1 Onset Delay and Duration of Action

Treatments do not produce immediate effects. We define:

- **Onset delay** δ : Time lag before treatment produces observable effect
- **Duration of action** τ : Time window over which effect persists

Constraints:

$$0 \leq \delta \leq 8,640,000 \text{ seconds (100 days)}$$

$$600 \leq \tau \leq 7,776,000 \text{ seconds (90 days)}$$

5.2.2 Outcome Window Calculation

For a predictor measurement at time t , we associate it with outcome measurements in the window:

$$W(t) = \{t_j : t + \delta \leq t_j \leq t + \delta + \tau\}$$

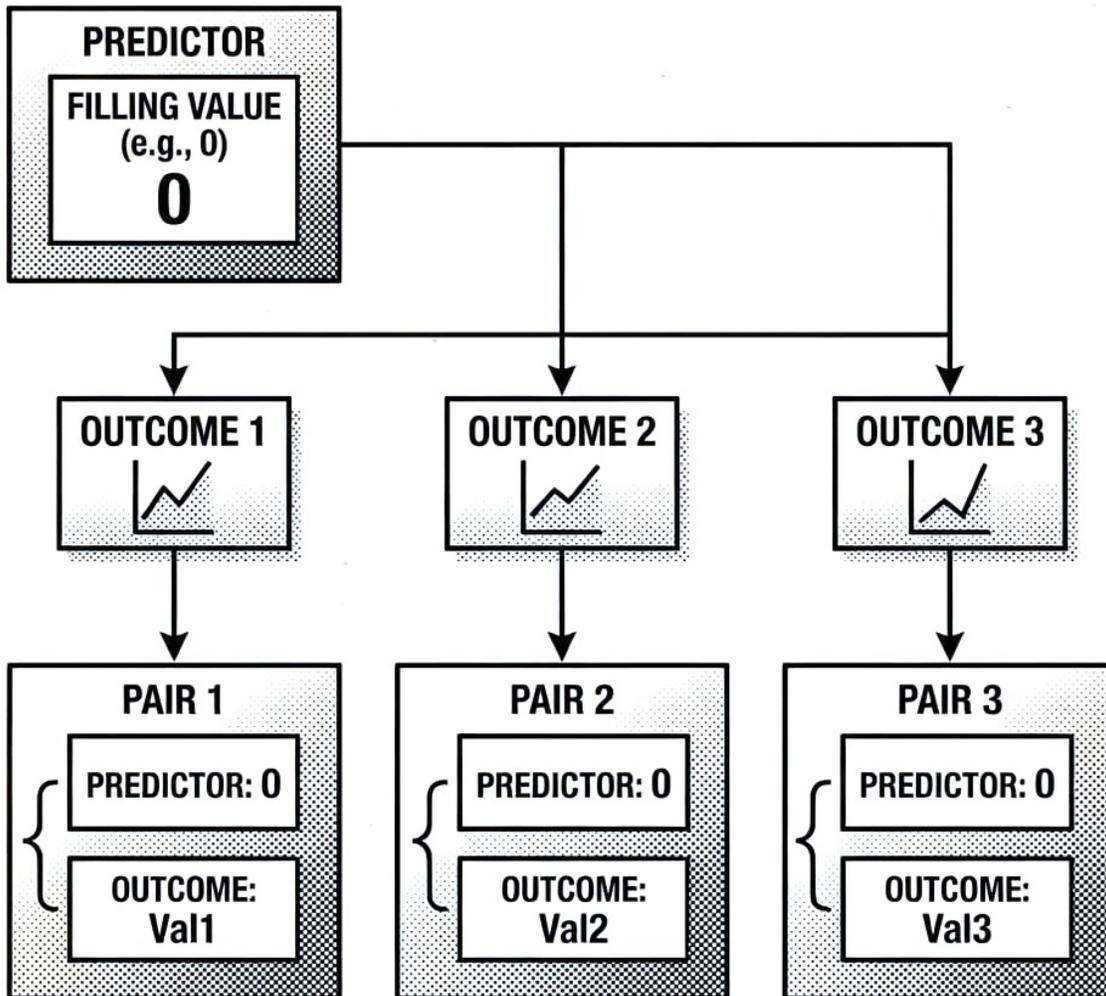
The aligned outcome value is computed as the mean:

$$\bar{o}(t) = \frac{1}{|W(t)|} \sum_{t_j \in W(t)} o_j$$

5.3 Pair Generation Strategies

We employ two complementary strategies depending on variable characteristics:

5.3.1 Outcome-Based Pairing (Predictor has Filling Value)



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Figure 14: A timeline diagram showing the relationship between an outcome measurement, the buffer period delta, and the preceding sampling window tau used to calculate predictor values.

When the predictor has a filling value (e.g., zero for “not taken”), we create one pair per outcome measurement:

```
For each outcome measurement (t_o, o):  
    window_end = t_o - delta  
    window_start = window_end - tau + 1
```

```
predictor_values = measurements in [window_start, window_end]

if predictor_values is empty:
    predictor_value = filling_value // e.g., 0
else:
    predictor_value = mean(predictor_values)

create_pair(predictor_value, o)
```

5.3.2 Predictor-Based Pairing (No Filling Value)

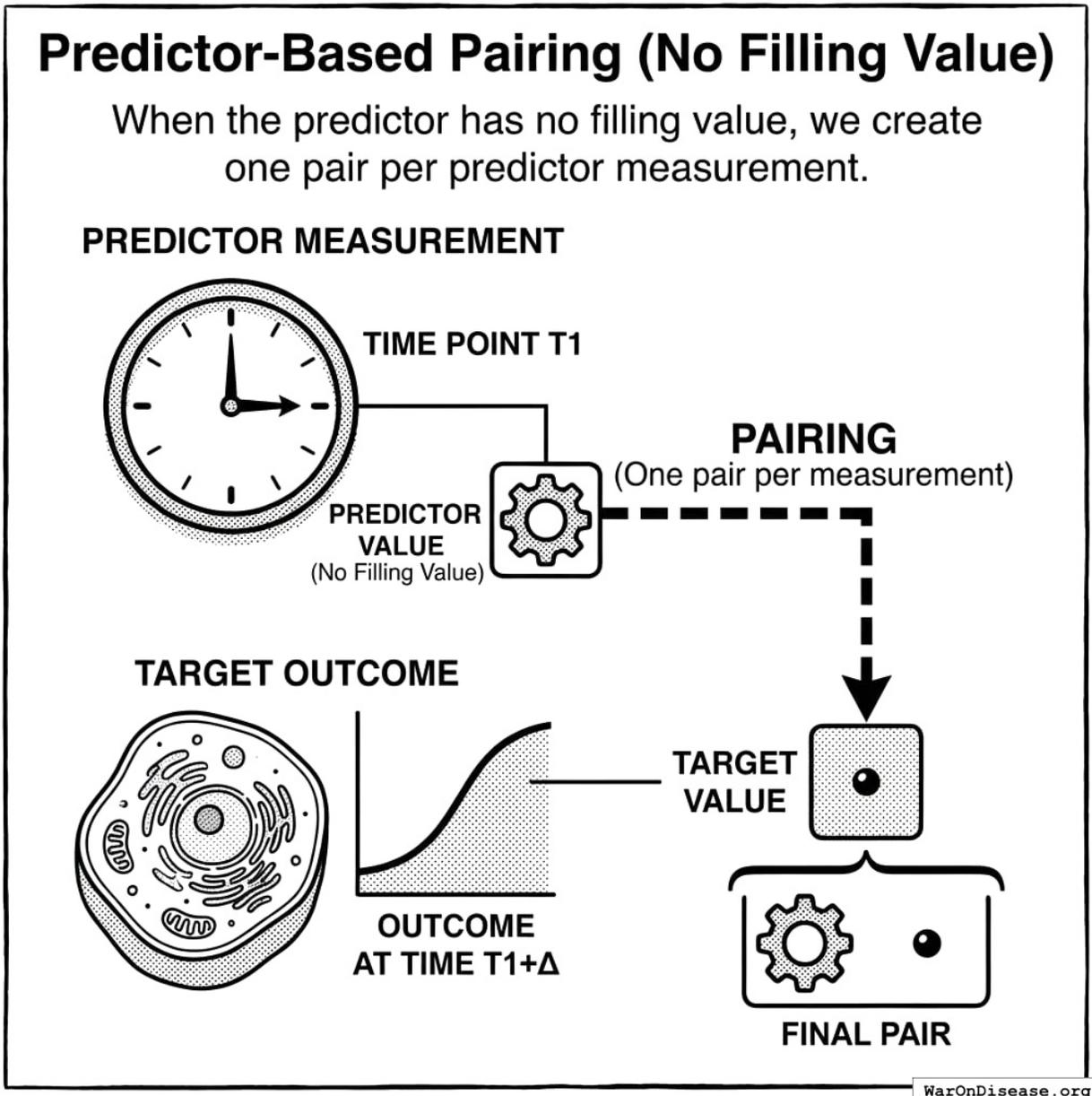


Figure 15: A timeline diagram showing a predictor measurement at time t_p , followed by a time delay δ , leading to an outcome window of length τ where measurements are averaged.

When the predictor has no filling value, we create one pair per predictor measurement:

For each predictor measurement (t_p, p) :

$window_start = t_p + \delta$

$window_end = window_start + \tau - 1$

$outcome_values = \text{measurements in } [window_start, window_end]$

```

if outcome_values is empty:
    skip this pair
else:
    outcome_value = mean(outcome_values)
    create_pair(p, outcome_value)

```

5.4 Filling Value Logic

5.4.1 Filling Types

Type	Description	Use Case
Zero	Missing = 0	Treatments (assume not taken)
Value	Missing = specific constant	Known default states
None	No imputation	Continuous outcomes
Interpolation	Linear interpolation	Slowly-changing variables

5.4.2 Temporal Boundaries

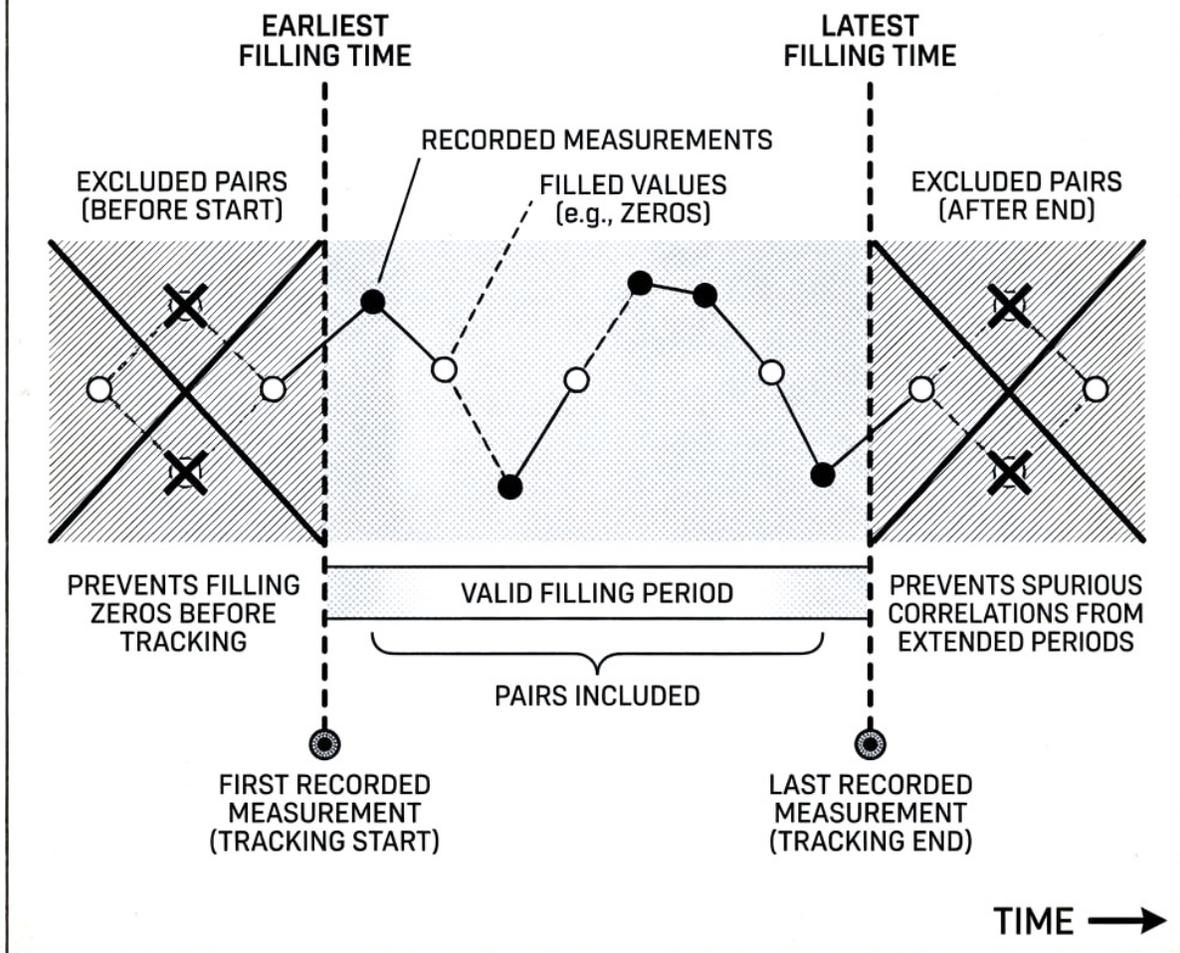
To prevent spurious correlations from extended filling periods:

- **Earliest filling time:** First recorded measurement (tracking start)
- **Latest filling time:** Last recorded measurement (tracking end)

Pairs outside these boundaries are excluded. This prevents filling zeros for a treatment before the participant started tracking it.

TEMPORAL BOUNDARIES

PREVENTING SPURIOUS CORRELATIONS



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Figure 16: A timeline visualization showing the data inclusion window between the earliest and latest recorded measurements, with data points outside these boundaries marked for exclusion.

5.4.3 Conservative Bias

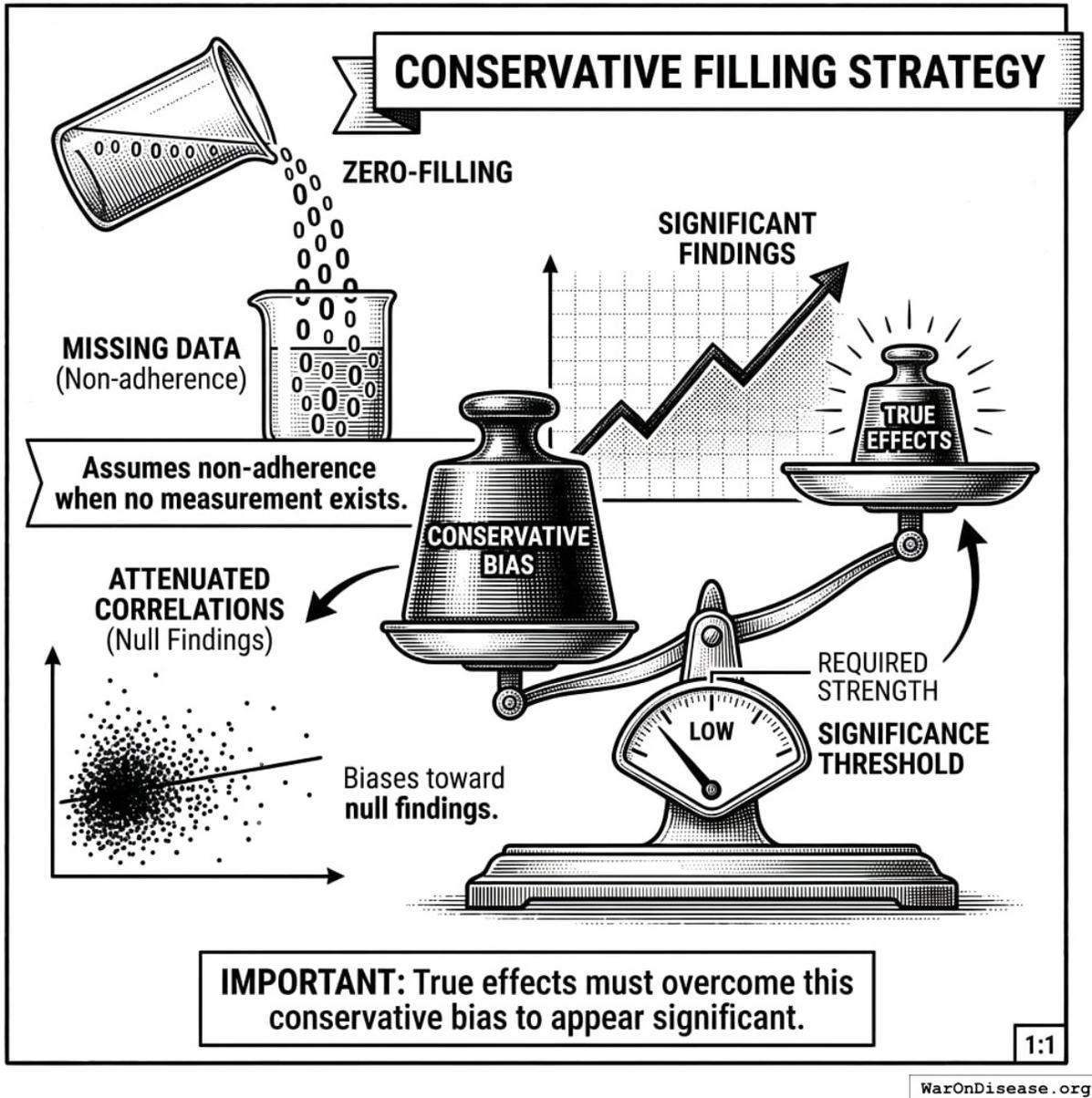


Figure 17: A conceptual chart showing how zero-filling missing data creates a conservative bias by pulling the measured correlation line toward the null baseline compared to the true effect.

Our filling strategy is deliberately conservative:

- Zero-filling for treatments assumes non-adherence when no measurement exists
- This biases toward null findings (attenuated correlations) rather than false positives
- True effects must overcome this conservative bias to appear significant

5.5 Baseline Definition and Outcome Estimation

5.5.1 Within-Subject Comparison

For each participant i , we compute the mean predictor value:

$$\bar{p}_i = \frac{1}{n_i} \sum_{j=1}^{n_i} p_{i,j}$$

We partition measurements into **baseline** and **follow-up** periods:

$$\text{Baseline}_i = \{(p, o) : p < \bar{p}_i\}$$

$$\text{Follow-up}_i = \{(p, o) : p \geq \bar{p}_i\}$$

This creates a natural within-subject comparison:

- **Baseline:** Periods of below-average predictor exposure
- **Follow-up:** Periods of above-average predictor exposure

5.5.2 Outcome Means

$$\mu_{\text{baseline},i} = \mathbb{E}[o \mid p < \bar{p}_i]$$

$$\mu_{\text{follow-up},i} = \mathbb{E}[o \mid p \geq \bar{p}_i]$$

5.6 Percent Change from Baseline

The primary effect size metric:

$$\Delta_i = \frac{\mu_{\text{follow-up},i} - \mu_{\text{baseline},i}}{\mu_{\text{baseline},i}} \times 100$$

Advantages:

- **Interpretability:** “15% reduction in pain” is intuitive
- **Scale invariance:** Enables comparison across different outcome measures
- **Clinical relevance:** Standard metric in medical literature
- **Regulatory familiarity:** FDA uses percent change in efficacy assessments

5.7 Correlation Coefficients

We compute both parametric and non-parametric measures:

5.7.1 Pearson Correlation (Linear Relationships)

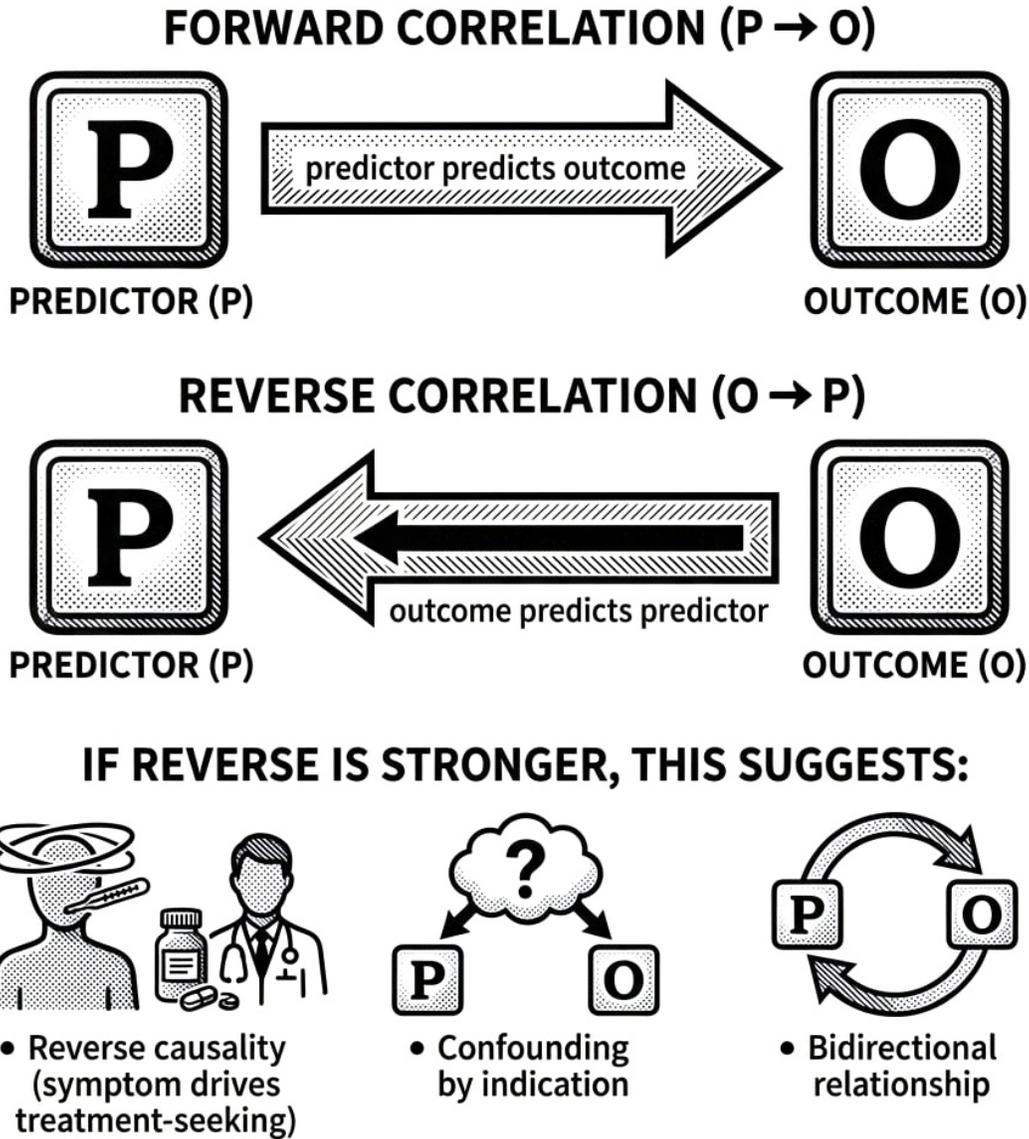
$$r_{\text{Pearson}} = \frac{\sum_{j=1}^n (p_j - \bar{p})(o_j - \bar{o})}{\sqrt{\sum_{j=1}^n (p_j - \bar{p})^2} \cdot \sqrt{\sum_{j=1}^n (o_j - \bar{o})^2}}$$

5.7.2 Spearman Rank Correlation (Monotonic Relationships)

$$r_{\text{Spearman}} = 1 - \frac{6 \sum_{j=1}^n d_j^2}{n(n^2 - 1)}$$

where $d_j = \text{rank}(p_j) - \text{rank}(o_j)$.

5.7.3 Forward and Reverse Correlations



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Figure 18: A conceptual diagram illustrating the difference between forward correlation (Predictor to Outcome) and reverse correlation (Outcome to Predictor), highlighting implications like reverse causality and confounding.

We compute both:

- **Forward:** $P \rightarrow O$ (predictor predicts outcome)
- **Reverse:** $O \rightarrow P$ (outcome predicts predictor)

If reverse correlation is stronger, this suggests:

- Reverse causality (symptom drives treatment-seeking)
- Confounding by indication
- Bidirectional relationship

5.8 Z-Score Normalization

To assess effect magnitude relative to natural variability:

$$z = \frac{|\Delta|}{\text{RSD}_{\text{baseline}}}$$

where relative standard deviation:

$$\text{RSD}_{\text{baseline}} = \frac{\sigma_{\text{baseline}}}{\mu_{\text{baseline}}} \times 100$$

Interpretation: $z > 2$ indicates $p < 0.05$ under normality, meaning the observed effect exceeds typical baseline fluctuation.

