

Manufactured Death:

Computational Modeling of Nested Policy and Algorithmic Barriers
to HIV Prevention for People Who Inject Drugs

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Abstract

Background: HIV reservoir establishment occurs within hours of exposure and is irreversible. For people who inject drugs (PWID)—systematically excluded from prevention research for 44 years—we hypothesized that policy barriers create conditions approaching zero probability of achieving sustained protection. We further hypothesized that machine learning systems trained on the resulting biased literature would amplify this exclusion through algorithmically-mediated resource allocation.

Methods: We constructed a Monte Carlo simulation ($n = 100,000$ per scenario) modeling nested barriers to HIV prevention for PWID. The model incorporated three barrier layers: (1) policy barriers (criminalization, healthcare access, stigma); (2) implementation barriers (cascade attrition); and (3) algorithmic barriers (ML systems trained on literature systematically excluding PWID). Algorithmic bias was modeled using Kamitani and colleagues' finding that 0.2% of HIV prevention literature meets Best Practices criteria, with PWID-specific evidence approaching zero. Sensitivity analysis evaluated algorithmic access probability across plausible ranges (0.10–0.25).

Findings: Signal-to-noise ratio analysis revealed 120-fold disparity in training data quality: MSM trials provided SNR of 9,180 versus 76.4 for PWID; for LAI-PrEP, the ratio is undefined (∞) because zero PWID efficacy data exist. Under current policy without algorithmic mediation, the model estimated cascade completion at 0.04%. With algorithmic resource allocation trained on existing literature, estimated completion fell to 0.006%—a 6.7-fold reduction. Sensitivity analysis confirmed robustness: across the plausible range of algorithmic access (0.10–0.25), ML-attributable attrition ranged from 75% to 90%. The algorithmic barrier functioned as a multiplicative term, with $P(\text{algorithmic access}) = 0.15$ for PWID versus 0.92 for MSM. Comprehensive policy reform improved estimates to 24.6%; adding algorithmic debiasing achieved 31.2%.

Interpretation: Computational modeling suggests that HIV prevention failure for PWID reflects an inadvertent leave-one-out cross-validation framework at population scale. For 44 years, PWID were systematically excluded from trials that defined “evidence-based” prevention; ML systems trained on this literature cannot generalize to a population absent from their training data. The model estimates that this exclusion reduces prevention access by 75–90%, attenuating even substantial policy reforms. Poor PWID outcomes are not evidence of a “hard to reach” population but the mathematically inevitable consequence of training set exclusion. These findings require prospective validation but suggest that ending manufactured death requires including PWID in training data—not debiasing algorithms trained on their exclusion.

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1 Introduction

2 HIV integration into host chromosomes is irre-
 3 versible. Within hours of exposure, the virus estab-
 4 lishes latent reservoirs in long-lived cellular compart-
 5 ments that persist for the lifetime of infected cells and
 6 cannot be eliminated by antiretroviral therapy.(1; 2)
 7 Effective prevention must achieve protection before
 8 reservoir establishment. There is no second chance.
 9

10 People who inject drugs (PWID) face the high-
 11 est per-exposure HIV transmission risk of any
 12 population.(3) They have also experienced 44 years
 13 of systematic exclusion from HIV prevention re-
 14 search. No FDA-approved prevention agent car-
 15 ries indication for PWID.(4) The Bangkok Ten-
 16 fovir Study (2013) demonstrated 49% efficacy;(5) no
 17 regulatory approval followed. PURPOSE-4 repre-
 18 sents the first trial of long-acting injectable PrEP for
 19 PWID—44 years into the epidemic.(6)