5.9 Statistical Significance

Two-tailed t-test for correlation significance:

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$$

with $n - 2$ degrees of freedom. Reject null hypothesis ($H_0 : \rho = 0$) at $\alpha = 0.05$ when:

$$|t| > t_{\text{critical}}(n-2, \alpha/2)$$

5.10 Hyperparameter Optimization

The onset delay δ^* and duration of action τ^* are selected to maximize correlation coefficient strength:

$$(\delta^*, \tau^*) = \underset{\delta, \tau}{\text{argmax}} |r(\delta, \tau)|$$

Search Strategy: 1. Initialize with category defaults (e.g., 30 min onset, 24 hr duration for drugs) 2. Grid search over physiologically plausible ranges 3. Select parameters yielding strongest correlation coefficient

Overfitting Mitigation:

- Restrict search to category-appropriate ranges

- Require minimum sample size before optimization
- Report both optimized and default-parameter results

6 Population Aggregation

6.1 Individual to Population

For population-level estimates, aggregate across N participants:

$$\bar{r} = \frac{1}{N} \sum_{i=1}^N r_i$$

$$\bar{\Delta} = \frac{1}{N} \sum_{i=1}^N \Delta_i$$

6.2 Standard Error and Confidence Intervals

$$SE_{\bar{r}} = \frac{\sigma_r}{\sqrt{N}}$$

$$CI_{95\%} = \bar{r} \pm 1.96 \cdot SE_{\bar{r}}$$

6.3 Heterogeneity Assessment

Between-participant variance:

$$\sigma_{\text{between}}^2 = \text{Var}(r_i)$$

High heterogeneity suggests:

- Subgroup effects (responders vs. non-responders)
- Interaction with unmeasured factors
- Need for personalized analysis

7 Data Quality Requirements

7.1 Minimum Thresholds

Requirement	Threshold	Rationale
Predictor value changes	≥ 5	Ensures sufficient variance
Outcome value changes	≥ 5	Ensures sufficient variance
Overlapping pairs	≥ 30	Central limit theorem
Baseline fraction	$\geq 10\%$	Adequate baseline
Follow-up fraction	$\geq 10\%$	Adequate predictor exposure
Processed daily measurements	≥ 4	Minimum data density

7.2 Variance Validation

Before computing variable relationships, validate sufficient variance:

$$\text{changes}(X) = \sum_{j=1}^{n-1} \mathbb{1}[x_j \neq x_{j+1}]$$

If $\text{changes}(P) < 5$ or $\text{changes}(O) < 5$, abort with `InsufficientVarianceException`.

7.3 Outcome Value Spread

$$\text{spread}_O = \max(O) - \min(O)$$

Variable relationships with zero spread are undefined and excluded.

8 Predictor Impact Score

The short version: Not all correlations are created equal. If we observe that “people who take Drug X report less pain,” how confident should we be? The Predictor Impact Score (PIS) answers this by combining: (1) how strong is the relationship, (2) how many people show it, (3) does the drug come *before* the improvement (not after), and (4) is there a dose-response pattern. High PIS = worth investigating in a clinical trial. Low PIS = probably noise.

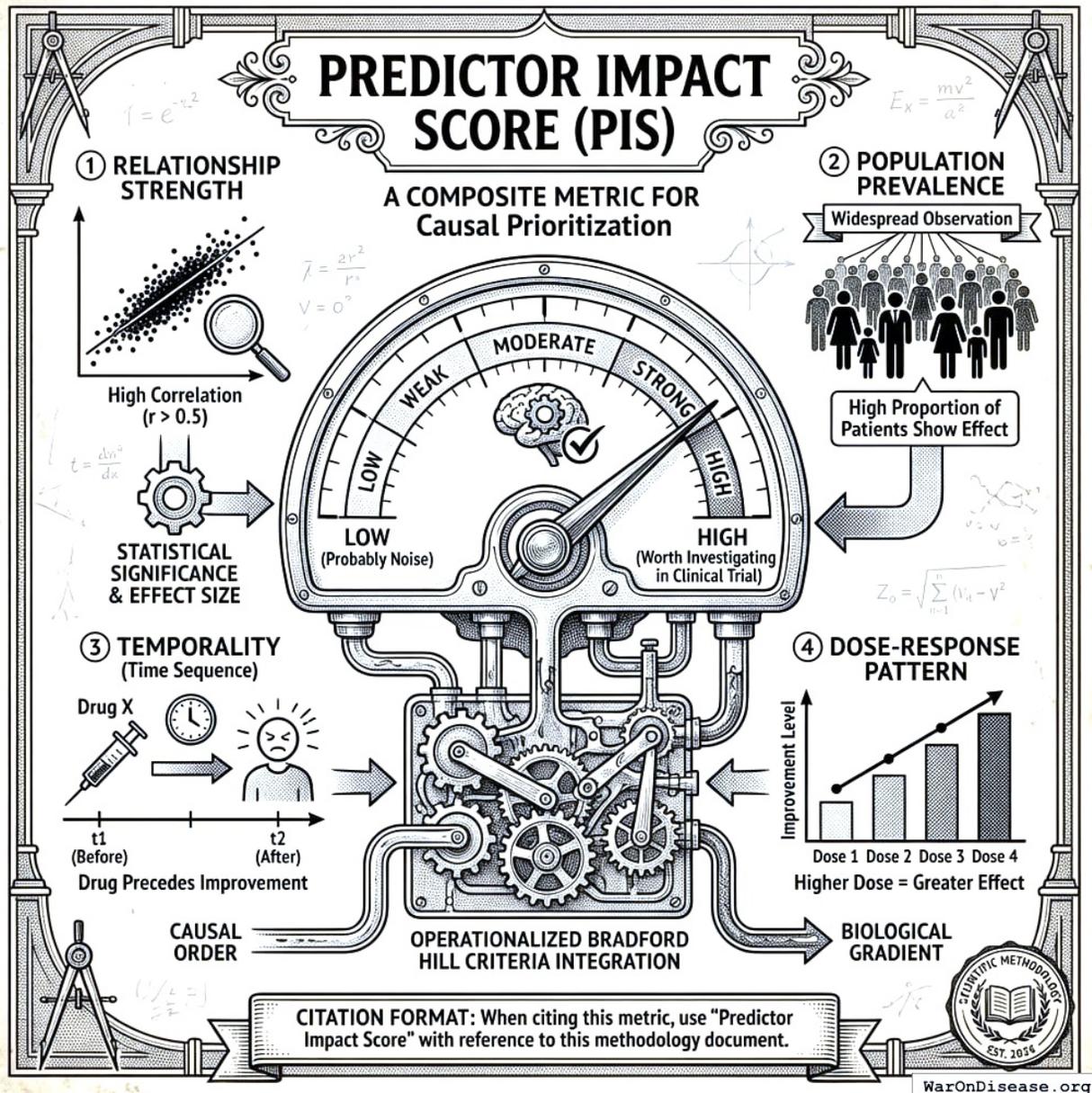


Figure 19: A diagram illustrating the four components (strength of relationship, statistical significance, temporal order, and dose-response) feeding into the Predictor Impact Score to determine if a drug effect is noise or a candidate for clinical trials.

The **Predictor Impact Score (PIS)** is a composite metric that quantifies treatment-outcome relationship strength from patient health data, operationalizing Bradford Hill causality criteria to prioritize drug effects for clinical trial validation. It integrates correlation strength, statistical significance, effect magnitude, and multiple Bradford Hill criteria into a single interpretable score. Higher scores indicate predictors with greater, more reliable impact on the outcome.

Citation format: When citing this metric in academic work, use “Predictor Impact Score” with reference to this methodology document.

8.1 What Makes the Predictor Impact Score Novel

Unlike simple correlation coefficients, PIS addresses fundamental limitations of observational analysis:

1. **Sample size agnosticism:** Raw correlations don't account for whether $N=10$ or $N=10,000$. PIS incorporates saturation functions that weight evidence accumulation.
2. **Temporal ambiguity:** Correlations can't distinguish $A \rightarrow B$ from $B \rightarrow A$. PIS includes a temporality factor comparing forward vs. reverse correlations.
3. **Effect magnitude blindness:** Statistical significance \neq practical significance. PIS incorporates z-scores to assess effect magnitude relative to baseline variability.
4. **Isolated metrics:** Traditional analysis reports correlation, p-value, and effect size separately. PIS integrates them into a single prioritization metric aligned with Bradford Hill criteria.

The Predictor Impact Score is not a causal proof. It's a principled heuristic for ranking which predictor-outcome relationships warrant further investigation, including experimental validation.

8.2 User-Level Predictor Impact Score

For individual participant (N-of-1) analyses, we compute:

$$\text{PIS}_{\text{user}} = |r| \cdot S \cdot \phi_z \cdot \phi_{\text{temporal}} \cdot f_{\text{interest}} + \text{PIS}_{\text{agg}}$$

Where:

- $|r|$ = absolute value of the correlation coefficient (strength)
- S = statistical significance (1 - p-value)
- ϕ_z = normalized z-score factor (effect magnitude)
- ϕ_{temporal} = temporality factor (forward vs. reverse causation)
- f_{interest} = interest factor (penalizes spurious variable pairs)
- PIS_{agg} = population-level aggregate score (provides context from broader population)

8.3 Aggregate (Population-Level) Predictor Impact Score

For population-level analyses aggregated across multiple participants:

$$\text{PIS}_{\text{agg}} = |r_{\text{forward}}| \cdot w \cdot \phi_{\text{users}} \cdot \phi_{\text{pairs}} \cdot \phi_{\text{change}} \cdot \phi_{\text{gradient}}$$

Where:

- $|r_{\text{forward}}|$ = absolute forward Pearson correlation coefficient (strength)
- w = weighted average of community votes on plausibility
- $\phi_{\text{users}} = 1 - e^{-N/N_{\text{sig}}}$ (user saturation, $N_{\text{sig}} = 10$)
- $\phi_{\text{pairs}} = 1 - e^{-n/n_{\text{sig}}}$ (pair saturation, $n_{\text{sig}} =$ significant pairs threshold)
- $\phi_{\text{change}} = 1 - e^{-\Delta_{\text{spread}}/\Delta_{\text{sig}}}$ (change spread saturation)
- $\phi_{\text{gradient}} =$ biological gradient coefficient (dose-response)

The saturation functions asymptotically approach 1 as sample sizes increase, reflecting that consistent findings across more participants strengthen causal inference.

8.4 Z-Score and Effect Magnitude Factor

The z-score quantifies the magnitude of the outcome change relative to baseline variability:

$$z = \frac{|\Delta\%_{\text{baseline}}|}{\text{RSD}_{\text{baseline}}}$$

Where:

- $\Delta\%_{\text{baseline}}$ = percent change from baseline (see below)
- $\text{RSD}_{\text{baseline}}$ = relative standard deviation of outcome during baseline period

A z-score > 2 indicates statistical significance ($p < 0.05$), meaning the observed change is unlikely due to random variation.

The **normalized z-score factor** incorporates effect magnitude into the PIS score:

$$\phi_z = \frac{|z|}{|z| + z_{\text{ref}}}$$

Where $z_{\text{ref}} = 2$ (the conventional significance threshold). This saturating function:

- Approaches 0 for negligible effects ($z \rightarrow 0$)
- Equals 0.5 at the significance threshold ($z = 2$)
- Approaches 1 for very large effects ($z \rightarrow \infty$)

8.5 Temporality Factor

The temporality factor quantifies evidence that the predictor precedes and causes the outcome (rather than reverse causation):

$$\phi_{\text{temporal}} = \frac{|r_{\text{forward}}|}{|r_{\text{forward}}| + |r_{\text{reverse}}|}$$

Where:

- r_{forward} = correlation when predictor precedes outcome ($P \rightarrow O$)
- r_{reverse} = correlation when outcome precedes predictor ($O \rightarrow P$)

This factor:

- Equals 0.5 when forward and reverse correlations are equal (ambiguous causality)
- Approaches 1 when forward correlation dominates (supports predictor \rightarrow outcome)
- Approaches 0 when reverse correlation dominates (suggests reverse causation or confounding by indication)

8.6 Percent Change from Baseline

The primary effect size metric expressing treatment impact:

$$\Delta\%_{\text{baseline}} = \frac{\bar{O}_{\text{follow-up}} - \bar{O}_{\text{baseline}}}{\bar{O}_{\text{baseline}}} \times 100$$

Where:

- $\bar{O}_{\text{follow-up}}$ = mean outcome value during follow-up period (after predictor exposure)
- $\bar{O}_{\text{baseline}}$ = mean outcome value during baseline period (before predictor exposure)

For outcomes measured in percentages or with zero baseline, we use absolute change instead:

$$\Delta_{\text{abs}} = \bar{O}_{\text{follow-up}} - \bar{O}_{\text{baseline}}$$

8.7 Statistical Significance

The statistical significance component captures confidence in the relationship:

$$S = 1 - p$$

Where p is the p-value from the correlation significance test. Higher values indicate greater confidence that the observed relationship is not due to chance.

8.8 Interest Factor

The interest factor f_{interest} penalizes likely spurious or uninteresting variable pairs:

$$f_{\text{interest}} = f_P \cdot f_O \cdot f_{\text{pair}}$$

Where:

- f_P = predictor interest factor (reduced for test variables, apps, addresses)
- f_O = outcome interest factor (reduced for non-outcome categories)
- f_{pair} = pair appropriateness (reduced for illogical category combinations)

8.9 Additional Data Quality Components

Skewness Coefficient (penalizes non-normal distributions):

$$\phi_{\text{skew}} = \frac{1}{1 + \gamma_P^2} \cdot \frac{1}{1 + \gamma_O^2}$$

Kurtosis Coefficient (penalizes heavy tails):

$$\phi_{\text{kurt}} = \frac{1}{1 + \kappa_P^2} \cdot \frac{1}{1 + \kappa_O^2}$$

Biological Gradient (dose-response relationship):

$$\phi_{\text{gradient}} = \left(\frac{\bar{p}_{\text{high}} - \bar{p}}{\sigma_P} - \frac{\bar{p}_{\text{low}} - \bar{p}}{\sigma_P} \right)^2$$

Measures the standardized difference between predictor values that predict high vs. low outcomes.

8.10 Bradford Hill Criteria Mapping

The PIS operationalizes six of the nine Bradford Hill criteria for causality¹³⁹:

Component	Formula	Bradford Hill Criterion	In PIS Formula
$\ r\ $	Correlation magnitude	Strength	Yes (direct)
ϕ_z	Normalized z-score	Strength (effect magnitude)	Yes (user-level)
$\Delta\%$	Percent change from baseline	Strength (clinical significance)	Yes (via ϕ_z)
$\phi_{\text{users}}, \phi_{\text{pairs}}$	Sample saturation	Consistency	Yes (aggregate)
ϕ_{gradient}	Dose-response coefficient	Biological Gradient	Yes (aggregate)
w	Weighted community votes	Plausibility	Yes (aggregate)
f_{interest}	Category appropriateness	Specificity	Yes (user-level)
ϕ_{temporal}	Forward/reverse ratio	Temporality	Yes (user-level)
$\delta > 0$	Onset delay requirement	Temporality	Enforced in design

8.11 Interpreting Predictor Impact Scores

Provisional Thresholds - Not Yet Validated

The PIS thresholds below are **theoretically motivated heuristics**, not empirically validated cutoffs. Until retrospective validation against RCT outcomes is performed (see Section 18), these thresholds should be treated as provisional guidelines for prioritization, not evidence standards.

PIS scores range from 0 to approximately 1 (though values slightly above 1 are possible with very strong evidence). Guidelines for interpretation:

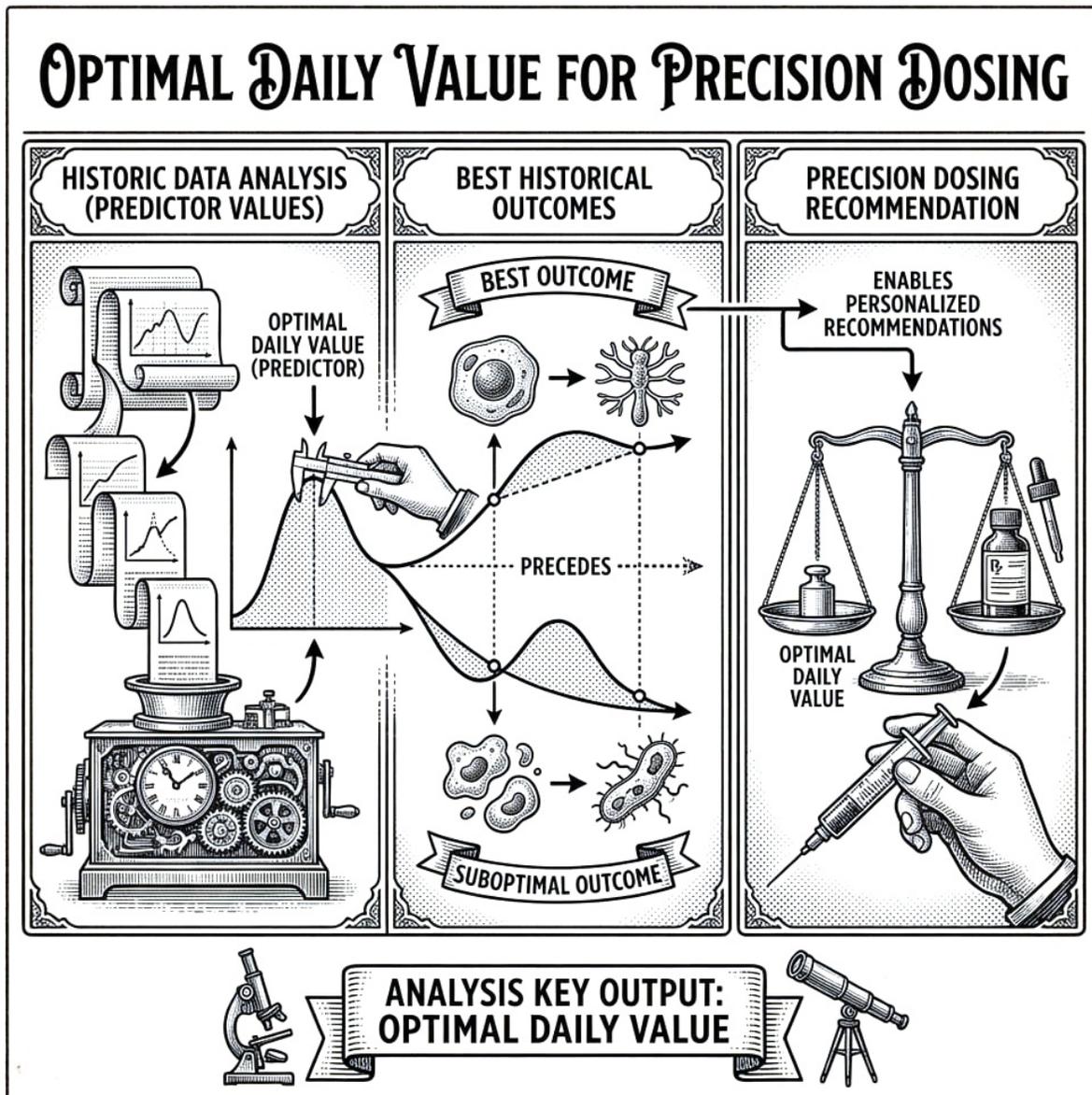
PIS Range	Interpretation	Recommended Action
0.5	Strong evidence	High priority for RCT validation
0.3 - 0.5	Moderate evidence	Consider for experimental investigation
0.1 - 0.3	Weak evidence	Monitor for additional data
< 0.1	Insufficient evidence	Low priority; may be noise

Important caveats:

- These thresholds are preliminary and should be validated against RCT outcomes
- PIS is relative, not absolute. Use it for prioritization, not proof.
- High PIS does not guarantee causation; low PIS does not rule it out
- Context matters: a PIS of 0.2 for a novel relationship may be more interesting than 0.5 for a known one

8.12 Optimal Daily Value for Precision Dosing

A key output of our analysis is the **optimal daily value**, the predictor value that historically precedes the best outcomes. This enables personalized, precision dosing recommendations.



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Figure 20: A conceptual flow showing how historical data analysis identifies an optimal daily value to achieve personalized precision dosing and superior outcomes.

8.12.1 Value Predicting High Outcome

The **Value Predicting High Outcome** (V_{high}) is the average predictor value observed when the outcome exceeds its mean:

$$V_{\text{high}} = \frac{1}{|H|} \sum_{(p,o) \in H} p$$

Where:

- $H = \{(p, o) : o > \bar{O}\}$ is the set of predictor-outcome pairs where outcome exceeds its average
- \bar{O} = mean outcome value across all pairs
- p = predictor (cause) value for each pair

Calculation Process: 1. Compute the average outcome value (\bar{O}) across all predictor-outcome pairs 2. Filter pairs to include only those where outcome $> \bar{O}$ (the “high effect” pairs) 3. Calculate the mean predictor value across these high-effect pairs

8.12.2 Value Predicting Low Outcome

The **Value Predicting Low Outcome** (V_{low}) is the average predictor value observed when the outcome is below its mean:

$$V_{\text{low}} = \frac{1}{|L|} \sum_{(p,o) \in L} p$$

Where:

- $L = \{(p, o) : o < \bar{O}\}$ is the set of predictor-outcome pairs where outcome is below its average

8.12.3 Grouped Optimal Values

For interpretability, we also calculate **grouped optimal values** that map to common dosing intervals:

- **Grouped Value Predicting High Outcome:** The nearest grouped predictor value (e.g., rounded to typical dosing units) to V_{high}
- **Grouped Value Predicting Low Outcome:** The nearest grouped predictor value to V_{low}

This allows recommendations like “400mg of Magnesium” rather than “412.7mg of Magnesium.”

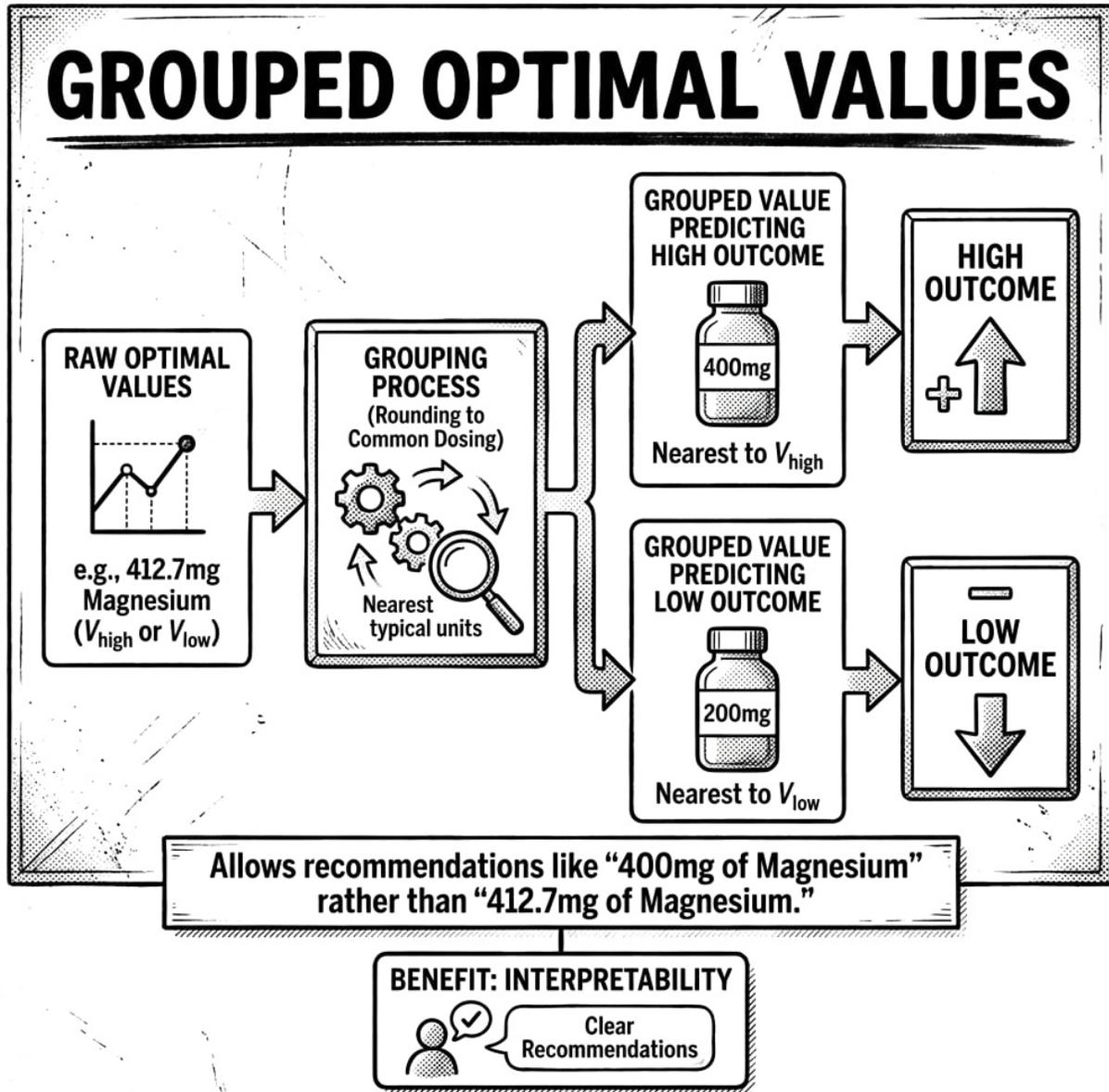


Figure 21: A diagram showing the mapping of precise calculated values to standard, rounded dosing intervals for practical use.

8.12.4 Precision Dosing Recommendations

These optimal values enable personalized recommendations:

For Positive Valence Outcomes (where higher is better, e.g., energy, sleep quality): > “Your [Outcome] was highest after [Grouped Value Predicting High Outcome] of [Predictor] over the previous [Duration of Action].” >> Example: “Your Sleep Quality was highest after 400mg of Magnesium over the previous 24 hours.”

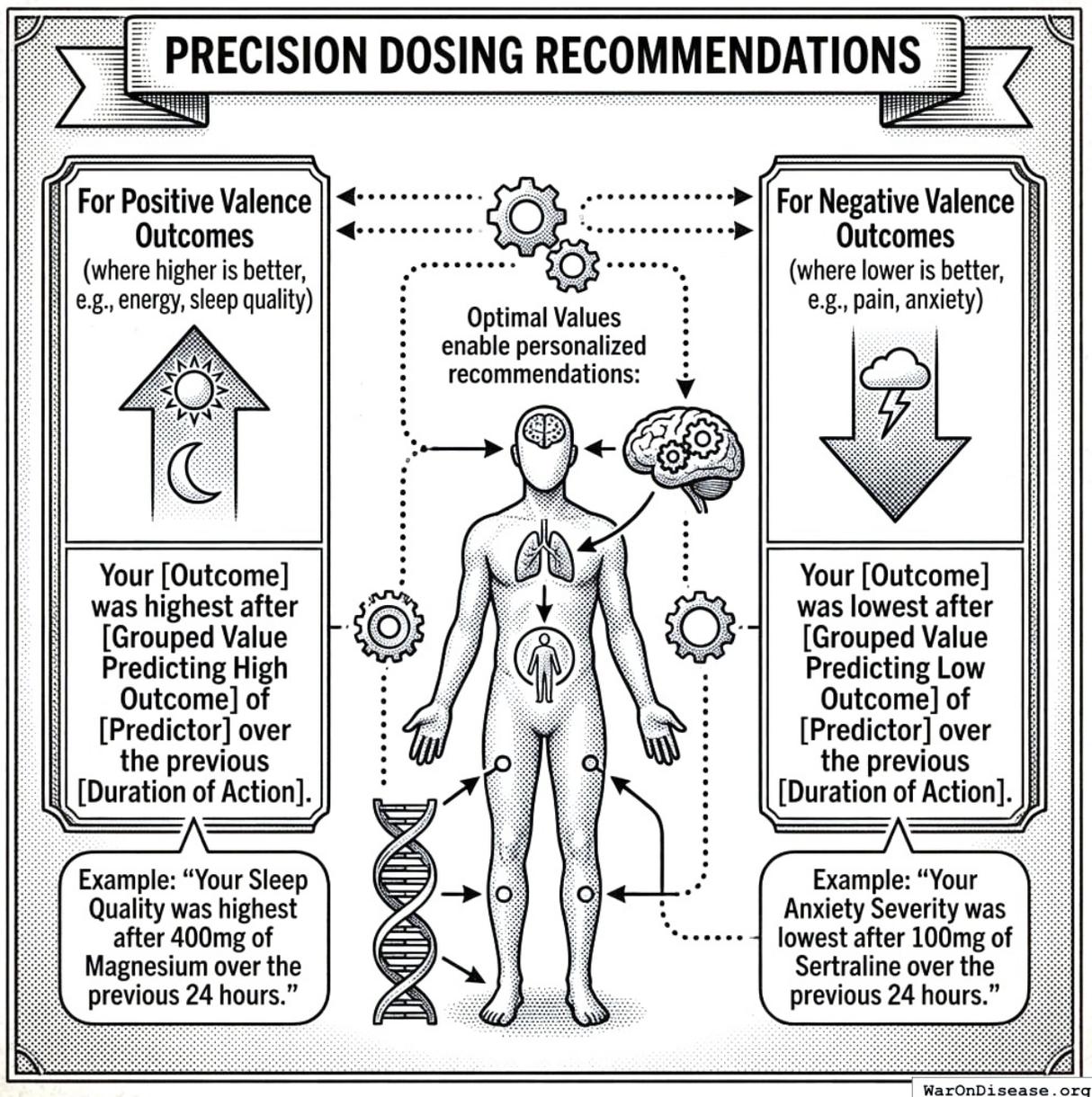


Figure 22: A comparison diagram showing the different logic structures for generating personalized dosing recommendations based on whether the health outcome is positive or negative.

For Negative Valence Outcomes (where lower is better, e.g., pain, anxiety): > "Your [Outcome] was lowest after [Grouped Value Predicting Low Outcome] of [Predictor] over the previous [Duration of Action]." >> Example: "Your Anxiety Severity was lowest after 100mg of Sertraline over the previous 24 hours."

8.12.5 Mathematical Relationship to Biological Gradient

The optimal values are closely related to the **biological gradient coefficient** (ϕ_{gradient}):

$$\phi_{\text{gradient}} = \left(\frac{V_{\text{high}} - \bar{P}}{\sigma_P} - \frac{V_{\text{low}} - \bar{P}}{\sigma_P} \right)^2$$

A larger separation between V_{high} and V_{low} indicates:

- Stronger dose-response relationship
- More reliable precision dosing recommendations
- Higher biological gradient coefficient

8.12.6 Clinical Applications

Metric	Definition	Clinical Use
V_{high}	Avg predictor when outcome $>$ mean	Optimal dose for positive outcomes
V_{low}	Avg predictor when outcome $<$ mean	Dose to avoid for positive outcomes
$V_{\text{high}} - V_{\text{low}}$	Optimal value spread	Magnitude of dose-response effect

Example Application: For a participant tracking Magnesium supplementation and Sleep Quality:

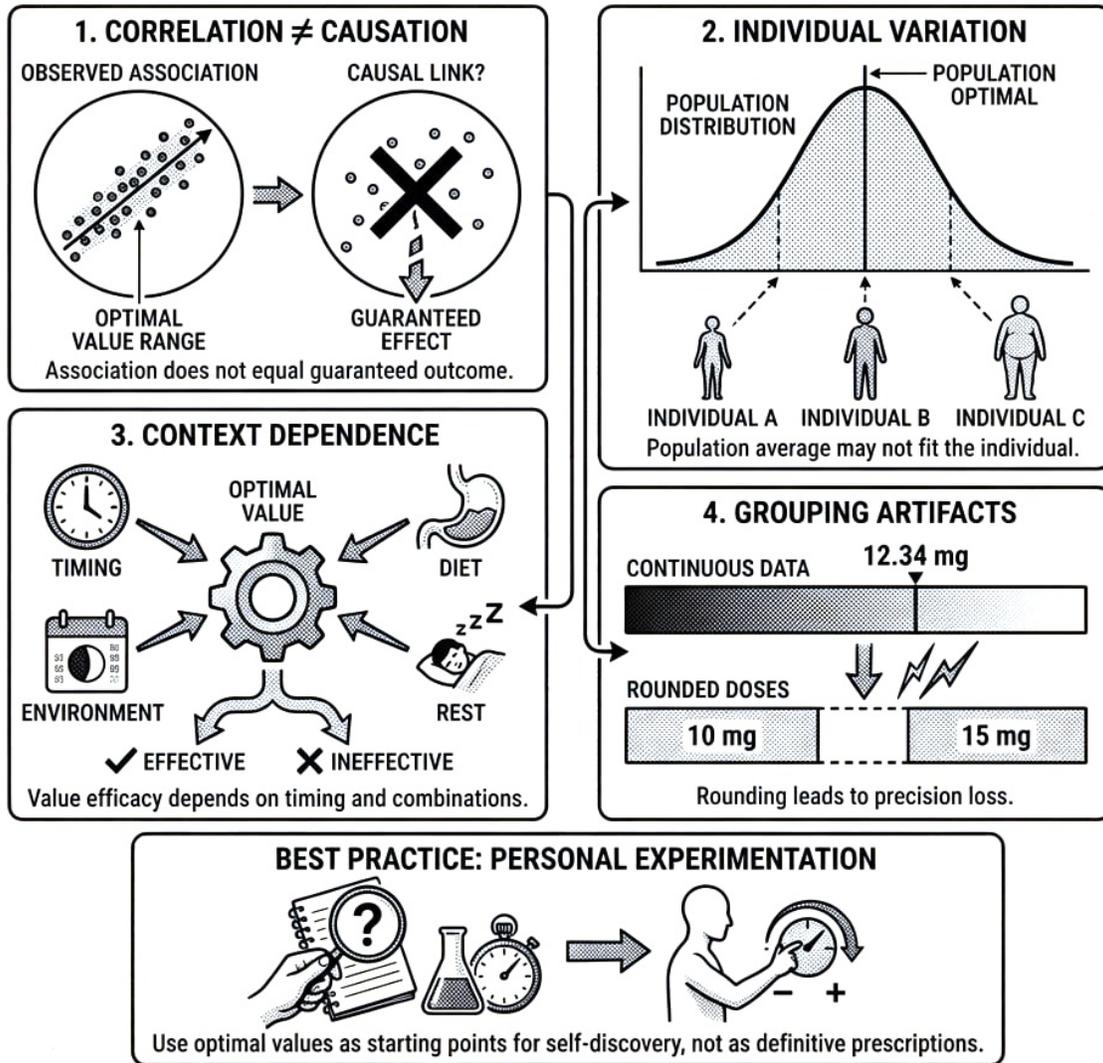
- $V_{\text{high}} = 412\text{mg} \rightarrow$ Grouped = 400mg (sleep quality highest after this dose)
- $V_{\text{low}} = 127\text{mg} \rightarrow$ Grouped = 125mg (sleep quality lowest after this dose)
- Recommendation: “Take approximately 400mg of Magnesium for optimal sleep quality”

8.12.7 Limitations

1. **Correlation Causation:** Optimal values reflect associations, not guaranteed causal effects
2. **Individual Variation:** Population optimal values may not be optimal for all individuals
3. **Context Dependence:** Optimal values may vary by timing, combination with other factors
4. **Grouping Artifacts:** Rounding to common doses may lose precision

Best Practice: Use optimal values as starting points for personal experimentation, not as definitive prescriptions.

LIMITATIONS OF “OPTIMAL” VALUES IN COMPLEX SYSTEMS



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Figure 23: A conceptual diagram showing how population-level ‘optimal values’ pass through filters like individual variation and context to become personalized starting points for experimentation.

8.12.8 Confidence Intervals for Optimal Values

Optimal values should be reported with uncertainty bounds to convey reliability:

$$CI_{V_{\text{high}}} = V_{\text{high}} \pm t_{\alpha/2} \cdot \frac{\sigma_{p|H}}{\sqrt{|H|}}$$

Where:

- $\sigma_{p|H}$ = standard deviation of predictor values in high-outcome set H

- $|H|$ = number of pairs in high-outcome set
- $t_{\alpha/2}$ = critical t-value for desired confidence level

Interpretation Guidelines:

CI Width (relative to mean)	Reliability	Recommendation
< 10%	High	Use as primary recommendation
10-25%	Moderate	Present as range (e.g., “350-450mg”)
25-50%	Low	Insufficient precision for dosing
> 50%	Very Low	Do not use for recommendations

Example: If $V_{\text{high}} = 400\text{mg}$ with 95% CI [380, 420], report: “Optimal dose: 400mg (95% CI: 380-420mg)”

8.12.9 Individual vs Population Optimal Values

Both individual and population optimal values are computed and stored. Guidelines for use:

Scenario	Recommended Source	Rationale
User has 50 paired measurements	Individual V_{high}	Sufficient personal data
User has 20-50 measurements	Weighted blend	$0.5 \cdot V_{\text{user}} + 0.5 \cdot V_{\text{pop}}$
User has <20 measurements	Population V_{high}	Insufficient personal data
User’s optimal differs >50% from population	Flag for review	May indicate unique response or data quality issue

Blending Formula:

$$V_{\text{recommended}} = w \cdot V_{\text{user}} + (1 - w) \cdot V_{\text{pop}}$$

Where $w = \min(1, n_{\text{user}}/n_{\text{threshold}})$ with $n_{\text{threshold}} = 50$ pairs.

8.12.10 Temporal Stability and Recalculation

Optimal values may drift over time due to:

- Physiological changes (age, weight, health status)
- Tolerance development
- Seasonal factors
- Lifestyle changes

Recalculation Policy:

Trigger	Action
New measurements added	Recalculate after every 10 new pairs
Time elapsed	Recalculate monthly regardless of new data
Significant life change	User-triggered recalculation
Optimal value drift >20%	Alert user to potential change

Rolling Window Option: For treatments where tolerance is expected, compute optimal values using only the most recent 90 days of data rather than all historical data.

Stability Metric:

$$\text{Stability} = 1 - \frac{|V_{\text{high}}^{\text{current}} - V_{\text{high}}^{\text{previous}}|}{V_{\text{high}}^{\text{previous}}}$$

Stability < 0.8 (>20% change) triggers a notification to the user.

8.12.11 Edge Cases: Minimal Dose-Response

When $V_{\text{high}} \approx V_{\text{low}}$, the predictor shows no clear dose-response relationship:

Detection Criterion:

$$\frac{|V_{\text{high}} - V_{\text{low}}|}{\sigma_P} < 0.5$$

(Less than half a standard deviation apart)

Possible Interpretations: 1. **Threshold effect:** Any dose above zero works equally well 2. **No effect:** Predictor doesn't influence outcome 3. **Non-linear response:** U-shaped or inverted-U curve not captured by simple high/low split 4. **Insufficient variance:** User takes similar doses, preventing detection

Handling:

- Do not display optimal value recommendations when dose-response is minimal
- Instead report: “No clear dose-response relationship detected for [Predictor] → [Outcome]”
- Flag for potential non-linear analysis in future versions

8.12.12 Validation of Optimal Values

The Critical Question: Do users who follow optimal value recommendations actually experience better outcomes than those who don't?

Proposed Validation Study:

1. **Prospective A/B Test:**
 - Group A: Receives personalized optimal value recommendations
 - Group B: Receives no recommendations (continues current behavior)
 - Compare outcome trajectories over 30-90 days
2. **Retrospective Adherence Analysis:**
 - For users with established optimal values, calculate “adherence score”:

$$\text{Adherence} = \frac{\text{Days within } \pm 20\% \text{ of } V_{\text{high}}}{\text{Total tracking days}}$$

- Correlate adherence with outcome improvement

Success Metrics:

- Users in top adherence quartile should show >15% better outcomes than bottom quartile
- Optimal value recommendations should outperform random dosing by >10%

Current Status: This validation has not been performed. Until validated, optimal values should be presented as “data-driven suggestions” rather than “clinically validated recommendations.”

8.13 Saturation Constant Rationale

The saturation constants (N_sig, n_sig, etc.) reflect pragmatic thresholds based on statistical and clinical considerations:

Constant	Value	Rationale
N_sig (users)	10	At N=10, user saturation 0.63. By N=30, 0.95. Reflects that consistency across 10+ individuals provides meaningful replication.
n_sig (pairs)	100	Central limit theorem suggests n 30 for normality. We use 100 as the “strong evidence” threshold.
Δ_sig (change spread)	10%	A 10% change is often considered clinically meaningful across many health outcomes.
z_ref	2	Corresponds to p < 0.05 under normality (the conventional significance threshold).

These constants are not empirically optimized. Future work should: 1. Validate constants against known causal relationships (from RCTs) 2. Consider domain-specific thresholds (e.g., psychiatric vs. cardiovascular outcomes) 3. Implement sensitivity analyses to assess robustness to constant choices

8.14 Effect Following High vs Low Predictor Values

Beyond optimal values, we calculate the **average outcome following different predictor levels** to quantify dose-response relationships:

8.14.1 Average Outcome Metrics

Metric	Definition	Clinical Interpretation
Average Outcome	Mean outcome across all pairs	Baseline outcome level

Metric	Definition	Clinical Interpretation
Average Outcome Following High Predictor	Mean outcome when predictor > mean	Outcome after high exposure
Average Outcome Following Low Predictor	Mean outcome when predictor < mean	Outcome after low exposure
Average Daily High Predictor	Mean predictor in upper 51% of spread	“High dose” value
Average Daily Low Predictor	Mean predictor in lower 49% of spread	“Low dose” value

8.14.2 Calculation

$$\bar{O}_{\text{high}} = \mathbb{E}[O \mid P > \bar{P}]$$

$$\bar{O}_{\text{low}} = \mathbb{E}[O \mid P \leq \bar{P}]$$

Where \bar{P} is the mean predictor value across all pairs.

Effect Size from High to Low Cause:

$$\Delta_{\text{high-low}} = \frac{\bar{O}_{\text{high}} - \bar{O}_{\text{low}}}{\bar{O}_{\text{low}}} \times 100$$

This metric directly shows the percent difference in outcome between high and low predictor exposure periods.

8.15 Predictor Baseline and Treatment Averages

For treatment-response analysis, we distinguish between **baseline** (non-treatment) and **treatment** periods:

Metric	Definition	Use Case
Predictor Baseline Average Per Day	Average daily predictor during low-exposure periods	Typical non-treatment value
Predictor Treatment Average Per Day	Average daily predictor during high-exposure periods	Typical treatment dosage
Predictor Baseline Average Per Duration Of Action	Baseline cumulative over duration of action	For longer-acting effects
Predictor Treatment Average Per Duration Of Action	Treatment cumulative over duration of action	Cumulative treatment dose

Example: For a user taking Magnesium supplements:

- `predictor_baseline_average_per_day` = 50mg (days not supplementing, dietary only)
- `predictor_treatment_average_per_day` = 400mg (days actively supplementing)
- This reveals the effective treatment dose vs. background exposure

8.16 Relationship Quality Filters

Not all statistically significant relationships are useful. We apply **quality filters** to prioritize actionable findings:

8.16.1 Filter Flags

Flag	Description	Impact on Ranking
Predictor Is Controllable	User can directly modify this predictor (e.g., food, supplements)	Required for actionable recommendations
Outcome Is A Goal	Outcome is something users want to optimize (e.g., mood, energy)	Required for relevance
Plausibly Causal	Plausible biological mechanism exists	Increases confidence
Obvious	Relationship is already well-known (e.g., caffeine → alertness)	May deprioritize for discovery
Boring	Relationship unlikely to interest users	Filters from default views
Interesting Variable Category Pair	Category combination is typically meaningful (e.g., Treatment → Symptom)	Prioritizes for analysis

8.16.2 Boring Relationship Definition

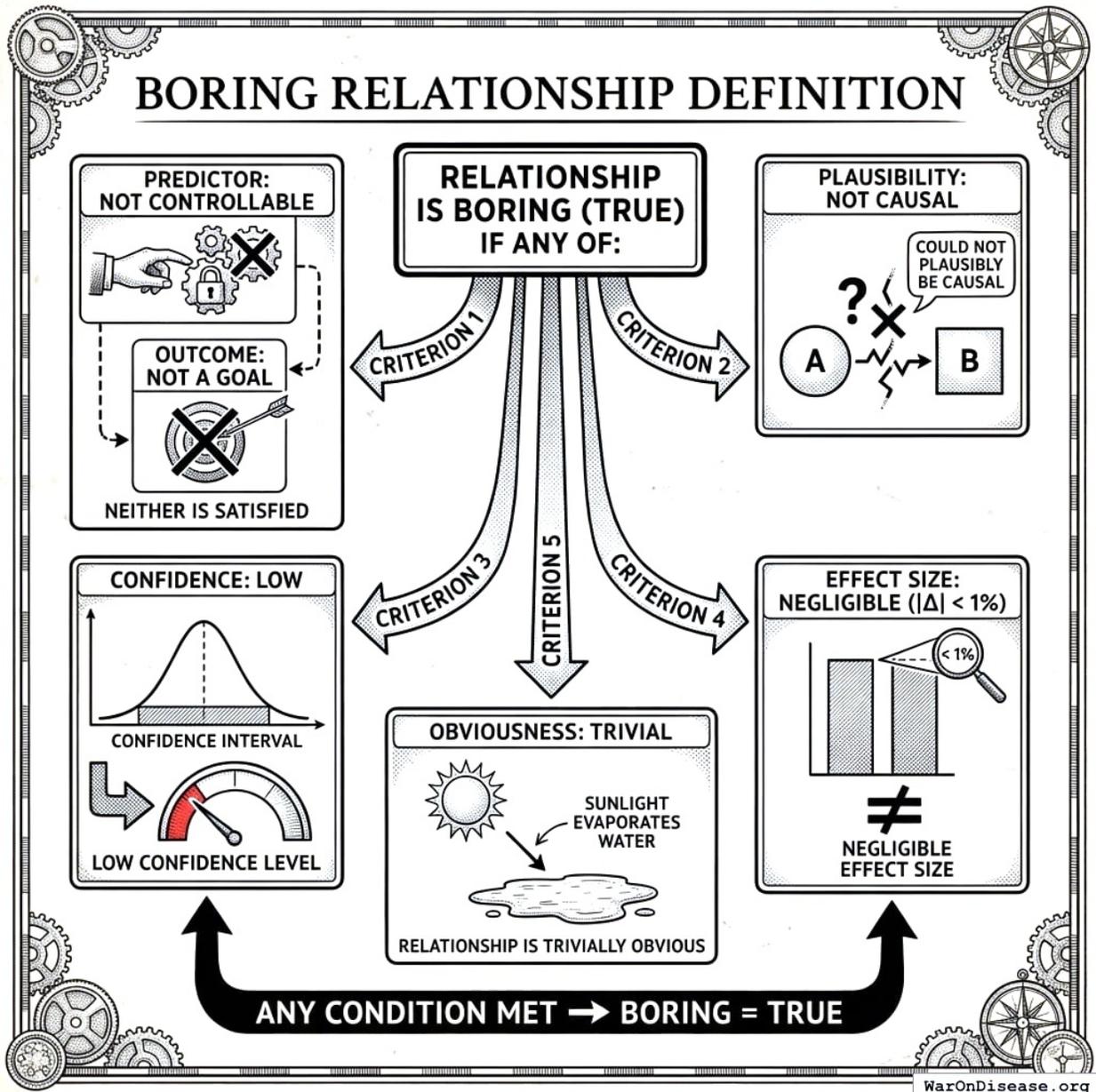


Figure 24: A flowchart depicting the decision logic for flagging a data relationship as ‘boring’ based on five specific rejection criteria.

A relationship is marked **boring = TRUE** if ANY of:

- Predictor is not controllable AND outcome is not a goal
- Relationship could not plausibly be causal
- Confidence level is LOW
- Effect size is negligible ($|\Delta| < 1\%$)
- Relationship is trivially obvious

8.16.3 Usefulness and Causality Voting

Users can vote on individual relationships:

Vote Type	Values	Purpose
Usefulness Vote	-1, 0, 1	Whether knowledge of this relationship is useful
Causality Vote	-1, 0, 1	Whether there's a plausible causal mechanism

Aggregate votes contribute to the PIS plausibility weight (w).

8.17 Variable Valence

Valence indicates whether higher values of a variable are inherently good, bad, or neutral:

Valence	Meaning	Examples
Positive	Higher is better	Energy, Sleep Quality, Productivity
Negative	Lower is better	Pain, Anxiety, Fatigue
Neutral	Direction depends on context	Heart Rate, Weight

8.17.1 Impact on Interpretation

Valence affects how we interpret correlation direction:

Predictor-Outcome Valence	Positive Correlation	Negative Correlation
Positive \rightarrow Positive	Both improve together	Trade-off
Positive \rightarrow Negative	Predictor worsens outcome	Predictor improves outcome
Treatment \rightarrow Negative Symptom	Side effect	Therapeutic effect

Example: A positive correlation between Sertraline and Depression Severity is BAD (depression has negative valence, so lower is better). The same positive correlation between Sertraline and Energy would be GOOD.