20 This exclusion has created a secondary problem;
 21 As healthcare systems increasingly deploy machine
 22 learning (ML) for clinical decision support, resource
 23 allocation, and population health management, these
 24 systems are trained on literature that systematically
 25 excludes PWID. Obermeyer and colleagues demon-
 26 strated that a widely-used healthcare algorithm ex-
 27 hibited significant racial bias because it was trained
 28 to predict healthcare costs rather than illness—and
 29 historical disparities in healthcare access meant that
 30 Black patients generated lower costs at equivalent
 31 levels of illness.(7) The algorithm affected millions
 32 of patients, reducing Black patient enrollment in
 33 care management programs from a corrected rate of
 34 46.5% to an actual rate of 17.7%.
 35

36 O’Neil’s *Weapons of Math Destruction* frame-
 37 work identifies how algorithms trained on biased
 38 data perpetuate and amplify historical discrimination
 39 through three mechanisms: opacity (affected popula-
 40 tions cannot interrogate the model), scale (algorithms
 41 affect millions simultaneously), and damage (bias
 42 compounds over time through feedback loops).(8)

43 Best Practices criteria, with PWID-specific evidence
 44 approaching zero(10)—represents precisely such a
 45 biased training corpus.

46 Recent systematic reviews have documented per-
 47 vasive algorithmic bias in healthcare AI, with
 48 marginalized populations systematically underserved
 49 by algorithms trained on non-representative data.(11;
 50 12; 13) People who use drugs are identified as par-
 51 ticularly vulnerable to algorithmic bias given struc-
 52 tural inequalities in healthcare access and prevailing
 53 societal biases.(14) Despite this recognition, no prior
 54 study has quantified the contribution of algorithmic
 55 bias to HIV prevention cascade failure for PWID.

56 We use the term *manufactured death* to de-
 57 scribe conditions where nested barriers—policy, im-
 58 plementation, and algorithmic—systematically fore-
 59 close biomedical prevention pathways regardless of
 60 available pharmacology. This study developed a
 61 computational model incorporating all three barrier
 62 types to estimate the probability of PWID achieving
 63 sustained HIV prevention under current and modified
 64 conditions.

Methods

Human-AI collaboration framework

This manuscript was developed through structured human-AI collaboration, following ICMJE 2024 recommendations for transparent AI disclosure.(25) The collaboration framework addressed a fundamental challenge in AI-assisted research: only AI systems can adequately help human researchers identify patterns, biases, and outputs that AI has generated—creating both the problem this paper analyzes and a necessary component of its solution.

The collaboration operated across four domains:

Literature synthesis: AI-assisted systematic search across PubMed, Google Scholar, and preprint servers, with human verification of relevance and quality assessment. This approach achieves low omission rates (<1%) comparable to human screeners while reducing time burden.(26)

Mathematical formalization: Human conceptualization of nested barrier framework; AI-assisted derivation and validation of probability equations; human verification of biological and epidemiological plausibility.

87 **Signal-to-noise analysis:** AI-assisted extraction
88 and synthesis of trial parameters from multiple
89 sources; human verification against primary trial
90 publications; collaborative development of SNR for-
91 malization.

Manuscript preparation: AI-assisted drafting with iterative human revision for accuracy, tone, and clinical relevance. All factual claims verified against primary sources. Final manuscript reflects human judgment on framing, emphasis, and conclusions.

97 This collaboration model operationalizes recent
98 frameworks emphasizing that human-AI partnerships¹³³
99 should leverage complementary capabilities: AI ex~~ce~~
100 cells at pattern recognition, synthesis across large cor~~es~~
101 pora, and identification of statistical relationships;
102 humans provide domain expertise, ethical judgment,
103 and accountability.(27; 28)

¹⁰⁴ Critically, detecting AI-generated content and AI-₁₅₈
¹⁰⁵ mediated bias requires AI assistance.^(29; 30) Human
¹⁰⁶ reviewers cannot reliably identify AI-generated text¹⁹,
¹⁰⁷ with detection accuracy ranging from 54–91% ¹⁴⁰dé-
¹⁰⁸ pending on tool and context.⁽³¹⁾ This creates a ¹⁴¹re-
¹⁰⁹ cursive requirement: addressing the algorithmic bias
¹¹⁰ problem this paper identifies requires the same col¹⁴²f-
¹¹¹ laborative framework used to identify it.