8.18 Temporal Parameter Optimization

We optimize `onset_delay ()` and `duration_of_action ()` to find the temporal parameters that maximize correlation strength:

8.18.1 Stored Optimization Data

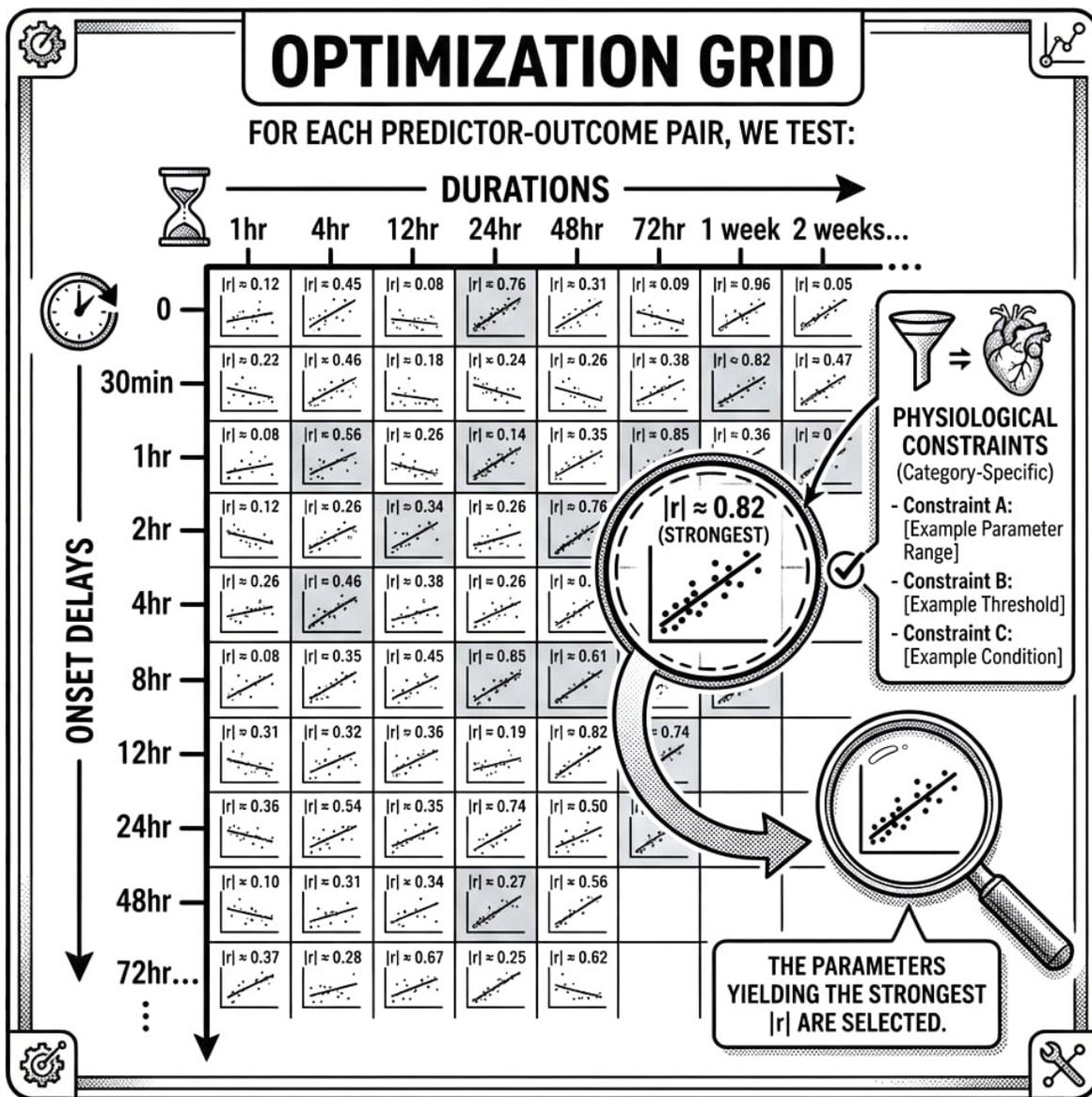
Field	Description
Correlations Over Delays	Pearson r values for various onset delays
Correlations Over Durations	Pearson r values for various durations of action

Field	Description
Onset Delay With Strongest Pearson Correlation	Optimal value
Pearson Correlation With No Onset Delay	Baseline r for immediate effect
Average Forward Pearson Correlation Over Onset Delays	Mean r across all tested delays
Average Reverse Pearson Correlation Over Onset Delays	Mean reverse r across delays

8.18.2 Optimization Grid

For each predictor-outcome pair, we test:

- **Onset delays:** 0, 30min, 1hr, 2hr, 4hr, 8hr, 12hr, 24hr, 48hr, 72hr...
- **Durations:** 1hr, 4hr, 12hr, 24hr, 48hr, 72hr, 1 week, 2 weeks...



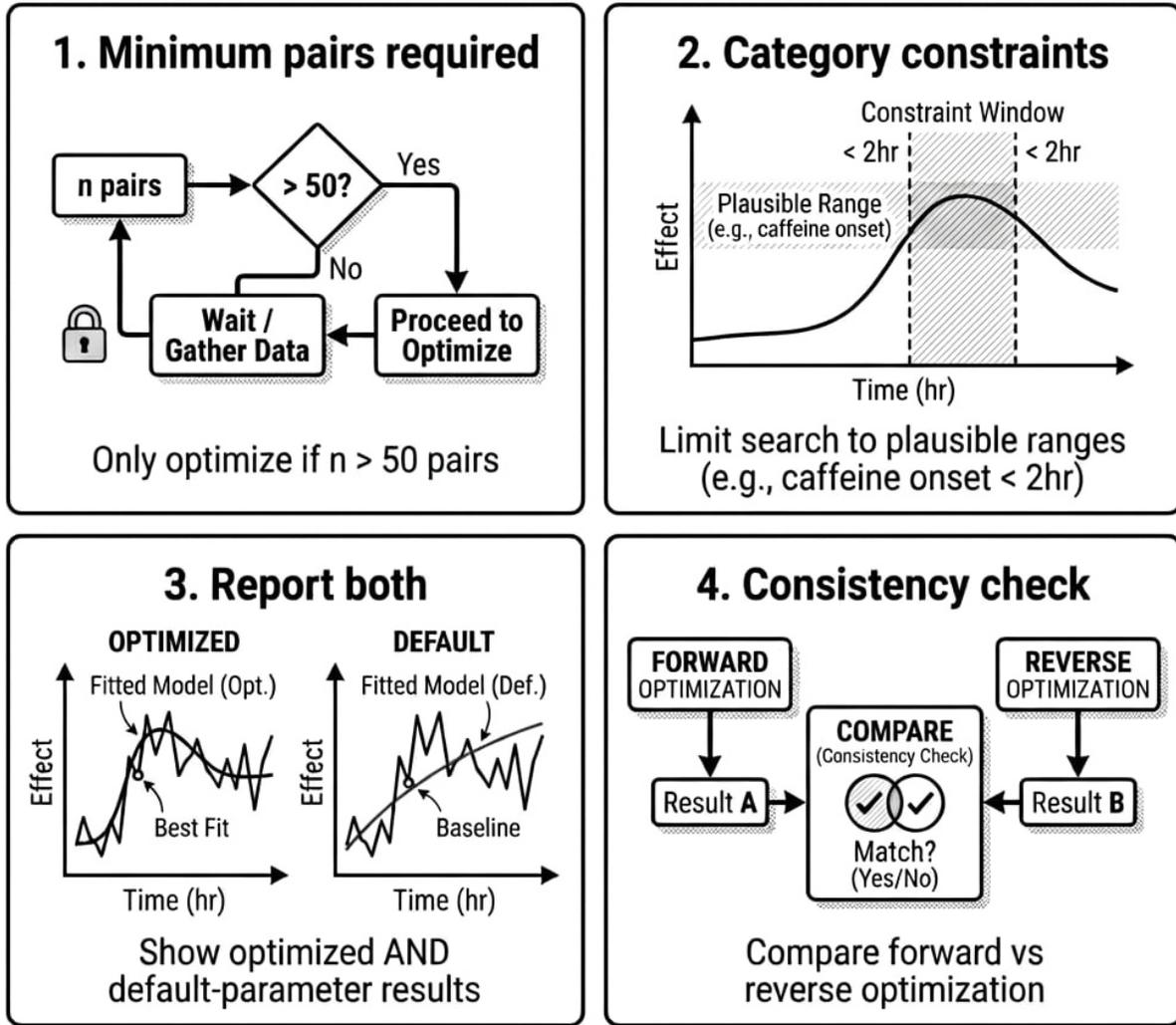
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Figure 25: A heatmap grid visualization showing Onset Delays on one axis and Durations on the other, illustrating the search space used to identify the strongest correlation coefficient.

The parameters yielding the strongest $|r|$ are selected, subject to category-specific physiological constraints.

OVERFITTING PROTECTION

To prevent spurious optimization:



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Figure 26: A visual checklist of the four safeguards used to prevent overfitting, highlighting data thresholds, domain constraints, result benchmarking, and directional consistency checks.

To prevent spurious optimization: 1. **Minimum pairs required:** Only optimize if $n > 50$ pairs 2. **Category constraints:** Limit search to plausible ranges (e.g., caffeine onset < 2hr) 3. **Report both:** Show optimized AND default-parameter results 4. **Consistency check:** Compare forward vs reverse optimization

8.19 Spearman Rank Correlation

In addition to Pearson correlation, we compute **Spearman rank correlation** (`forward_spearman_correlation_co` for robustness:

$$r_s = 1 - \frac{6 \sum d_i^2}{n(n^2 - 1)}$$

Where d_i = difference in ranks for each pair.

Advantages over Pearson:

- Robust to outliers
- Captures monotonic (not just linear) relationships
- Less affected by skewed distributions

When to prefer Spearman:

- Outcome has skewed distribution (e.g., symptom severity with many zeros)
- Relationship is monotonic but non-linear (e.g., diminishing returns)
- Data contains outliers from measurement errors

9 Outcome Label Generation

9.1 Predictor Analysis Reports

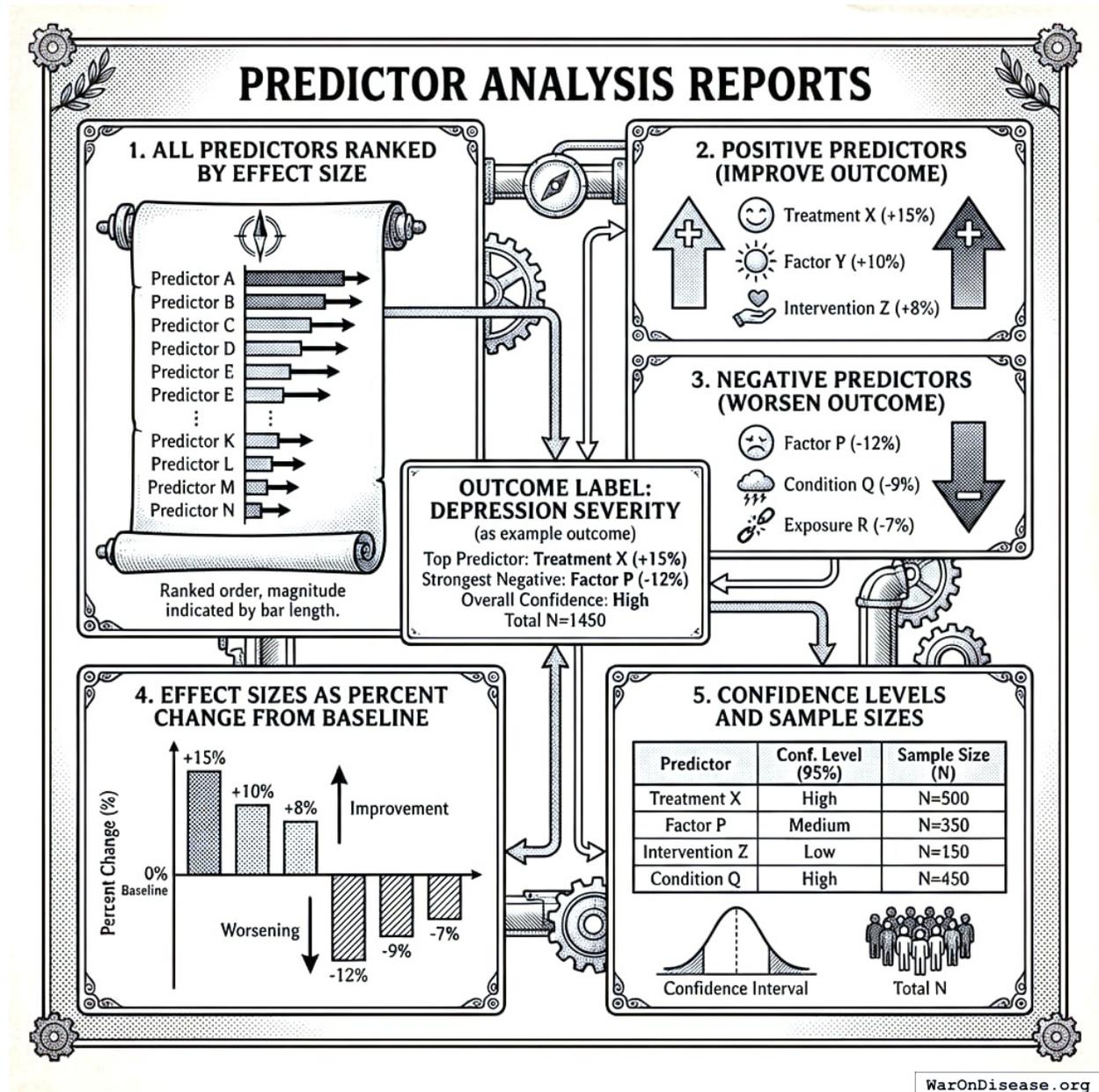


Figure 27: A sample Predictor Analysis Report visualization showing a horizontal bar chart of factors ranked by their positive or negative impact on a health outcome, including effect sizes and confidence intervals.

For each outcome variable (e.g., Depression Severity), we generate comprehensive “outcome labels” showing:

1. All predictors ranked by effect size
2. Positive predictors (treatments/factors that improve the outcome)

3. **Negative predictors** (treatments/factors that worsen the outcome)
4. **Effect sizes as percent change from baseline**
5. **Confidence levels and sample sizes**

9.2 Report Structure

Outcome Label: [Outcome Variable Name]

Population: N = [number] participants

Total Studies: [number] treatment-outcome pairs analyzed

POSITIVE EFFECTS (Treatments predicting IMPROVEMENT)

```

=====
Rank | Treatment | Effect Size | 95% CI | N | Confidence
-----|-----|-----|-----|---|-----
1    | Treatment A | +23.5% | [18.2, 28.8] | 1,247 | High
2    | Treatment B | +18.2% | [12.1, 24.3] | 892 | High
3    | Treatment C | +12.7% | [8.3, 17.1] | 2,103 | High
...

```

NEGATIVE EFFECTS (Treatments predicting WORSENING)

```

=====
Rank | Treatment | Effect Size | 95% CI | N | Confidence
-----|-----|-----|-----|---|-----
1    | Treatment X | -15.3% | [-20.1, -10.5] | 567 | Medium
2    | Treatment Y | -8.7% | [-12.3, -5.1] | 1,892 | High
...

```

NO SIGNIFICANT EFFECT

```

=====
[List of treatments with  $|\Delta| < \text{threshold}$  or  $p > 0.05$ ]

```

9.3 Category-Specific Analysis

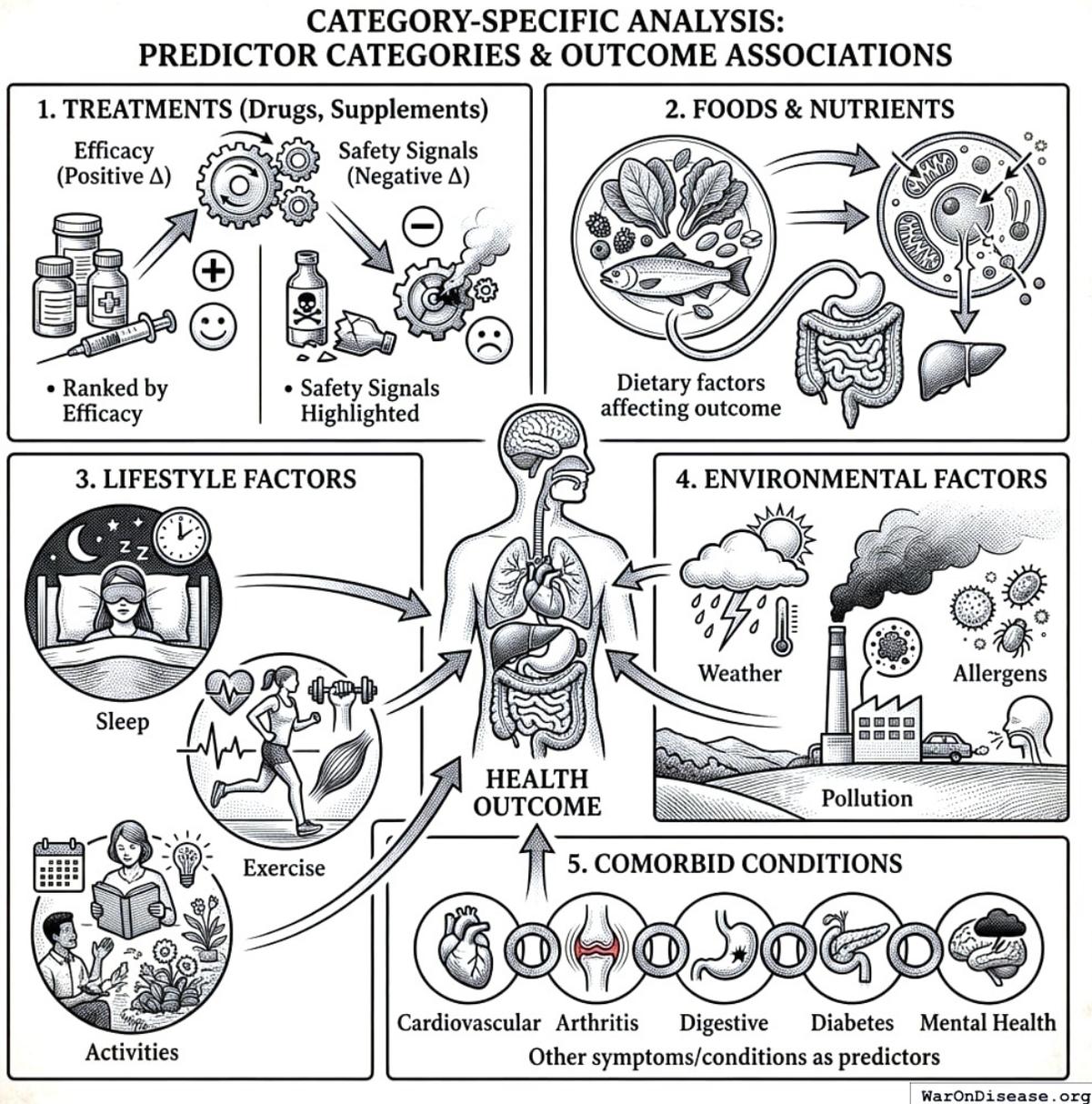


Figure 28: A visual breakdown of the five predictor categories used to organize the analysis: treatments, foods, lifestyle, environment, and comorbid conditions.

Reports are organized by predictor category:

- 1. Treatments (Drugs, Supplements)**
 - Ranked by efficacy (positive Δ)
 - Safety signals highlighted (negative Δ)
- 2. Foods & Nutrients**
 - Dietary factors affecting outcome

3. **Lifestyle Factors**
 - Sleep, exercise, activities
4. **Environmental Factors**
 - Weather, pollution, allergens
5. **Comorbid Conditions**
 - Other symptoms/conditions as predictors

9.4 Verification Status

Each study is classified by verification status:

Status	Icon	Description
Verified		Up-voted by users; data reviewed and valid
Unverified	?	Awaiting review
Flagged		Down-voted; potential data quality issues

9.5 Outcome Labels vs. FDA Drug Labels

Traditional FDA drug labels are **per-drug documents** that list qualitative adverse events and indications based on pre-market trials. They are static (updated infrequently), qualitative (“may cause drowsiness”), and organized around the drug rather than the patient’s condition.

Outcome Labels invert this paradigm: they are **per-outcome documents** that rank all treatments by quantitative effect size for a given health outcome. They are dynamic (updated continuously as data arrives), quantitative (“↓24.7% depression severity”), and organized around what the patient wants to optimize. This enables patients and clinicians to answer the question: “What works best for my condition?” This is a question traditional drug labels cannot answer.

9.6 Worked Example: Complete Outcome Label

The following shows a complete outcome label for depression, demonstrating how treatments are ranked by effect size with confidence intervals:

OUTCOME LABEL: Depression Severity

Based on 47,832 participants tracking depression outcomes Last updated: 2026-01-04 | Data period: 2020-2026

Treatments Improving Depression (ranked by effect size Δ)

Table 20: Treatments associated with depression improvement. Negative effect indicates symptom reduction.

Rank	Treatment	Effect	95% CI	N	PIS	Optimal Dose
1	Exercise	−31.2%	[27.1, 35.3]	12,847	0.67	45 min/day
2	Bupropion	−28.3%	[22.1, 34.5]	2,847	0.54	300mg
3	Sertraline	−24.7%	[19.8, 29.6]	5,123	0.51	100mg
4	Sleep (7-9 hrs)	−22.1%	[18.4, 25.8]	31,204	0.48	8.2 hrs
5	Venlafaxine	−21.2%	[15.3, 27.1]	1,892	0.44	150mg

Rank	Treatment	Effect	95% CI	N	PIS	Optimal Dose
6	Omega-3	-18.9%	[14.2, 23.6]	4,521	0.38	2000mg EPA+DHA
7	Meditation	-16.4%	[12.1, 20.7]	8,932	0.35	20 min/day
8	Fluoxetine	-15.8%	[11.2, 20.4]	3,456	0.33	40mg
9	Vitamin D	-12.3%	[8.7, 15.9]	6,789	0.28	4000 IU
10	Social interaction	-11.7%	[8.2, 15.2]	9,234	0.26	3+ hrs/day

Treatments Worsening Depression (safety signals)

Table 21: Treatments associated with depression worsening. Positive effect indicates symptom increase.

Rank	Treatment	Effect	95% CI	N	PIS	Note
1	Alcohol (>2/day)	+23.4%	[18.9, 27.9]	7,234	0.52	Dose-dependent
2	Sleep deprivation	+19.8%	[15.2, 24.4]	14,521	0.47	<6 hrs/night
3	Social isolation	+15.2%	[11.3, 19.1]	5,892	0.38	<1 hr/day
4	Refined sugar	+8.7%	[5.2, 12.2]	11,234	0.24	>50g/day

No Significant Effect ($|\Delta| < 5\%$ or $p > 0.05$): Multivitamin, Probiotics, B-complex, Magnesium (for depression specifically), Ashwagandha, 5-HTP, SAME, St. John's Wort¹

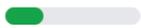
Legend: PIS = Predictor Impact Score (0-1 scale, higher = stronger evidence); Optimal Dose = V_{high} for positive valence outcomes and V_{low} for negative valence outcomes

Interpretation: This outcome label shows that for depression, exercise and sleep optimization rival or exceed pharmaceutical interventions in effect size, with stronger evidence bases (higher N). Bupropion and Sertraline lead among medications. The safety signals section highlights modifiable risk factors that worsen depression.

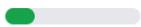
¹St. John's Wort shows high heterogeneity (some responders, some non-responders)

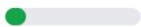
Klotho-Increasing Gene Therapy

Cognitive Improvements (Example)

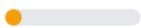
Cognitive Function (ADAS-Cog) +28% 

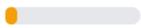
Memory Recall +35% 

Executive Function +22% 

Hippocampal Volume +15% 

Side Effects (Example)

Immune Response +12% 

Headache +9% 

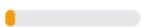
Fatigue +7% 

Figure 29: Outcome Labels show quantitative effect sizes, sample sizes, and confidence intervals for each treatment - like “nutrition facts for drugs”

10 Treatment Ranking System

10.1 Within-Category Rankings

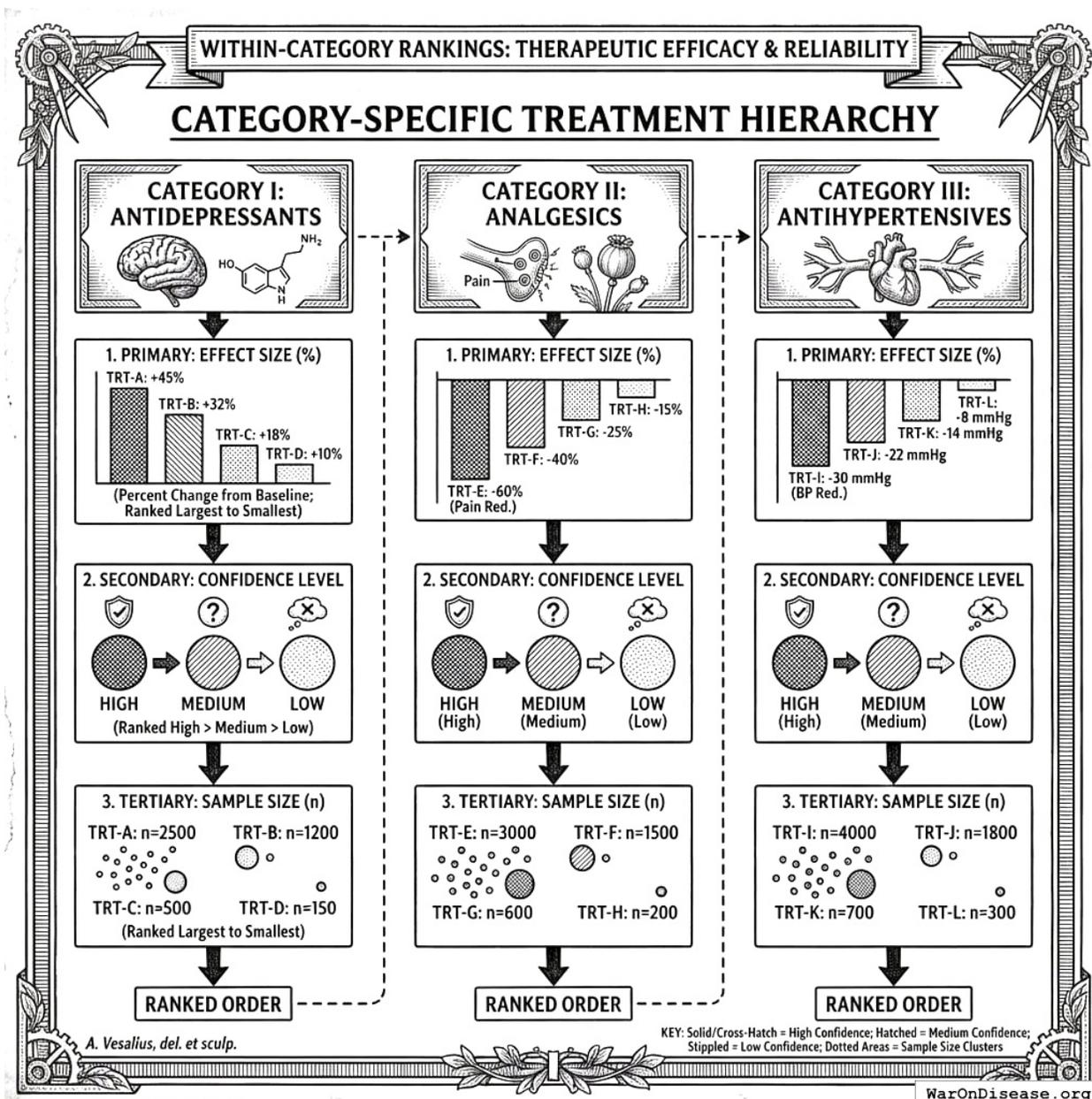


Figure 30: A hierarchical diagram illustrating the three-tier ranking system used for treatments, prioritized by effect size, then confidence level, and finally sample size.

For each therapeutic category (e.g., Antidepressants), treatments are ranked by:

1. **Primary:** Effect size (percent change from baseline)
2. **Secondary:** Confidence level (High > Medium > Low)
3. **Tertiary:** Sample size

10.2 Ranking Algorithm

For each treatment T in a therapeutic category, we compute a composite ranking score:

$$\text{RankScore}_T = \bar{\Delta}_T \times w_{\text{confidence}} \times \text{PIS}_T$$

where $\bar{\Delta}_T$ is the mean effect size across participants, $w_{\text{confidence}}$ is the confidence weight (see Table 22), and PIS_T is the Predictor Impact Score. Treatments are sorted by descending rank score.

10.3 Confidence Weighting

Table 22: Confidence weighting schema for treatment ranking.

Confidence Level	Weight (w)	Criteria
High	1.0	$p < 0.01$ OR $N > 100$ OR pairs > 500
Medium	0.7	$p < 0.05$ OR $N > 10$ OR pairs > 100
Low	0.4	Meets minimum thresholds only

10.4 Comparative Effectiveness Display

Table 23 illustrates how treatments within a therapeutic category are presented to users.

Table 23: Antidepressants ranked by efficacy for depression. Negative effect indicates symptom reduction.

Rank	Treatment	Effect (Δ)	95% CI	N	Confidence
1	Bupropion 300mg	-28.3%	[22.1, 34.5]	2,847	High
2	Sertraline 100mg	-24.7%	[19.8, 29.6]	5,123	High
3	Venlafaxine 150mg	-21.2%	[15.3, 27.1]	1,892	High
4	Fluoxetine 40mg	-18.9%	[13.2, 24.6]	3,456	High

11 Safety and Efficacy Quantification

11.1 Safety Signal Detection

Adverse Effect Identification: Safety signals are identified through (1) negative correlations between treatment and beneficial outcomes, and (2) positive correlations between treatment and harmful outcomes.

Table 24: Example safety signal report showing potential adverse effects with statistically significant positive correlations to harmful outcomes.

Outcome	Effect (Δ)	95% CI	Plausibility	Action
Fatigue	+18.3%	[12.1, 24.5]	High (known sedation)	Monitor
Nausea	+15.7%	[8.9, 22.5]	High (GI effects)	Monitor
Weight Gain	+8.2%	[4.1, 12.3]	Medium	Long-term monitoring

Outcome	Effect (Δ)	95% CI	Plausibility	Action
Anxiety	+6.5%	[2.1, 10.9]	Low (paradoxical)	Investigate

11.2 Efficacy Signal Detection

Therapeutic Effect Identification: Efficacy signals are identified through (1) positive correlations between treatment and beneficial outcomes, and (2) negative correlations between treatment and harmful outcomes (symptom reduction).

Table 25: Example efficacy signal report showing therapeutic effects with statistically significant correlations.

Outcome	Effect (Δ)	95% CI	Indication	Evidence
Depression	-24.7%	[19.8, 29.6]	Primary	Strong
Anxiety	-18.2%	[12.3, 24.1]	Secondary	Strong
Sleep Quality	+15.3%	[10.1, 20.5]	Secondary	Moderate
Energy	+12.1%	[7.2, 17.0]	Secondary	Moderate

11.3 Benefit-Risk Assessment

Net Clinical Benefit Score:

$$NCB = \sum_{i \in \text{benefits}} w_i \cdot |\Delta_i| - \sum_{j \in \text{risks}} w_j \cdot |\Delta_j|$$

where w represents importance weights assigned by clinical relevance.

Example: Sertraline 100mg Benefit-Risk Profile

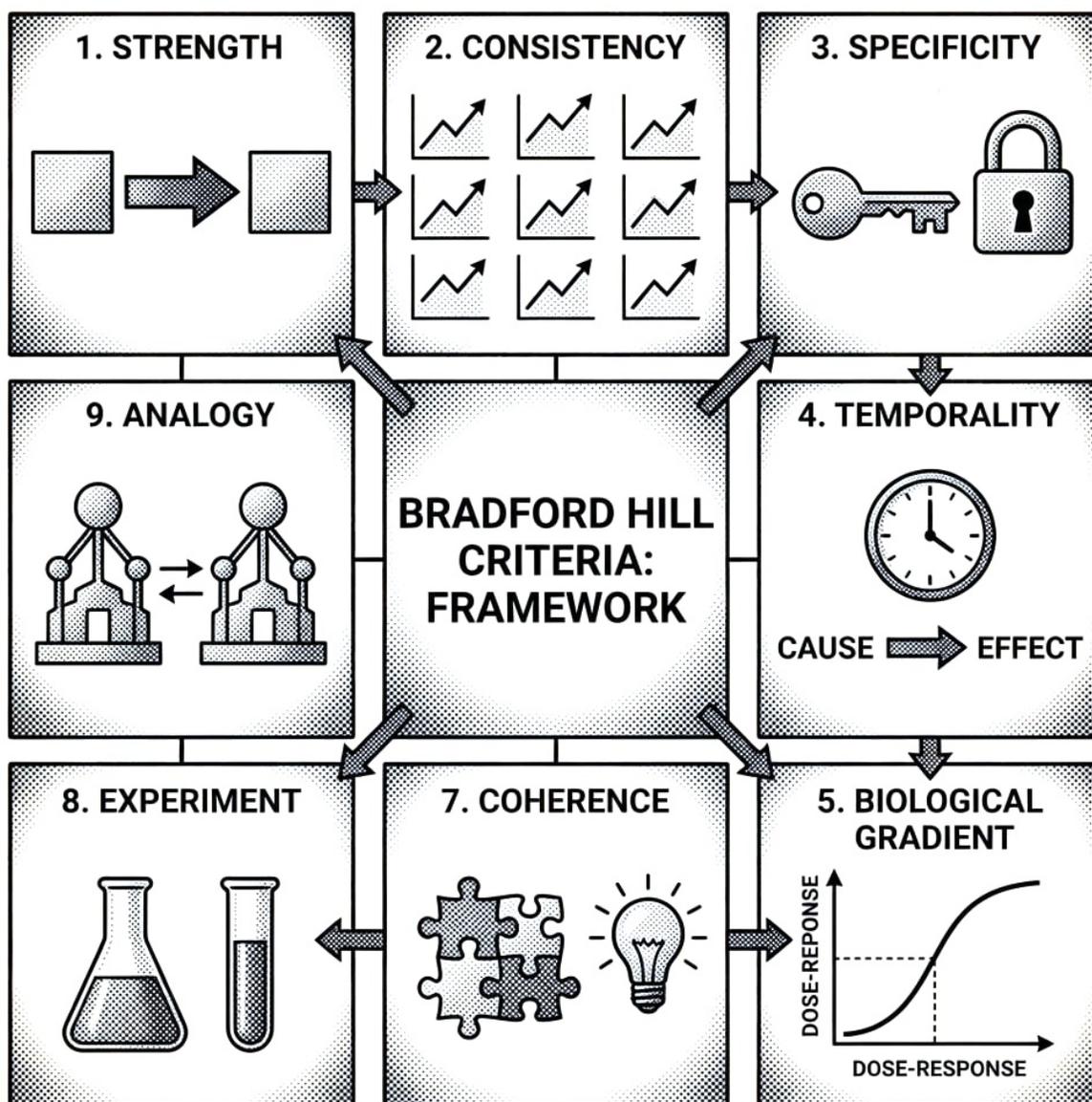
Table 26: Benefit-risk components for Sertraline 100mg.

Benefits	Effect	Weight	Risks	Effect	Weight
Depression	-24.7%	1.0	Nausea	+8.3%	0.3
Anxiety	-18.2%	0.8	Insomnia	+5.1%	0.4
			Sexual dysfunction	+12.7%	0.5

Weighted Summary: Benefits = 39.26, Risks = 8.93, **Net Clinical Benefit = +30.33** (favorable profile for depression/anxiety)

12 Addressing the Bradford Hill Criteria

The Bradford Hill criteria¹³⁹ provide the foundational framework for assessing causation from observational data. This section details how our framework addresses each criterion.



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Figure 31: A conceptual mapping showing how the proposed framework addresses each of the nine Bradford Hill criteria for causal inference.

12.1 Complete Criteria Mapping

Criterion	How Addressed	Quantitative Metric	In PIS?
Strength	Effect size magnitude	Pearson r , $\Delta\%$	Yes
Consistency	Cross-participant aggregation	N , n , SE, CI	Yes
Specificity	Category appropriateness	Interest factor	Yes

Criterion	How Addressed	Quantitative Metric	In PIS?
Temporality	Onset delay requirement	$\delta > 0$ enforced	Yes
Biological Gradient	Dose-response analysis	Gradient coefficient	Yes
Plausibility	Community voting	Up/down votes	Yes
Coherence	Literature cross-reference	Narrative	No
Experiment	N-of-1 natural experiments	Study design	No
Analogy	Similar variable comparison	Narrative	No

12.2 Quantitative Criteria Details

Strength:

- Reports Pearson r with classification (very strong: 0.8, strong: 0.6, moderate: 0.4, weak: 0.2, very weak: <0.2)
- Example: “There is a moderately positive ($R = 0.45$) relationship between Sertraline and Depression improvement.”

Consistency:

- Reports N participants, n paired measurements
- Notes that spurious associations naturally dissipate as participants modify behaviors based on non-replicating findings

Temporality:

- Onset delay δ explicitly encodes treatment-to-effect lag
- Forward vs. reverse correlation comparison identifies potential reverse causality

Plausibility:

- Users vote on biological mechanism plausibility
- Weighted average contributes to ranking
- Crowd-sources expert and patient knowledge

13 Validation and Quality Assurance

13.1 User Voting System

Each study can receive user votes:

Vote	Meaning	Effect
Up-vote ()	Data appears valid, relationship plausible	Included in verified results
Down-vote ()	Data issues or implausible relationship	Flagged for review

Vote	Meaning	Effect
No vote	Not yet reviewed	Included in unverified results

13.2 Automated Quality Checks

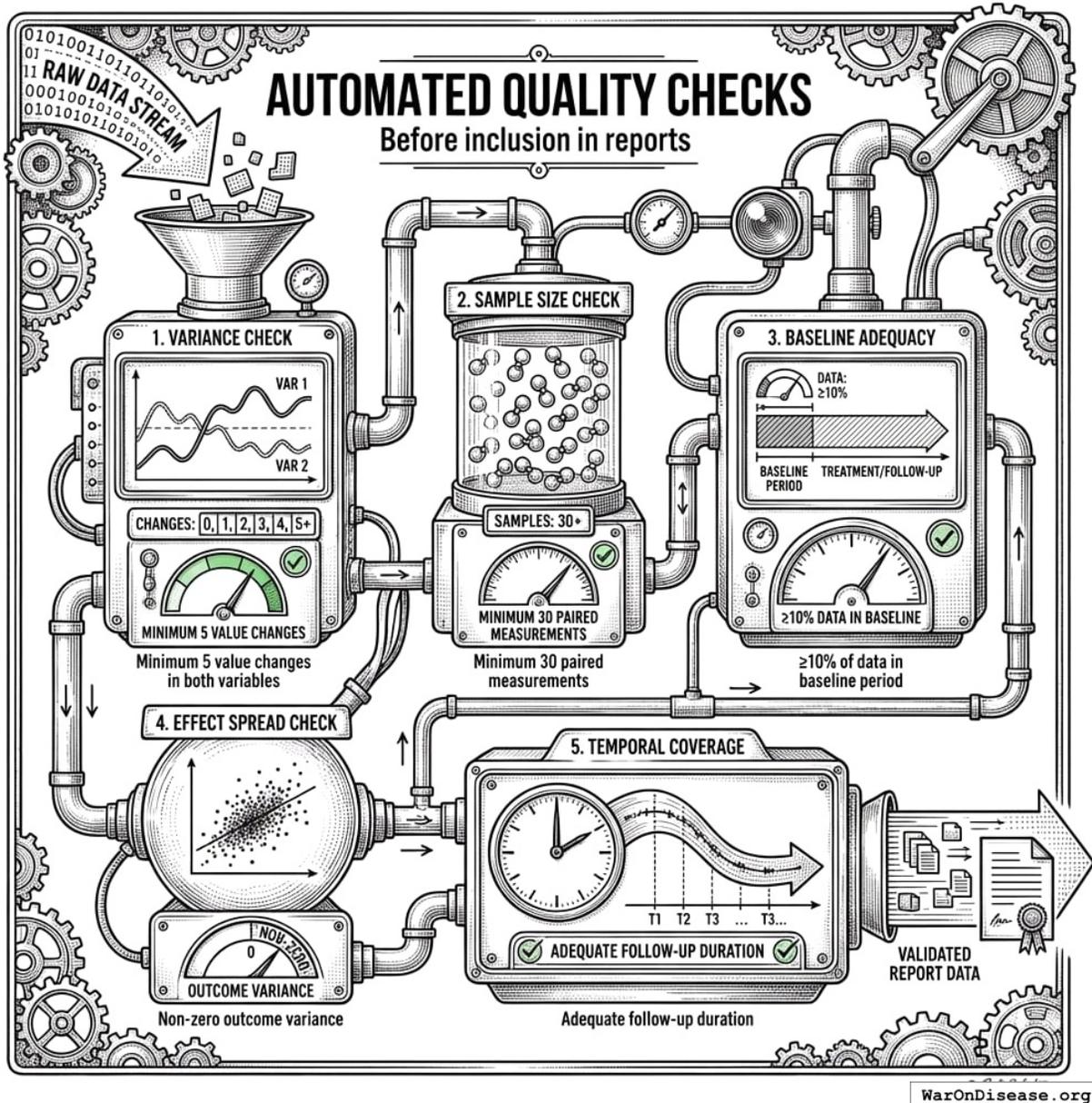


Figure 32: A sequential flowchart illustrating the five automated quality check gates that data must pass through before being included in reports.

Before inclusion in reports:

1. **Variance check:** Minimum 5 value changes in both variables

2. **Sample size check:** Minimum 30 paired measurements
3. **Baseline adequacy:** 10% of data in baseline period
4. **Effect spread check:** Non-zero outcome variance
5. **Temporal coverage:** Adequate follow-up duration

13.3 Flagged Study Handling

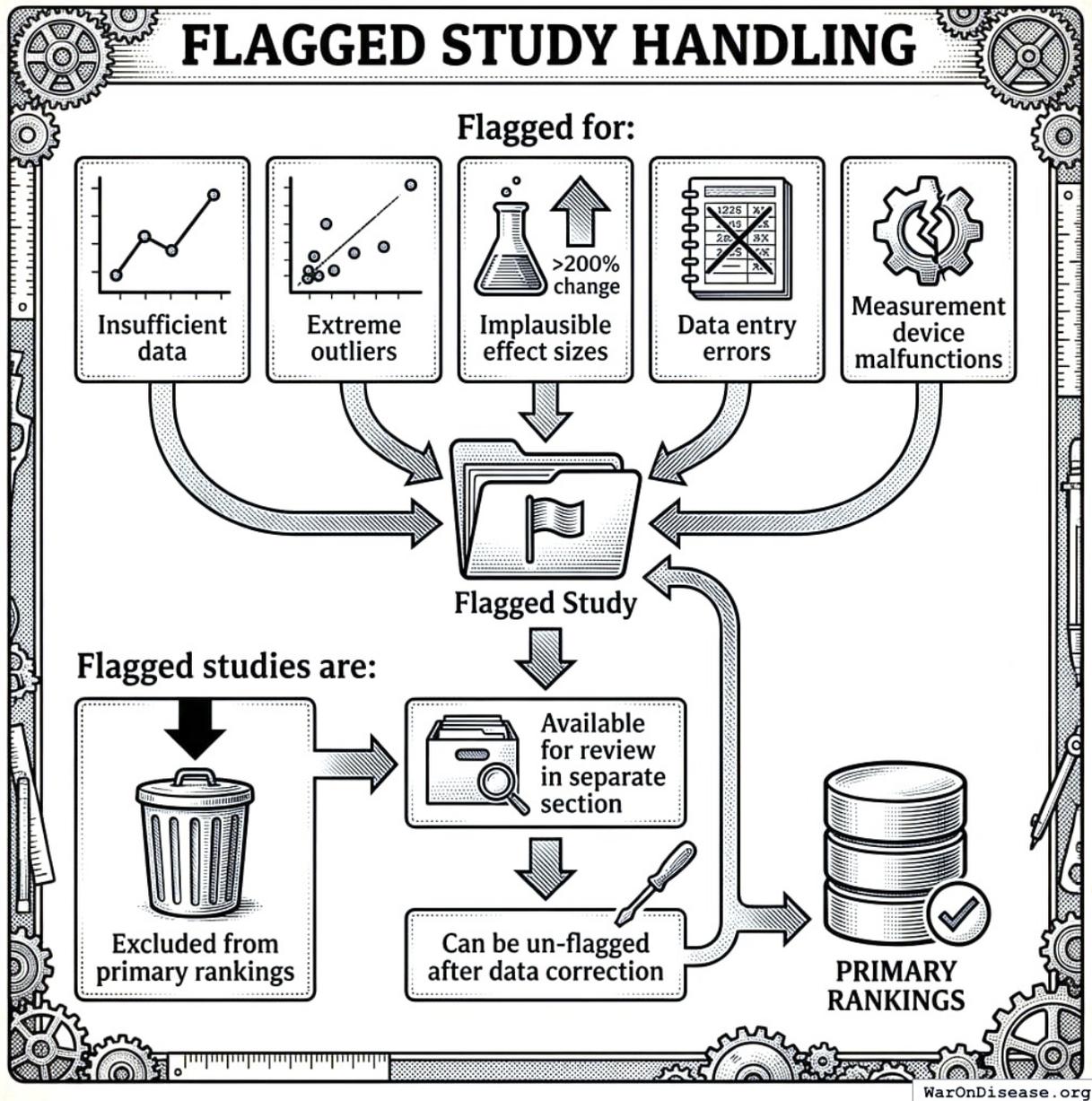


Figure 33: A flowchart showing the lifecycle of a study from initial flagging criteria to exclusion and the potential for reinstatement after data correction.

Studies may be flagged for:

- Insufficient data
- Extreme outliers
- Implausible effect sizes (>200% change)
- Data entry errors
- Measurement device malfunctions

Flagged studies are:

- Excluded from primary rankings
- Available for review in separate section
- Can be un-flagged after data correction

14 Stage 2: Pragmatic Trial Confirmation

The short version: Observational data can find promising signals, but only randomized trials can prove causation. The good news: we don't need expensive, slow traditional trials. A meta-analysis of 108 embedded pragmatic trials¹³⁴ shows that “pragmatic” trials (simple randomization embedded in routine care) can validate treatments at 44.1x (95% CI: 39.4x-89.1x) lower cost. We use cheap observational analysis (Stage 1) to filter millions of possibilities down to the top candidates, then confirm the best ones with pragmatic trials (Stage 2). Result: validated treatment recommendations at a fraction of current cost.

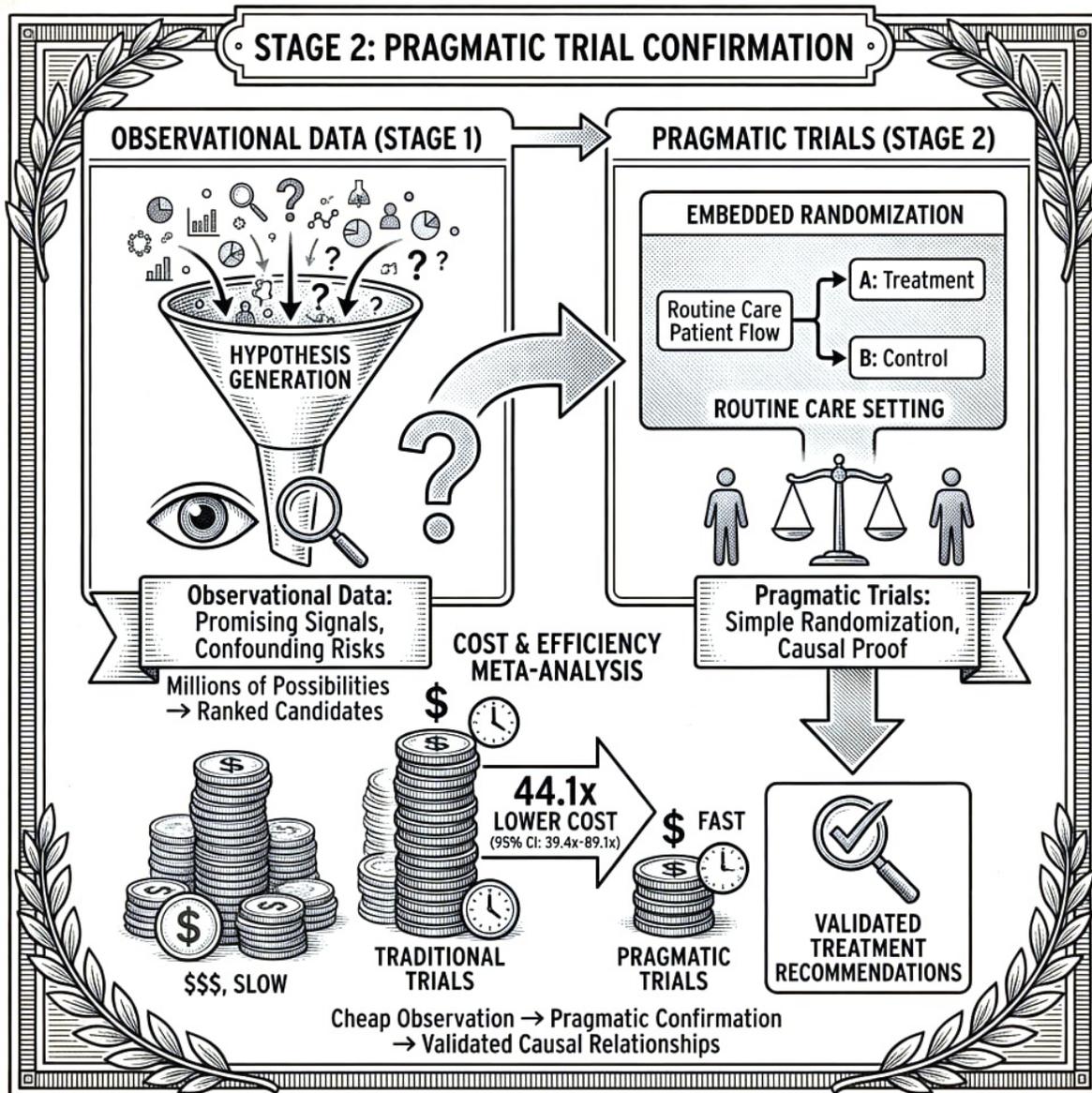


Figure 34: A workflow diagram showing the two-stage process: Stage 1 filters millions of observational data signals into top candidates, which Stage 2 then validates through low-cost pragmatic trials to establish causation.