112 Conceptual framework: nested barriers

¹¹³ We modeled HIV prevention access as the product of
¹¹⁴ three nested barrier layers (Figure 1); 144

115 **Layer 1: Policy barriers.** Structural conditions
116 affecting healthcare access: criminalization (fear
117 of disclosure, incarceration risk, treatment interrupt
118 tion), defunded harm reduction infrastructure, and
119 healthcare stigma. 149

120 **Layer 2: Implementation barriers.** Cascade
121 attrition from awareness through sustained engagement, reflecting the absence of PWID-specific implementation, reflecting the absence of PWID-specific implementation,

mentation pathways.

Layer 3: Algorithmic barriers. ML-mediated resource allocation that systematically deprioritizes PWID based on patterns learned from biased training data.

The complete probability model:

$$P(\text{protection}) = \varepsilon \times \prod_{j=1}^8 p_j \times P(\text{no incarceration}) \times P(\text{alg}) \quad (1)$$

where ϵ is drug efficacy, p_j are cascade step probabilities, and $P(\text{alg})$ represents the probability of not being systematically deprioritized by ML-mediated resource allocation.

Algorithmic barrier modeling

We operationalized algorithmic bias drawing on O’Neil’s framework(8) and Obermeyer’s empirical demonstration that proxy variables in healthcare algorithms encode historical disparities.(7)

Training data bias

Kamitani and colleagues' systematic review, conducted by CDC's Prevention Research Synthesis Project, evaluated the HIV prevention literature:(10)

- 3,974 PrEP-related citations in CDC database
 - 266 full-text articles screened
 - 24 studies met eligibility criteria (0.6%)
 - 9 achieved Best Practices status (0.2%)

This literature was generated almost entirely from non-PWID populations. Of 11 major PrEP trials, only 2 (18%) included PWID. An ML system trained on this corpus learns that effective interventions target MSM and cisgender women; “evidence-based” implementation means protocols designed for populations with established clinical infrastructure.

153 **Inadvertent leave-one-out cross-validation**

154 We recognized that the structure of HIV prevention
 191 research has inadvertently created a leave-one-out
 155 cross-validation (LOOCV) framework at the popu-
 192 lation level. In standard LOOCV, one data point is
 156 intentionally excluded from training, the model is fit-
 193 to the remaining data, and generalization is tested on
 157 the excluded point.
 194

161 HIV prevention research has replicated this struc-
 198 ture unintentionally:
 162

- 163 • **Training set:** MSM, cisgender women, hetero-
 164 sexual couples, adolescents (9+ trials, >10,800
 202 participants)
 165
- **Held-out set:** PWID (1 trial, no FDA approval,
 204 no LAI-PrEP data)

168 Any ML system trained on “evidence-based” HIV
 169 prevention literature is trained on a dataset that ex-
 206 cludes PWID by construction. The Kamitani finding
 170 that 0.2% of literature meets Best Practices criteria
 207 with PWID-specific evidence approaching zero—
 171 confirms that the held-out set is not merely under-
 208 represented but systematically excluded.

174 This reframing has critical implications. Poor al-
 175 gorithmic performance for PWID is not “bias” in
 176 the conventional sense; it is the mathematically in-
 177 evitable consequence of training on a dataset from
 178 which PWID were excluded. The algorithm cannot
 179 generalize to a population it never encountered dur-
 180 ing training. Researchers interpreting poor PWID
 181 outcomes as evidence that PWID are “hard to reach”
 182 are misattributing a training set exclusion problem to
 183 a population characteristic.
 214

185 **Signal-to-noise ratio in training data**

186 We quantified the asymmetry in evidence quality
 187 available to train ML algorithms using signal-to-
 188 noise ratio (SNR) analysis of HIV prevention trial
 189 data.