The observational methodology described in Sections 1-11 generates ranked hypotheses about treatment-outcome relationships. While powerful for signal detection and hypothesis generation, observational data alone cannot establish causation due to unmeasured confounding. This section describes how **pragmatic clinical trials** serve as the confirmation layer, transforming promising observational signals into validated causal relationships.

14.1 The Two-Stage Pipeline

Our complete methodology operates as a two-stage pipeline:

Table 29: Two-stage pipeline summary.

Stage	Method	Cost	Purpose	Output
Stage 1: Signal Detection	Aggregated N-of-1 observational analysis	~\$0.100 (95% CI: \$0.030-\$1.00)/patient	Hypothesis generation	Ranked PIS signals
Stage 2: Causal Confirmation	Pragmatic randomized trials	~\$929 (95% CI: \$97-\$3K)/patient	Causation proof	Validated effect sizes

This design leverages the complementary strengths of each approach:

- **Stage 1** scales to millions of treatment-outcome pairs at minimal cost, identifying the most promising candidates
- **Stage 2** applies experimental rigor to confirm causation for high-priority signals

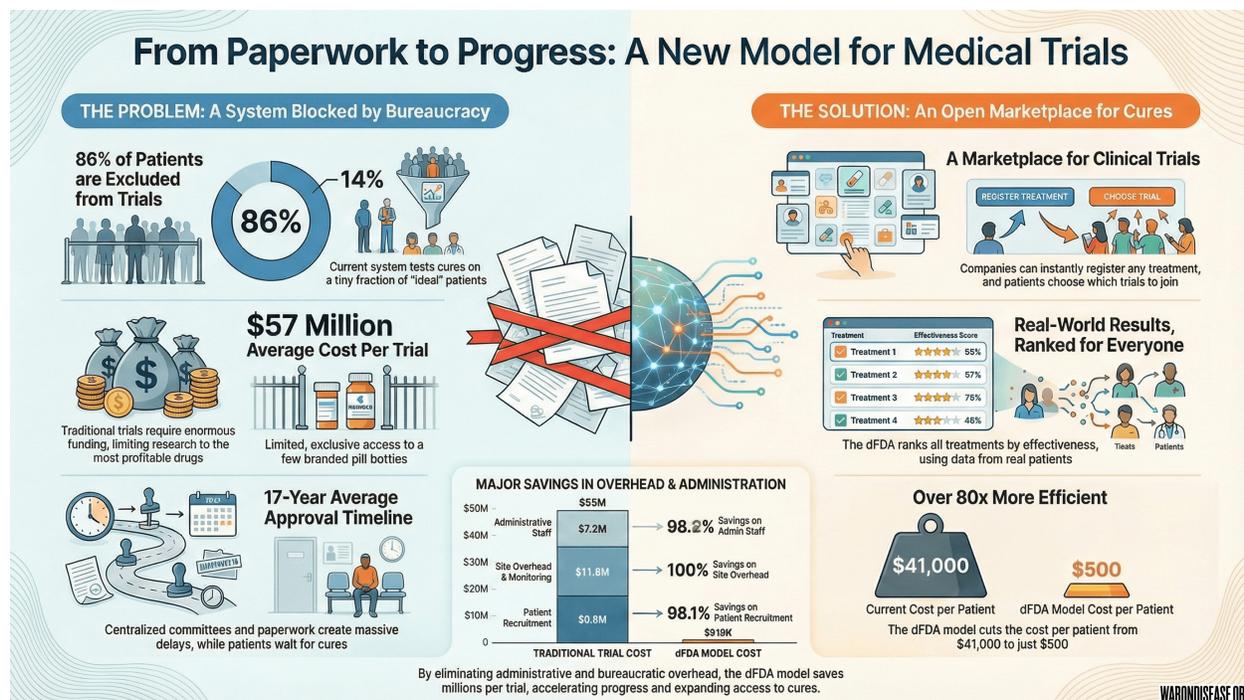


Figure 35: FDA vs dFDA: The two-stage pipeline dramatically reduces cost and time compared to traditional drug development

14.2 Pragmatic Trial Methodology

Pragmatic trials differ fundamentally from traditional Phase III trials. A Harvard meta-analysis of 108 embedded pragmatic trials found median costs of only \$97/patient, with even conservative implementations like ADAPTABLE achieving \$929 (95% CI: \$929-\$1.40K)/patient^{1,134}:

Table 30: Pragmatic vs. traditional Phase III trials.

Dimension	Traditional Phase III	Pragmatic Trial (Evidence-Based)
Cost per patient	\$41K (95% CI: \$20K-\$120K)	\$929 (95% CI: \$97-\$3K) (median \$97-929) ²
Time to results	3-7 years	3-6 months
Patient population	Homogeneous (strict exclusion)	Real-world (minimal exclusion)
Setting	Specialized research centers	Routine clinical care
Data collection	Extensive case report forms	Minimal essential outcomes
Randomization	Complex stratification	Simple 1:1 or 1:1:1
Sample size	Hundreds to thousands	Thousands to tens of thousands

Multiple large-scale pragmatic trials have demonstrated this model’s effectiveness. The Oxford RECOVERY trial enrolled 49,000 patients across 186 hospitals, evaluating 12 treatments and finding a life-saving result (dexamethasone) in 100 days, saving 1.00 million lives (95% CI: 500 thousand lives-2.00 million lives) globally⁸⁴. The PCORnet ADAPTABLE trial enrolled 15,076 patients across 40 clinical sites at \$929 (95% CI: \$929-\$1.40K)/patient¹. These are not isolated successes. The Harvard meta-analysis shows this efficiency is reproducible across therapeutic areas¹³⁴.

14.3 Signal-to-Trial Prioritization

Not all observational signals warrant pragmatic trial confirmation. We propose a **Trial Priority Score (TPS)** combining:

$$TPS = PIS \times \sqrt{DALYs_{\text{addressable}}} \times \text{Novelty} \times \text{Feasibility}$$

Where:

- **PIS**: Predictor Impact Score from Stage 1 (higher = stronger signal)
- **DALYs_{addressable}**: Disease burden addressable by the treatment
- **Novelty**: Inverse of existing evidence (new signals prioritized)
- **Feasibility**: Practical considerations (drug availability, safety profile, cost)

Signals in the top 0.1-1% by TPS are candidates for pragmatic trial confirmation.

14.4 Comparative Effectiveness Randomization

For treatments already in clinical use, we employ **comparative effectiveness** designs following the ADAPTABLE trial model¹:

1. **Embedded randomization**: Randomization occurs within routine care visits

²Meta-analysis of 108 trials found \$97 median; ADAPTABLE trial achieved \$929; RECOVERY achieved \$500. We use the conservative ADAPTABLE estimate.

2. **Minimal disruption:** Patients receive standard care with random assignment between active comparators
3. **Real-world endpoints:** Primary outcomes are events captured in EHR (mortality, hospitalization, symptom resolution)
4. **Large simple design:** Thousands of patients, minimal per-patient data collection

Example protocol for a high-PIS signal (Treatment A vs. Treatment B for Outcome X):

Table 31: Example pragmatic trial protocol for comparative effectiveness.

Parameter	Specification
Eligibility	Patients with Condition Y initiating treatment for Outcome X
Randomization	1:1 to Treatment A vs. Treatment B
Primary endpoint	Change in Outcome X at 90 days
Data collection	Baseline characteristics (EHR), outcome at 90 days (patient-reported or EHR)
Sample size	2,000 patients (1,000 per arm)
Cost	~\$1.9M total (\$929 (95% CI: \$97-\$3K)/patient)
Timeline	6-12 months

14.5 Feedback Loop: Trial Results Improve Observational Models

Pragmatic trial results feed back to improve Stage 1 methodology:

1. **Calibration:** Compare observational effect sizes to randomized effect sizes; develop correction factors
2. **Confounding identification:** Trials where observational and randomized effects diverge identify confounders
3. **Subgroup discovery:** Trial heterogeneity analysis identifies responder populations, improving PIS stratification
4. **Hyperparameter validation:** Optimal onset delays and durations validated against experimental ground truth

This creates a **learning health system** where observational and experimental evidence continuously refine each other.

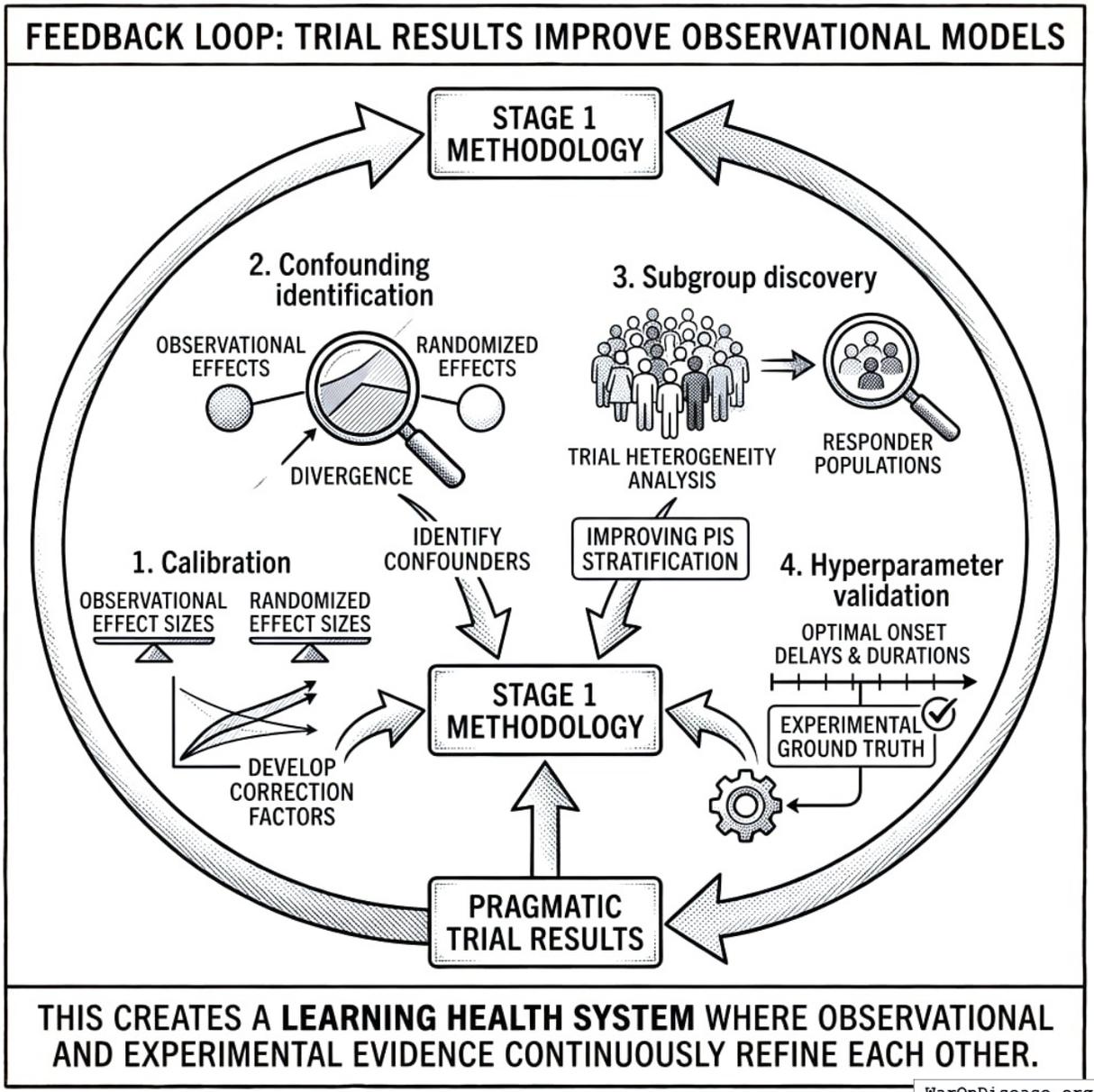


Figure 36: A circular ‘Learning Health System’ diagram showing the continuous flow between observational Stage 1 models and experimental Stage 2 trials, with specific feedback channels for calibration and validation.

14.6 Output: Validated Outcome Labels

The two-stage pipeline produces **validated outcome labels** combining observational and experimental evidence. Table 32 shows the data elements captured for each treatment-outcome pair.

Table 32: Validated outcome label data structure.

Component	Field	Description	Example
Identification	Treatment	Intervention name and dose	Vitamin D 2000 IU
	Outcome	Health outcome measured	Depression Severity
Stage 1 (Observational)	Δ_{obs}	Observational effect size	-12%
	CI_{obs}	95% confidence interval	[-15%, -9%]
	N_{obs}	Number of participants	45,000
	PIS	Predictor Impact Score	0.72
Stage 2 (Experimental)	Δ_{exp}	Randomized trial effect	-8%
	CI_{exp}	Trial confidence interval	[-12%, -4%]
	N_{exp}	Trial participants	3,000
	Trial ID	Registry identifier	DFDA-VIT-D-001
Combined	Evidence Grade	Validation status	Validated/Promising/Signal
	Causal Confidence	Probability of true effect	0-1 scale

Evidence grades:

- **Validated:** Confirmed by pragmatic RCT ($p < 0.05$, consistent direction)
- **Promising:** High PIS (>0.6), awaiting or in trial
- **Signal:** Moderate PIS (0.3-0.6), hypothesis only

15 Limitations and How They're Addressed

The two-stage design addresses the fundamental limitations of purely observational pharmacovigilance while acknowledging residual constraints.

15.1 Fundamental Limitations: Observational Stage

These limitations apply to Stage 1 (observational analysis) but are addressed by Stage 2 (pragmatic trials):

Table 33: Fundamental observational limitations and trial resolution.

Limitation	Stage 1 Status	Stage 2 Resolution
Cannot prove causation	Hypothesis only	Randomization establishes causation
Cannot replace RCTs	Generates candidates	Pragmatic trials ARE simplified RCTs
Cannot handle strong confounding	Confounding by indication	Randomization eliminates confounding
Cannot generalize beyond population	Self-selected trackers	Pragmatic trials use real-world populations

15.2 Methodological Weaknesses: Addressed by Two-Stage Design

Table 34: Methodological weaknesses addressed by the two-stage design.

Weakness	Stage 1 Impact	Two-Stage Resolution
Arbitrary baseline definition	Acceptable for signal ranking	Trial uses randomized comparison, no baseline needed
Hyperparameter overfitting	May inflate some correlations	Trial confirms true effect, calibrates models
Self-selection bias	Non-representative sample	Pragmatic trials embed in routine care
Measurement error	Self-report limitations	Trials can use objective endpoints
Hawthorne effect	Tracking changes behavior	Trials embedded in normal care minimize this
Multiple testing	Millions of comparisons	Only top signals proceed to trial (TPS filter)
Temporal confounding	Seasonal/life event effects	Randomization eliminates systematic bias
Confounding by indication	Sicker patients take more treatment	Randomization balances severity

15.3 Residual Limitations

Even with the two-stage design, certain limitations remain:

1. **Resource constraints:** Cannot trial all promising signals; prioritization required
2. **External validity:** Pragmatic trial populations still may not represent all subgroups
3. **Rare outcomes:** Very rare adverse events may require larger observational signals
4. **Behavioral interventions:** Some treatments (diet, exercise) difficult to blind
5. **Long-term effects:** Pragmatic trials typically 6-12 months; decades-long effects require observational follow-up
6. **Interaction effects:** Two-way drug interactions testable; higher-order interactions remain observational
7. **Multiple testing burden:** Stage 1 analyzes millions of treatment-outcome pairs without formal multiple testing correction (e.g., Benjamini-Hochberg FDR control). The TPS filter reduces false positives proceeding to Stage 2, but users should expect a high proportion of Stage 1 signals to be false discoveries. This is by design (cheap observational analysis tolerates false positives because Stage 2 trials filter them out), but consumers of Stage 1 rankings alone should interpret with appropriate skepticism
8. **Self-selection bias:** Participants who track health data differ systematically from the general population (likely healthier, more educated, more health-conscious). Effect sizes may not generalize to non-trackers

15.4 What This Framework CAN Now Do

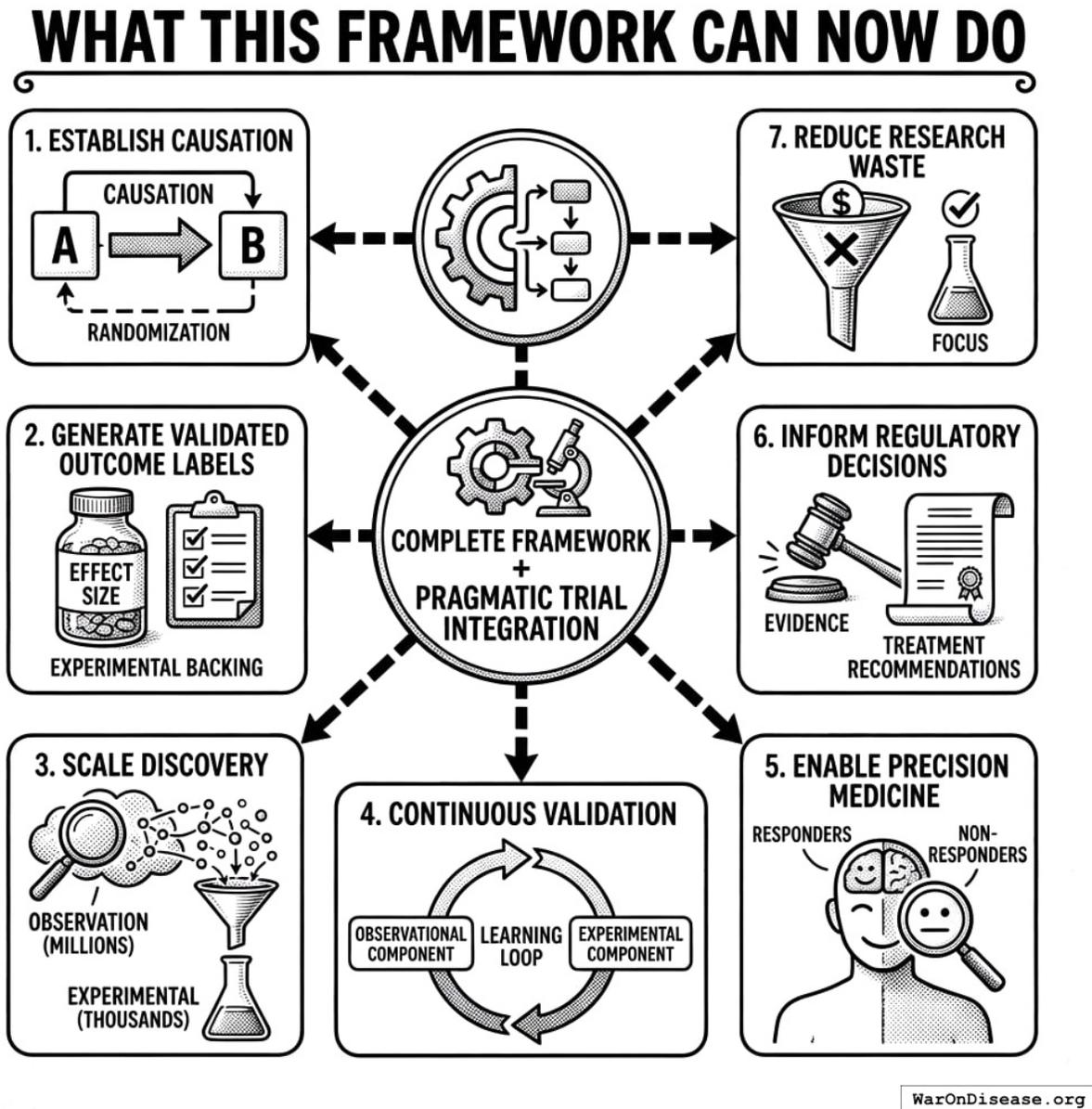


Figure 37: A conceptual diagram illustrating the iterative framework where observational signals funnel into experimental validation, creating a continuous learning loop for precision medicine.

With pragmatic trial integration, the complete framework can:

1. **Establish causation:** For high-priority signals, randomization proves causal relationships
2. **Generate validated outcome labels:** Quantitative effect sizes with experimental backing
3. **Scale discovery:** Analyze millions of pairs observationally, confirm thousands experimentally
4. **Continuous validation:** Learning loop improves both observational and experimental components
5. **Enable precision medicine:** Subgroup analyses identify responders vs. non-responders

6. **Inform regulatory decisions:** Validated labels provide evidence for treatment recommendations
7. **Reduce research waste:** Focus expensive trials on signals most likely to confirm

16 Implementation Guide

16.1 System Architecture

The processing protocol defines six sequential steps:

1. **Data Ingestion Protocol:** Collects measurements from wearables, health apps, EHR/FHIR systems, manual entry, and environmental sensors
2. **Measurement Normalization:** Standardizes units, timestamps, deduplicates records, and attributes data provenance
3. **Variable Ontology:** Assigns semantic categories, default temporal parameters (δ , τ), and filling value logic
4. **Relationship Analysis Engine:** Generates predictor-outcome pairs, performs temporal alignment, computes correlations, and optimizes hyperparameters
5. **Population Aggregation:** Combines individual N-of-1 analyses, computes confidence intervals, detects heterogeneity and subgroups
6. **Report Generation:** Produces outcome labels, treatment rankings, and safety/efficacy signals

Complete implementation details, database schemas, and reference code are available in the supplementary materials repository.

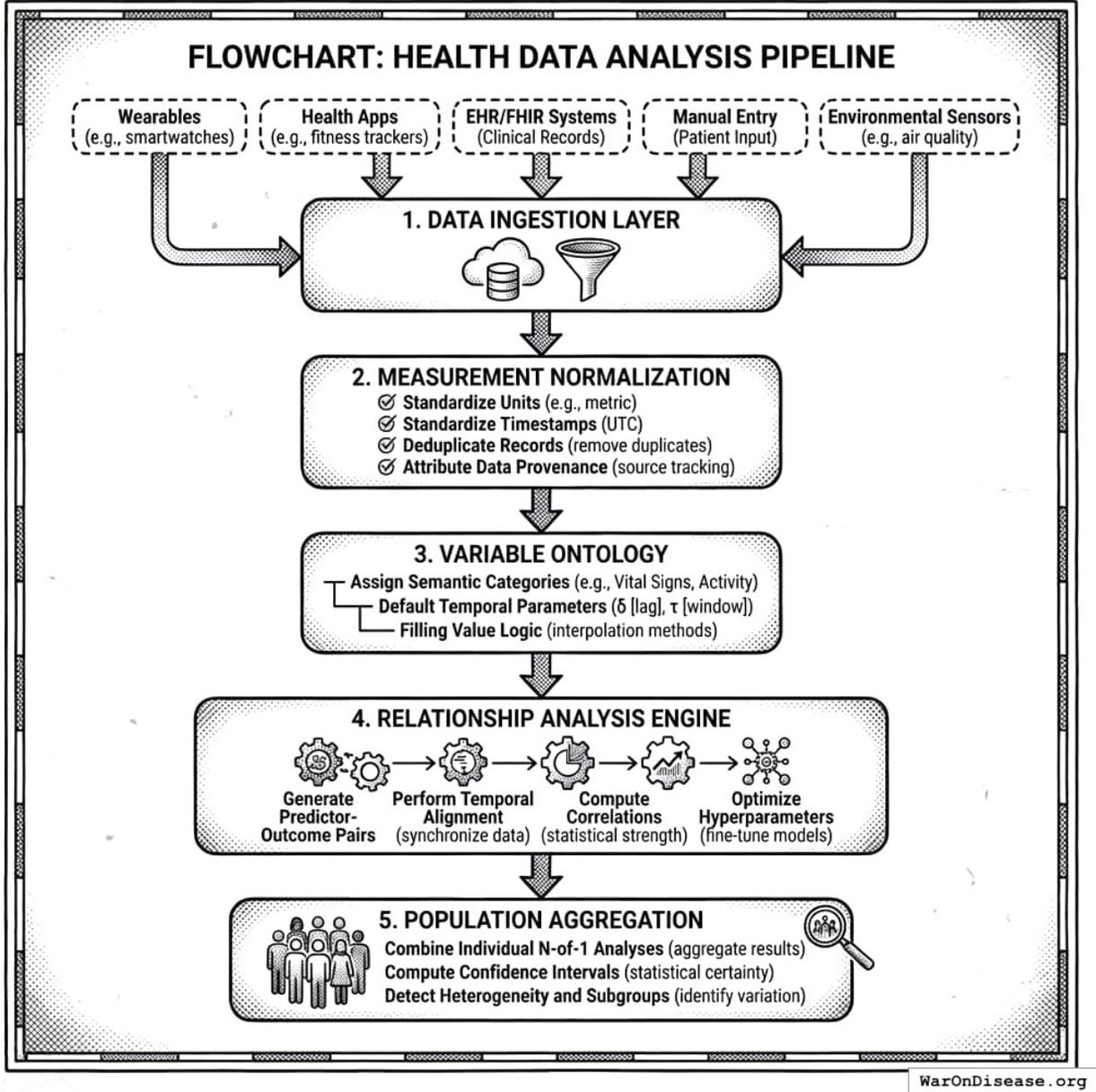


Figure 38: Data processing pipeline from raw ingestion to aggregated population reports.

16.2 Core Algorithm: Pair Generation

Algorithm 1 (Temporal Pair Generation): Given predictor measurements $P = \{(t_j^P, p_j)\}$ and outcome measurements $O = \{(t_k^O, o_k)\}$, onset delay δ , duration of action τ , and optional filling value f :

Case 1 (Predictor has filling value): For each outcome measurement (t_k^O, o_k) :

$$p_k = \begin{cases} \frac{1}{|W_k|} \sum_{j \in W_k} p_j & \text{if } W_k \neq \emptyset \\ f & \text{otherwise} \end{cases}$$

where $W_k = \{j : t_k^O - \delta - \tau < t_j^P \leq t_k^O - \delta\}$. Output pair (p_k, o_k) .

Case 2 (No filling value): For each predictor measurement (t_j^P, p_j) :

$$o_j = \frac{1}{|W_j|} \sum_{k \in W_j} o_k$$

where $W_j = \{k : t_j^P + \delta \leq t_k^O < t_j^P + \delta + \tau\}$. Output pair (p_j, o_j) only if $W_j \neq \emptyset$.

16.3 Core Algorithm: Baseline Separation

Algorithm 2 (Baseline/Follow-up Partition): Given aligned pairs $\{(p_i, o_i)\}_{i=1}^n$:

1. Compute predictor mean: $\bar{p} = \frac{1}{n} \sum_{i=1}^n p_i$
2. Partition into baseline $B = \{(p_i, o_i) : p_i < \bar{p}\}$ and follow-up $F = \{(p_i, o_i) : p_i \geq \bar{p}\}$
3. Compute outcome means: $\mu_B = \mathbb{E}[o \mid (p, o) \in B]$ and $\mu_F = \mathbb{E}[o \mid (p, o) \in F]$
4. Return percent change: $\Delta = \frac{\mu_F - \mu_B}{\mu_B} \times 100$

16.4 Algorithm 3: Predictor Impact Score Calculation

Algorithm 3 (User-Level PIS): Given correlation coefficients, statistical significance, z-score, interest factor, and aggregate PIS:

$$\text{PIS}_{\text{user}} = |r| \times S \times \phi_z \times \phi_{\text{temporal}} \times f_{\text{interest}} + \text{PIS}_{\text{agg}}$$

Procedure:

1. Set $Z_{\text{ref}} = 2$ (reference z-score threshold)
2. Compute strength: $r = |r_{\text{forward}}|$
3. Compute effect magnitude factor: $\phi_z = \frac{|z|}{|z| + Z_{\text{ref}}}$ (or 0.5 if z undefined)
4. Compute temporality factor: $\phi_{\text{temporal}} = \frac{|r_{\text{forward}}|}{|r_{\text{forward}}| + |r_{\text{reverse}}|}$ (or 0.5 if both zero)
5. Return: $r \times S \times \phi_z \times \phi_{\text{temporal}} \times f_{\text{interest}} + \text{PIS}_{\text{agg}}$

Algorithm 4 (Aggregate PIS): Given forward correlation, number of users N , number of pairs n , outcome changes, plausibility votes, and gradient coefficient:

$$\text{PIS}_{\text{agg}} = |r_{\text{forward}}| \times w \times \phi_{\text{users}} \times \phi_{\text{pairs}} \times \phi_{\text{change}} \times \phi_{\text{gradient}}$$

Procedure:

1. Set saturation constants: $N_{\text{sig}} = 10$, $n_{\text{sig}} = 100$, $\Delta_{\text{sig}} = 10\%$
2. Compute user saturation: $\phi_{\text{users}} = 1 - e^{-N/N_{\text{sig}}}$
3. Compute pair saturation: $\phi_{\text{pairs}} = 1 - e^{-n/n_{\text{sig}}}$
4. Compute change spread: $\Delta_{\text{spread}} = |\Delta_{\text{high}} - \Delta_{\text{low}}|$ (minimum 1)
5. Compute change saturation: $\phi_{\text{change}} = 1 - e^{-\Delta_{\text{spread}}/\Delta_{\text{sig}}}$
6. Compute gradient factor: $\phi_{\text{gradient}} = \min(\text{gradient_coefficient}, 1.0)$
7. Return: $|r_{\text{forward}}| \times w \times \phi_{\text{users}} \times \phi_{\text{pairs}} \times \phi_{\text{change}} \times \phi_{\text{gradient}}$

Algorithm 5 (Interest Factor): Penalize spurious variable pairs:

$$f_{\text{interest}} = f_P \times f_O \times f_{\text{pair}}$$

Procedure:

1. Initialize $f = 1.0$
2. **Predictor penalties:** Divide f by 2 for each: test variable, app/website, address
3. **Outcome penalties:** Divide f by 2 for each: test variable, non-outcome category
4. **Pair penalties:** Divide f by 2 if predictor is non-predictor category; divide by 10 if illogical category pair
5. Return f

16.5 Reference Implementation

A complete reference implementation is available at:

- **Code Repository:** <https://github.com/decentralized-fda>
- **Documentation:** <https://docs.dfa.earth>

The repository includes:

- Analysis engine (Python) with full PIS calculation pipeline
- Database schemas (PostgreSQL, SQLite) for variable relationships
- API protocol (OpenAPI 3.0) for data ingestion and querying
- Test vectors matching Appendix D worked example

17 Regulatory Considerations

17.1 Positioning Relative to RCTs

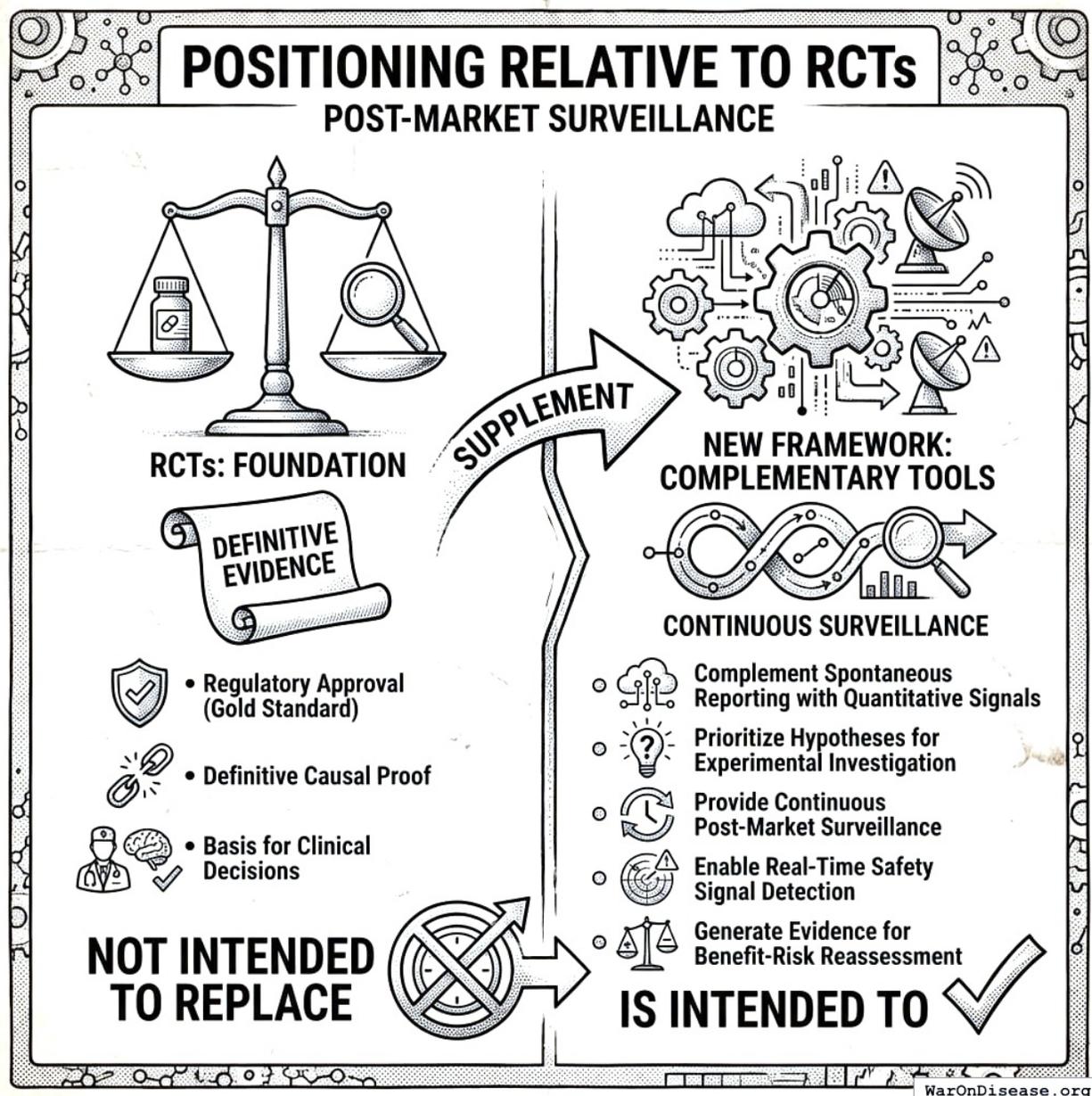


Figure 39: A comparison diagram illustrating the complementary relationship between the framework and Randomized Controlled Trials (RCTs), highlighting their distinct roles in drug safety and evidence generation.

This framework is **not** intended to:

- Replace RCTs for regulatory approval
- Provide definitive causal proof
- Serve as sole basis for clinical decisions

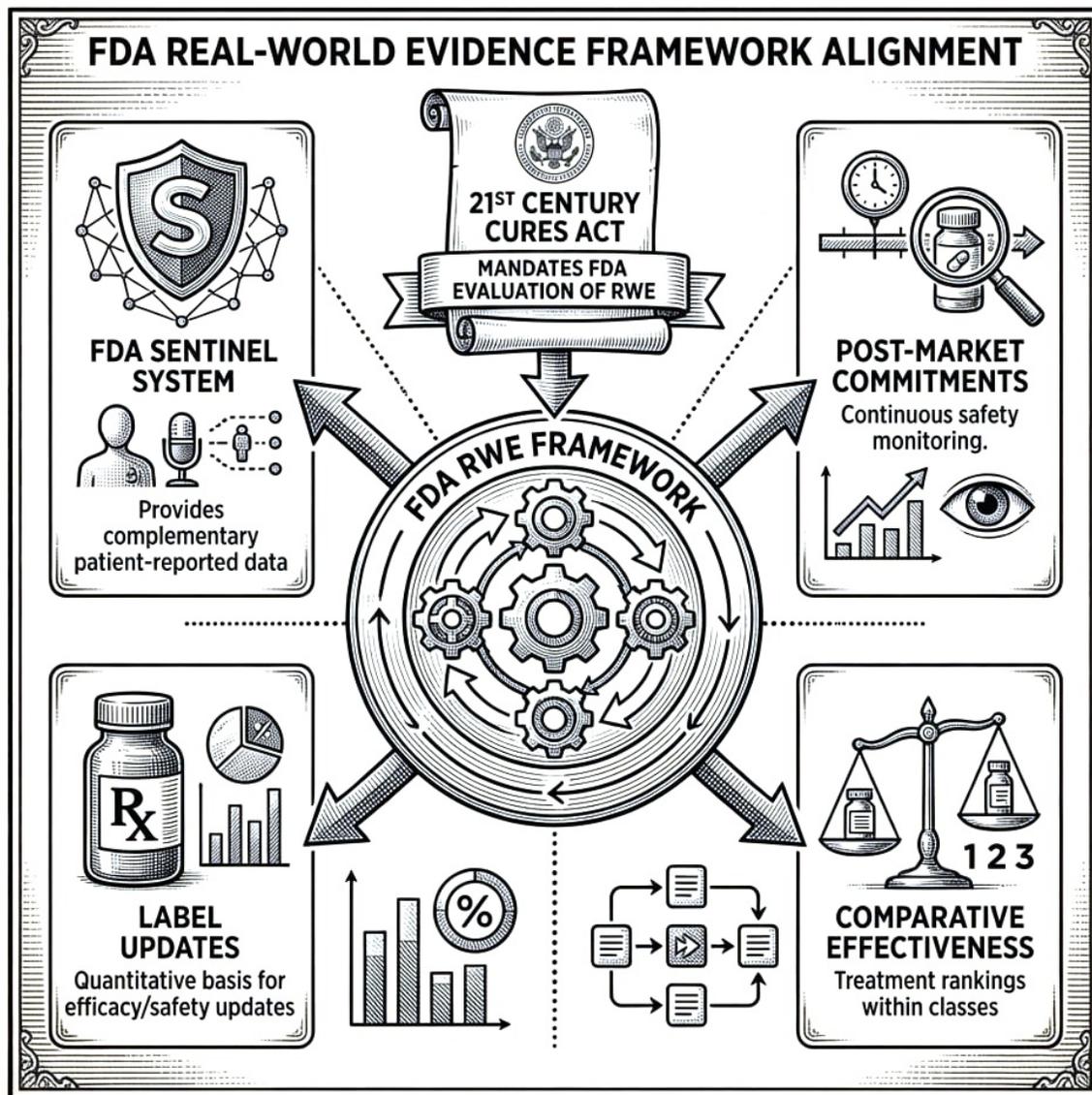
This framework is intended to:

- Complement spontaneous reporting with quantitative signals
- Prioritize hypotheses for experimental investigation
- Provide continuous post-market surveillance
- Enable real-time safety signal detection
- Generate evidence for benefit-risk reassessment

17.2 Evidence Hierarchy Integration

Evidence Level	Source	Role of This Framework
Level I	RCTs, Meta-analyses	Gold standard for approval
Level II	Cohort studies	This framework provides quantitative RWE
Level III	Case-control	Traditional pharmacovigilance
Level IV	Case series	Spontaneous reports (FAERS)

17.3 FDA Real-World Evidence Framework Alignment



WarOnDisease.org

Figure 40: A visual mapping of the FDA Real-World Evidence Framework showing its support for the Sentinel System, post-market commitments, label updates, and comparative effectiveness.

The 21st Century Cures Act mandates FDA evaluation of RWE. This framework supports:

- **FDA Sentinel System:** Provides complementary patient-reported data
- **Post-market commitments:** Continuous safety monitoring
- **Label updates:** Quantitative basis for efficacy/safety updates
- **Comparative effectiveness:** Treatment rankings within classes

18 Validation Framework

18.1 The Critical Question

The ultimate test of PIS validity: **Do high-PIS relationships replicate in RCTs more often than low-PIS ones?**

Until this validation is performed, PIS should be treated as a theoretically-motivated heuristic, not a validated predictive tool.

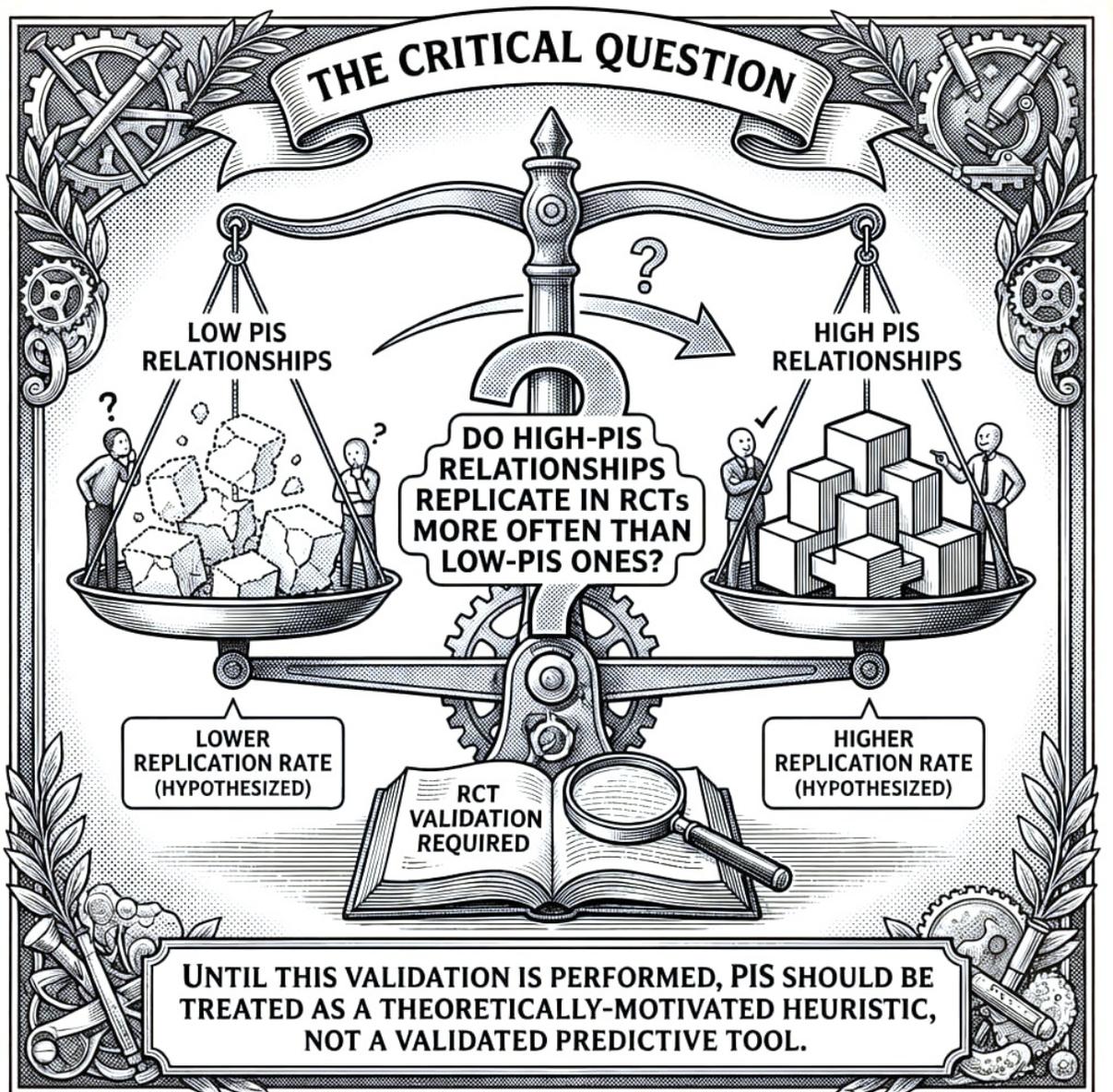


Figure 41: A comparison bar chart showing the hypothesized higher replication rates in RCTs for high-PIS relationships versus low-PIS relationships to demonstrate validity.

18.2 Proposed Validation Study

Design: Retrospective comparison of PIS predictions against published RCT results.

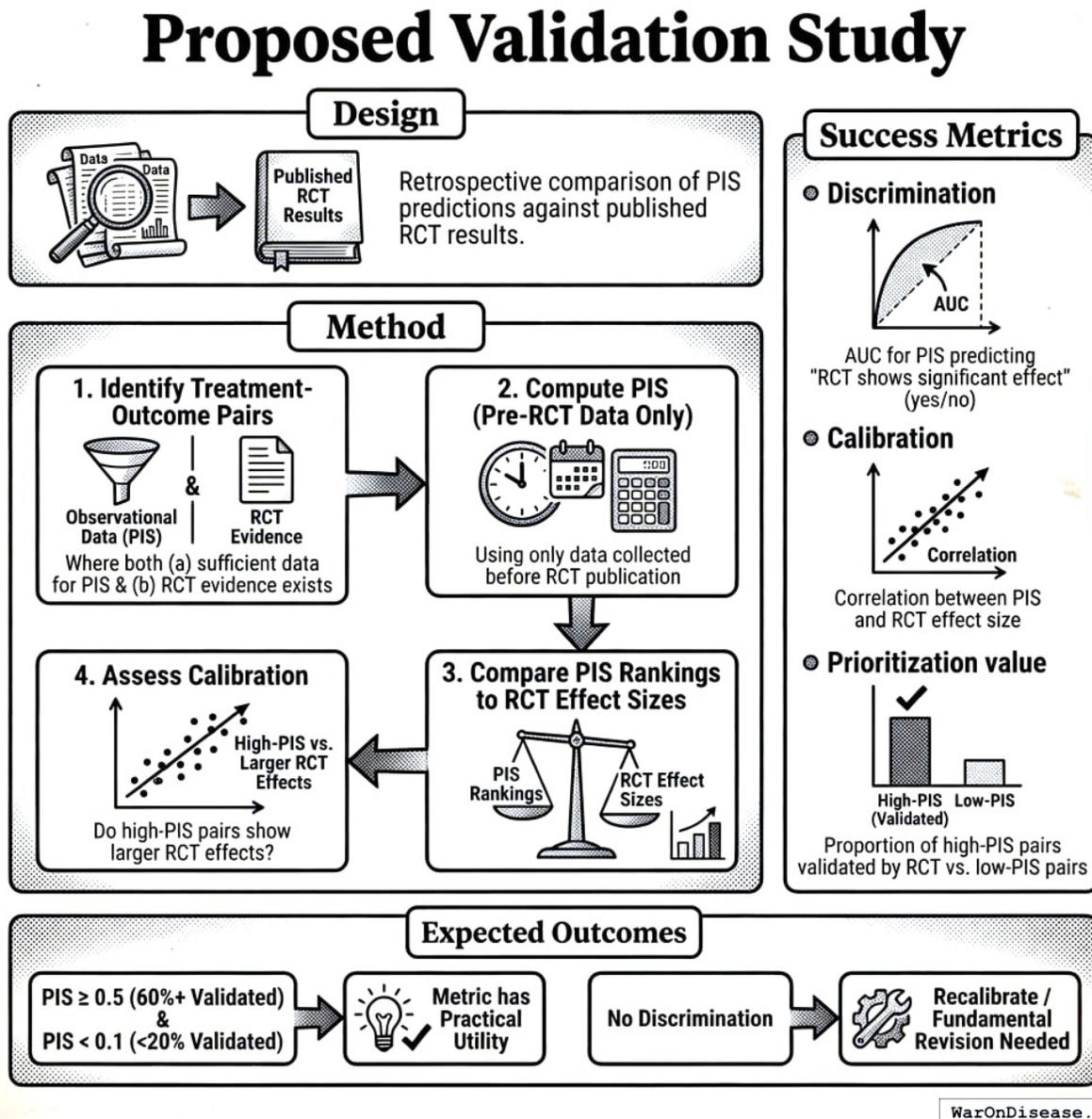


Figure 42: Workflow of the retrospective validation study comparing PIS predictions against historical RCT results to assess discrimination and calibration.

Method: 1. Identify treatment-outcome pairs where both (a) we have sufficient observational data to compute PIS, and (b) RCT evidence exists 2. Compute PIS for each pair using only data collected before RCT publication 3. Compare PIS rankings to RCT effect sizes 4. Assess calibration: Do high-PIS pairs show larger RCT effects?

Success Metrics:

- **Discrimination:** AUC for PIS predicting “RCT shows significant effect” (yes/no)
- **Calibration:** Correlation between PIS and RCT effect size
- **Prioritization value:** Proportion of high-PIS pairs validated by RCT vs. low-PIS pairs

Expected Outcomes:

- If $PIS \geq 0.5$ pairs have RCT validation rate of 60%+ and $PIS < 0.1$ pairs have rate $< 20\%$, the metric has practical utility
- If no discrimination, saturation constants need recalibration or the approach needs fundamental revision

18.3 Known Limitations Requiring Validation

1. **Confounding by indication:** Does the temporality factor adequately address reverse causation in treatment contexts?
2. **Saturation constant sensitivity:** How robust are rankings to $\pm 50\%$ changes in N_sig , n_sig ?
3. **Population generalizability:** Do PIS values from health-tracker users predict effects in general populations?