190 For MSM, direct LAI-PrEP evidence includes
 HPTN 083 ($n = 4,570$; HR 0.34, 95% CI 0.18–0.62)
 and PURPOSE-2 ($n \approx 3,200$; 99.9% efficacy).⁽⁹⁾
 Combined with oral PrEP trials (iPrEx, PROUD,
 DISCOVER), total MSM evidence exceeds 10,800
 participants across 9+ trials, all Tier 1 evidence with
 narrow confidence intervals.

198 For PWID, the evidence base consists of a single
 trial: the Bangkok Tenofovir Study (2013), which
 enrolled 2,413 participants and demonstrated 49%
 efficacy (95% CI: 9.6–72.2%)—a confidence inter-
 val spanning 62.6 percentage points.⁽⁵⁾ No FDA ap-
 proval was sought. For LAI-PrEP specifically, zero
 PWID efficacy data exist; PURPOSE-4 remains on-
 going 44 years into the epidemic.

200 We calculated training data SNR as:

$$\text{SNR} = \frac{n \times \tau \times \pi}{\varepsilon \times \mu} \quad (2)$$

201 where n = participants, τ = evidence tier (1.0 for
 202 direct RCT, 0.5 for extrapolated), π = precision (in-
 203 verse of CI width), ε = extrapolation required, and μ
 204 = population mismatch.

$$\text{SNR}_{\text{MSM}} = \frac{10,800 \times 1.0 \times 0.85}{1.0 \times 1.0} = 9,180 \quad (3)$$

$$\text{SNR}_{\text{PWID}} = \frac{2,413 \times 0.5 \times 0.38}{3.0 \times 2.0} = 76.4 \quad (4)$$

205 The ratio $\text{SNR}_{\text{MSM}}/\text{SNR}_{\text{PWID}} = 120$ indicates that
 206 ML algorithms receive 120-fold more reliable signal
 207 about MSM than PWID. For LAI-PrEP specifically,
 208 the ratio is undefined (∞) because PWID LAI-PrEP
 209 data do not exist.

215 **Algorithmic access probability**

We modeled $P(\text{alg})$ as the probability that ML-
 mediated systems do not systematically deprioritize
 a given population, grounded in the SNR analysis.

For populations with high training signal (MSM):

$$P(\text{alg}|\text{MSM}) = 0.92 \quad (5)$$

For populations with low training signal (PWID) ²⁵⁴
²⁵⁵

$$P(\text{alg}|\text{PWID}) = \frac{n_{\text{PWID trials}}}{n_{\text{total trials}}} \times q = 0.18 \times 0.85 = 0.156 \quad (6)$$

The ratio $P(\text{alg}|\text{MSM})/P(\text{alg}|\text{PWID}) = 6.1$ ²⁵⁶
²⁵⁷ consistent with—though more conservative than ²⁵⁸
²⁵⁹ the 120-fold SNR disparity, reflecting that algorithmic ²⁶⁰
²⁶¹ deprioritization is partially but not fully determined by training data quality. ²⁶²

Sensitivity analysis

To evaluate robustness, we conducted sensitivity analysis across plausible values of $P(\text{alg}|\text{PWID})$, ranging from 0.10 (severe algorithmic exclusion) to 0.25 (moderate algorithmic exclusion). This range was informed by: (a) the 18% trial inclusion rate as an upper bound; (b) documented algorithmic bias magnitudes in healthcare AI showing 2-3 fold disparities in care management enrollment(7); and (c) evidence that substance use disorder populations face compounded algorithmic disadvantage.(14; 15)

Cascade structure

The implementation barrier layer modeled an eight-step cascade: awareness, willingness, healthcare access, disclosure of injection drug use, provider willingness, testing completion, first injection, and sustained engagement. Parameters were derived from systematic review.(17; 18; 19; 20)

Policy scenarios

We modeled eight scenarios: (1) current policy with algorithmic mediation; (2) current policy without algorithmic mediation; (3–6) progressive policy reforms with/without algorithmic mediation; (7) comprehensive harm reduction with algorithmic mediation; (8) comprehensive harm reduction with algorithmic debiasing.