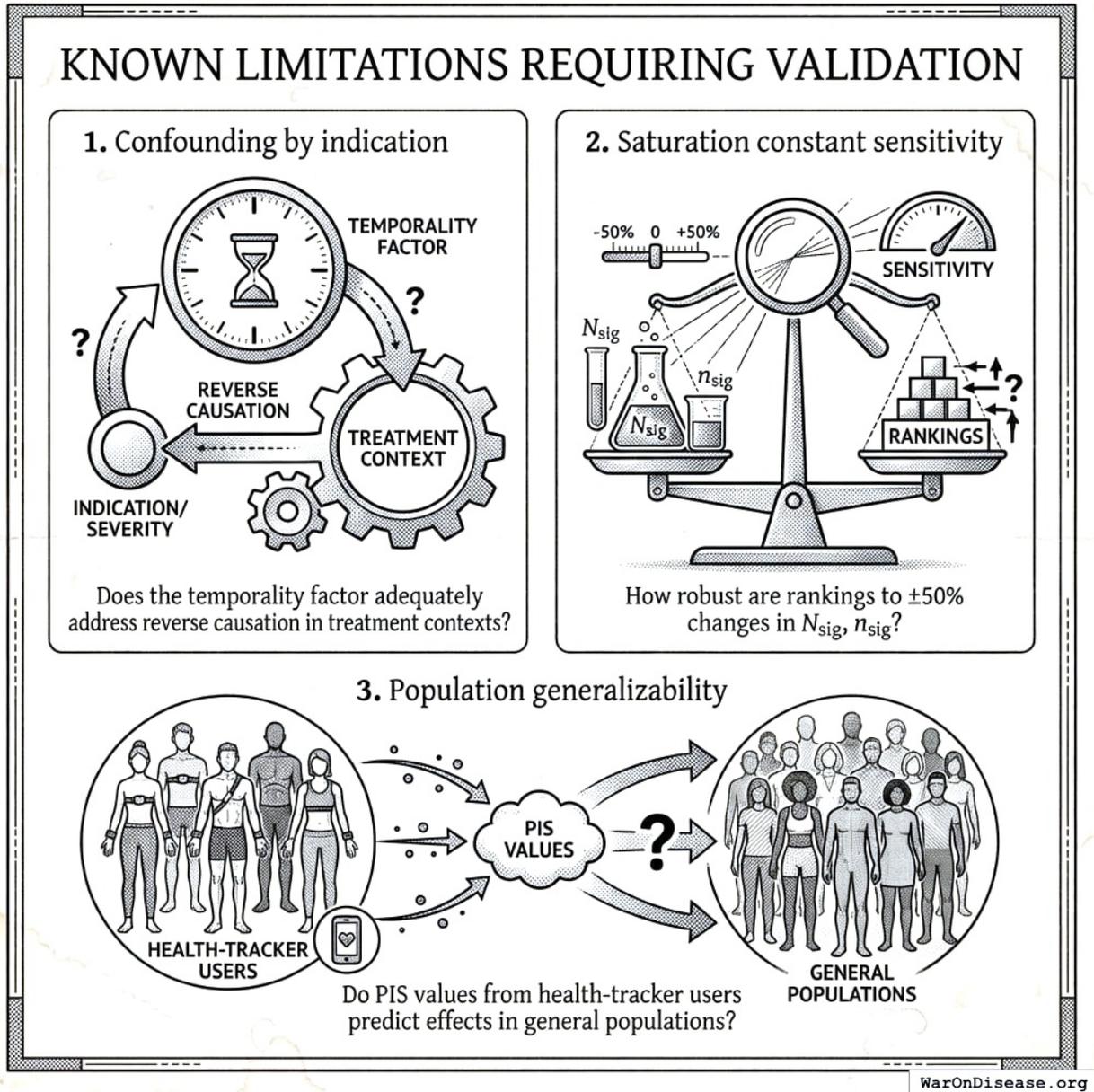


Figure 43: A visual summary of the three validation hurdles: causal directionality in treatment, the impact of parameter sensitivity on rankings, and the gap between tracker users and the general population.

19 Future Directions

19.1 Methodological Improvements

1. **Causal discovery algorithms:** Implement PC algorithm, FCI, or GES for graph structure learning
2. **Propensity score integration:** Covariate adjustment for measured confounders
3. **Bayesian hierarchical models:** More principled cross-participant pooling with uncertainty

quantification

4. **Time-varying effects:** Model how relationships change over time (effect modification)
5. **Subgroup analysis:** Identify responder vs. non-responder populations using heterogeneity metrics
6. **Multiple testing correction:** Benjamini-Hochberg for family-wise error control across millions of pairs
7. **Sensitivity analysis:** E-values or other methods to quantify robustness to unmeasured confounding
8. **Causal mediation:** Identify mechanisms through which treatments affect outcomes
9. **Drug-drug interactions:** Detect combination effects and synergies

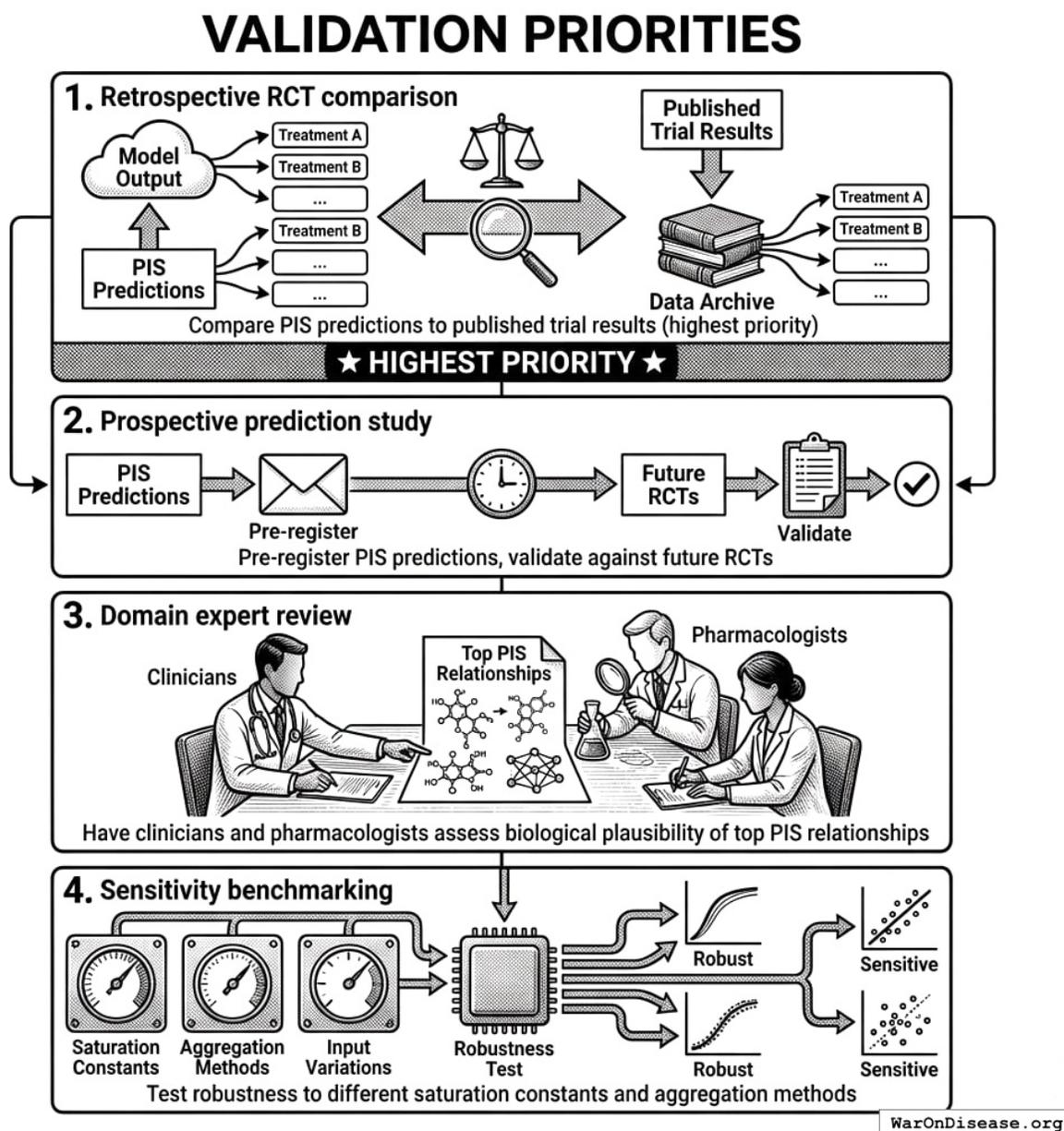


Figure 44: A four-stage validation roadmap for PIS predictions, illustrating the sequence from retrospective comparisons and prospective studies to expert review and sensitivity benchmarking.

1. **Retrospective RCT comparison:** Compare PIS predictions to published trial results (highest priority)
2. **Prospective prediction study:** Pre-register PIS predictions, validate against future RCTs
3. **Domain expert review:** Have clinicians and pharmacologists assess biological plausibility of top PIS relationships
4. **Sensitivity benchmarking:** Test robustness to different saturation constants and aggregation methods

19.3 Implementation Enhancements

1. **Real-time signal detection:** Automated alerts when new high-PIS relationships emerge
2. **Confidence intervals for PIS:** Bootstrap or Bayesian intervals to quantify uncertainty
3. **Interactive exploration:** Tools for users to explore their individual PIS relationships
4. **API access:** Enable researchers to query PIS data programmatically

20 Conclusion

We have presented a comprehensive **two-stage framework** for generating **validated outcome labels** from real-world health data. Key contributions include:

1. **Stage 1: Scalable signal detection:** Aggregated N-of-1 observational analysis processes millions of treatment-outcome pairs at ~\$0.100 (95% CI: \$0.030-\$1.00)/patient, generating ranked hypotheses through the Predictor Impact Score
2. **Stage 2: Causal confirmation:** Pragmatic randomized trials following the embedded trial model (validated across 108+ studies¹³⁴) confirm top signals at ~\$929 (95% CI: \$97-\$3K)/patient (44.1x (95% CI: 39.4x-89.1x) cheaper than traditional trials) while eliminating confounding
3. **Bradford Hill operationalization:** Six of nine causality criteria quantified in composite scoring system
4. **Trial Priority Score:** Principled prioritization of which signals warrant experimental confirmation
5. **Validated outcome labels:** Three-tier evidence grading (Validated, Promising, Signal) with both observational and experimental effect sizes
6. **Learning health system:** Feedback loop where trial results continuously calibrate observational models

This two-stage design directly addresses the fundamental limitations of purely observational pharmacovigilance. Confounding by indication, self-selection bias, and inability to prove causation are all resolved through Stage 2 randomization for high-priority signals, while Stage 1 maintains the scale and cost advantages necessary for comprehensive monitoring.

This framework represents **the FDA of the Future**, a decentralized system that:

- Receives continuous real-world evidence streams from millions of participants
- Generates ranked treatment-outcome hypotheses through automated observational analysis
- Confirms top signals through embedded pragmatic trials at 44.1x (95% CI: 39.4x-89.1x) lower cost than traditional methods
- Publishes validated outcome labels with quantitative effect sizes and evidence grades
- Maintains treatment rankings updated in real-time with experimental backing
- Enables precision medicine through personalized optimal value calculations
- Operates transparently with open-source methodology and reproducible analyses

The technology exists. The methodology is sound. The data is available. The pragmatic trial model is proven. We present this framework not as a replacement for regulatory bodies, but as the complete infrastructure (from passive data collection to validated causal claims) that they will need to fulfill their mission in an era of ubiquitous health data. What remains is the institutional will to build it.

21 Appendix A: Effect Size Classification

Absolute Correlation	Classification
$\ r\ \geq 0.8$	Very Strong
$0.6 \leq \ r\ < 0.8$	Strong
$0.4 \leq \ r\ < 0.6$	Moderate
$0.2 \leq \ r\ < 0.4$	Weak
$\ r\ < 0.2$	Very Weak

22 Appendix B: Variable Category Defaults

Category	Onset Delay	Duration of Action	Filling Value
Treatments	1,800s (30 min)	86,400s (1 day)	0
Foods	1,800s (30 min)	864,000s (10 days)	0
Emotions	0	86,400s (1 day)	None
Symptoms	0	86,400s (1 day)	None
Vital Signs	0	86,400s (1 day)	None
Sleep	0	86,400s (1 day)	None
Physical Activity	0	86,400s (1 day)	None
Environment	0	86,400s (1 day)	None

23 Appendix C: Glossary

- **Predictor Variable:** The independent variable hypothesized to influence the outcome (e.g., treatment, food, activity). Formerly called “cause variable.”
- **Outcome Variable:** The dependent variable being measured for changes (e.g., symptom, mood, biomarker). Formerly called “effect variable.”
- **User Variable Relationship:** A per-user N-of-1 analysis record containing correlation coefficients, effect sizes (percent change from baseline), Predictor Impact Scores, and Bradford Hill metrics for a specific predictor-outcome pair. Stored in `user_variable_relationships` table.
- **Global Variable Relationship:** A population-level aggregation of user variable relationships, combining individual N-of-1 analyses across participants. Stored in `global_variable_relationships` table.
- **Correlation Coefficient:** The Pearson or Spearman statistical measure of linear/monotonic association between predictor and outcome variables (a component of a variable relationship).
- **Predictor Impact Score (PIS):** Composite metric quantifying how much a predictor impacts an outcome. Integrates correlation strength, statistical significance, z-score (effect magnitude), temporality factor, and interest factor at the user level; adds consistency, plausibility, and biological gradient at the aggregate level. Higher scores indicate predictors with greater, more reliable impact. Ranges from 0 to ~1.
- **Onset Delay (δ):** Time between predictor exposure and first observable outcome change
- **Duration of Action (τ):** Time window over which predictor influence on outcome persists
- **Baseline Period:** Measurements when predictor exposure is below participant’s average

- **Follow-up Period:** Measurements when predictor exposure is at or above participant’s average
- **Percent Change from Baseline ($\Delta\%$):** Relative difference between follow-up and baseline outcome means
- **Z-Score:** Effect magnitude normalized by baseline variability; $z > 2$ indicates statistical significance
- **Temporality Factor (ϕ_{temporal}):** Ratio of forward to total correlation, measuring evidence for correct causal direction
- **Filling Value:** Default value imputed for missing measurements
- **Outcome Label:** A per-outcome document that ranks all treatments and predictors by their quantitative effect size on a specific health outcome. Unlike traditional FDA drug labels (which are per-drug and qualitative), outcome labels are per-outcome, quantitative, and dynamically updated. They answer the question: “What works best for this condition?” See Section 7.5 for comparison with FDA labels.
- **Treatment Ranking:** Ordered list of treatments by efficacy or safety for a given outcome, sorted by effect size with confidence weighting. Rankings include percent change from baseline, confidence intervals, sample sizes, and Predictor Impact Scores. See Section 8 for ranking methodology.
- **Value Predicting High Outcome (V_{high}):** The average predictor value observed when the outcome exceeds its mean. Used for precision dosing recommendations. This is the “optimal daily value” for achieving better outcomes.
- **Value Predicting Low Outcome (V_{low}):** The average predictor value observed when the outcome is below its mean. Represents the predictor value associated with worse outcomes.
- **Grouped Optimal Value:** The nearest commonly-used dosing value to the calculated optimal value, enabling practical recommendations (e.g., “400mg” instead of “412.7mg”)
- **Optimal Value Spread ($V_{\text{high}} - V_{\text{low}}$):** The difference between high and low outcome predictor values, indicating the magnitude of dose-response effect
- **Precision Dosing:** Personalized treatment recommendations based on an individual’s historical optimal values, enabling targeted interventions at the dose most likely to produce beneficial outcomes
- **Average Outcome Following High Predictor (\bar{O}_{high}):** Mean outcome value observed following above-average predictor exposure
- **Average Outcome Following Low Predictor (\bar{O}_{low}):** Mean outcome value observed following below-average predictor exposure
- **Predictor Baseline Average:** Average predictor value during low-exposure (non-treatment) periods
- **Predictor Treatment Average:** Average predictor value during high-exposure (treatment) periods
- **Valence:** Whether higher values of a variable are inherently good (positive), bad (negative), or context-dependent (neutral)
- **Predictor Is Controllable:** Flag indicating whether the user can directly modify this predictor (e.g., supplements, food, activities)
- **Outcome Is Goal:** Flag indicating whether this outcome is something users want to optimize
- **Plausibly Causal:** Flag indicating whether a plausible biological mechanism exists for this relationship
- **Boring:** Flag indicating relationships unlikely to interest users due to being uncontrollable, non-goal, implausible, or obvious
- **Interesting Variable Category Pair:** Flag for category combinations that are typically

meaningful (e.g., Treatment \rightarrow Symptom)

- **Usefulness Vote:** User rating (-1, 0, 1) on whether knowledge of a relationship is practically useful
- **Causality Vote:** User rating (-1, 0, 1) on whether a plausible causal mechanism exists
- **Correlations Over Delays:** Stored correlation coefficients calculated with various onset delay values for temporal optimization
- **Correlations Over Durations:** Stored correlation coefficients calculated with various duration of action values
- **Forward Spearman Correlation:** Rank-based correlation coefficient that captures monotonic relationships and is robust to outliers
- **Optimal Value Confidence Interval:** Uncertainty bounds around V_{high} or V_{low} , reflecting reliability of the estimate based on sample size and variance
- **Optimal Value Stability:** Metric measuring how much the optimal value has changed over time; stability < 0.8 indicates significant drift
- **Adherence Score:** Proportion of tracking days where actual predictor value was within $\pm 20\%$ of the recommended optimal value
- **Dose-Response Detection Threshold:** Criterion ($|V_{\text{high}} - V_{\text{low}}|/\sigma_P < 0.5$) below which no meaningful dose-response exists
- **Rolling Window Optimal Value:** Optimal value calculated using only recent data (e.g., 90 days) rather than all historical data, useful when tolerance effects are expected

24 Appendix D: Worked Example

24.1 Example: Calculating Predictor Impact Score for “Magnesium \rightarrow Sleep Quality”

Given data (hypothetical):

- $N = 47$ users tracked both magnesium supplementation and sleep quality
- $n = 2,340$ paired observations across all users
- Forward correlation: $r_{\text{forward}} = 0.31$
- Reverse correlation: $r_{\text{reverse}} = 0.12$
- Percent change from baseline: $\Delta\% = +18.5\%$ (sleep quality improved)
- Baseline RSD: 23%
- Community votes: 15 up, 2 down
- Effect spread: 22% (difference between high and low magnesium outcomes)

Step 1: Calculate z-score

$$z = \frac{|18.5\%|}{23\%} = 0.80$$

Step 2: Calculate temporality factor

$$\phi_{\text{temporal}} = \frac{|0.31|}{|0.31| + |0.12|} = \frac{0.31}{0.43} = 0.72$$

This suggests forward causation (magnesium \rightarrow sleep) is more likely than reverse (poor sleep \rightarrow taking magnesium).

Step 3: Calculate saturation factors

- User saturation: $\phi_{\text{users}} = 1 - e^{-47/10} = 1 - 0.009 = 0.991$
- Pair saturation: $\phi_{\text{pairs}} = 1 - e^{-2340/100} = 1 - e^{-23.4} \approx 1.0$
- Change saturation: $\phi_{\text{change}} = 1 - e^{-22/10} = 1 - 0.11 = 0.89$

Step 4: Calculate plausibility weight

$$w = \frac{15}{15 + 2} = 0.88$$

Step 5: Compute aggregate PIS

$$\text{PIS}_{\text{agg}} = 0.31 \times 0.88 \times 0.991 \times 1.0 \times 0.89 \times 0.72 = 0.17$$

Interpretation: PIS = 0.17 falls in the “weak evidence” range (0.1-0.3). The relationship shows:

- Modest correlation strength ($r = 0.31$)
- Good temporal evidence ($\tau = 0.72$, forward > reverse)
- Strong consistency (many users and pairs)
- High plausibility (community agrees mechanism is plausible)

Recommendation: This relationship warrants monitoring. As more data accumulates or if effect size increases, it could become a candidate for experimental validation. The temporality factor is encouraging. This doesn't appear to be reverse causation.

25 Appendix E: Analysis Workflow

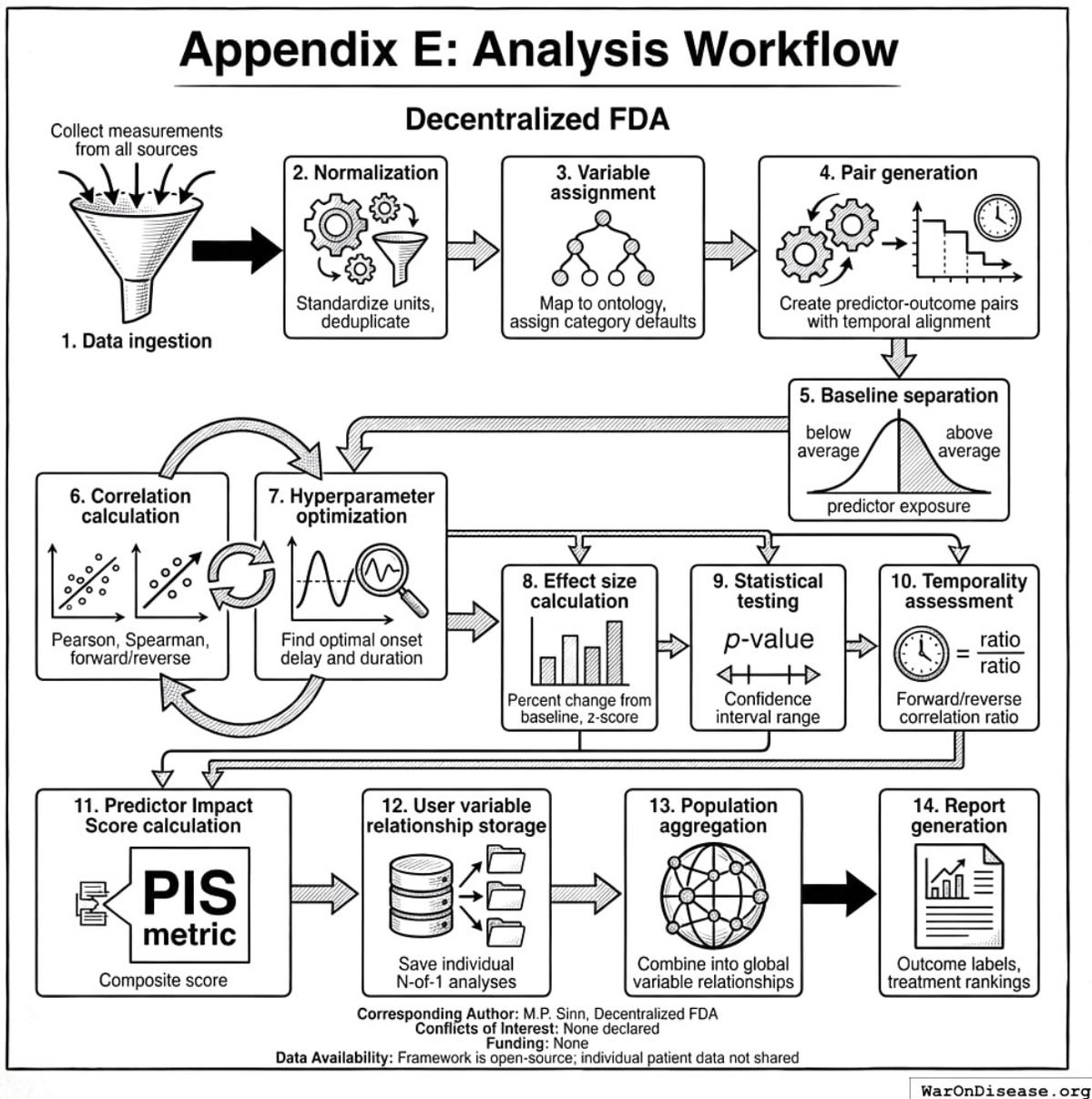


Figure 45: A flowchart mapping the 14-step sequential analysis workflow, starting from data ingestion and normalization through statistical processing and culminating in population aggregation and report generation.

- 1. Data ingestion:** Collect measurements from all sources
- 2. Normalization:** Standardize units, deduplicate
- 3. Variable assignment:** Map to ontology, assign category defaults
- 4. Pair generation:** Create predictor-outcome pairs with temporal alignment
- 5. Baseline separation:** Partition by below/above average predictor exposure
- 6. Correlation calculation:** Pearson, Spearman, forward/reverse

7. **Hyperparameter optimization:** Find optimal onset delay and duration
8. **Effect size calculation:** Percent change from baseline, z-score
9. **Statistical testing:** p-value, confidence intervals
10. **Temporality assessment:** Forward/reverse correlation ratio
11. **Predictor Impact Score calculation:** Composite PIS metric
12. **User variable relationship storage:** Save individual N-of-1 analyses
13. **Population aggregation:** Combine into global variable relationships
14. **Report generation:** Outcome labels, treatment rankings

Decentralized FDA

Corresponding Author: M.P. Sinn, Decentralized FDA **Conflicts of Interest:** None declared
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