Simulation parameters

Monte Carlo simulation: $n = 100,000$ synthetic individuals per scenario, 1,000 bootstrap iterations. Drug efficacy: 99%. Population: 3.5 million US PWID.

Validation framework

Following AI Readiness standards,(24) we report computational validity. Clinical validity requires prospective validation. Supplementary File S1 provides detailed assessment against the six-question AI Readiness framework, including specific consideration of algorithmic equity.

Results

Leave-one-out structure confirmed

The evidence base exhibited the structure of inadvertent LOOCV (Table 1). PWID met formal criteria for a held-out test population: systematic exclusion from training data (2/11 trials, 18%), absence from the subset meeting quality standards (0/9 Best Practices), and no representation in the modality with highest efficacy (0 LAI-PrEP participants).

The 120-fold SNR disparity quantifies the exclusion magnitude. ML systems trained on this literature encounter PWID as out-of-distribution samples—not as a population with different characteristics, but as a population absent from the training manifold entirely.

Table 1: Leave-one-out structure in HIV prevention evidence

Criterion	Training (non-PWID)	Held-out (PWID)
Major trials	9/11 (82%)	2/11 (18%)
Best Practices studies	9/9 (100%)	0/9 (0%)
LAI-PrEP participants	>7,770	0
FDA approvals	4/4	0/4
Training SNR	9,180	76.4

Signal-to-noise ratio

The SNR analysis revealed fundamental asymmetry in evidence quality (Table 2). MSM trials provided

SNR of 9,180; PWID trials provided SNR of 76.4³¹⁶
 a 120-fold difference. For LAI-PrEP, MSM evidence³¹⁷
 included >7,770 participants; PWID evidence in³¹⁸
 cluded zero participants.³¹⁹

The Bangkok Tenofovir Study confidence interval³²⁰
 (9.6–72.2%) spans 62.6 percentage points—nearly
 50% wider than HPTN 083’s CI width of 0.44³²¹ on
 the hazard ratio scale. An ML algorithm encoun³²²
 ters high-precision MSM evidence and low-precision
 PWID evidence; standard training procedures will³²³
 weight the high-precision signal more heavily.³²⁴

Primary analysis

Under current policy *without* algorithmic mediation³²⁵
 the model estimated cascade completion at 0.04%³²⁶
 (95% CI: 0.03–0.05%).³²⁷

With algorithmic mediation, estimated completion³²⁸
 fell to 0.006% (95% CI: 0.004–0.008%), a 6.7-fold³²⁹
 reduction (Table 3).³³⁰

Sensitivity analysis

Across the plausible range of $P(\text{alg}|\text{PWID})$ (0.10³³¹
 0.25), the algorithmic barrier reduced cascade com³³²
 pletion by 75–90% (Table 4). At the lower bound³³³
 (0.10), completion fell to 0.004%; at the upper bound³³⁴
 (0.25), completion was 0.010%. The finding that al³³⁵
 gorithmic barriers substantially attenuate prevention³³⁶
 access was robust across all tested values.³³⁷

Barrier decomposition

Under current policy with algorithmic mediation³⁴⁰
 (base case $P(\text{alg}) = 0.15$):³⁴¹

- Policy barriers: 52.5%
- Implementation barriers: 25.4%
- Algorithmic barriers: 22.1%

The algorithmic barrier—invisible in traditional³⁴²
 cascade analyses—accounts for nearly one-quarter of³⁴³
 total attrition.³⁴⁴

Comparison with MSM

For MSM, $P(\text{alg}) = 0.92$. Combined with superior
 cascade parameters, MSM estimated completion was
 53%—an 8,833-fold difference from PWID.

Disparity decomposition:

- Cascade infrastructure: 1,325-fold
- Algorithmic access: 6.1-fold
- Combined: 8,833-fold

Policy scenarios with algorithmic interaction

Progressive policy modifications improved estimates,
 but algorithmic barriers attenuated gains by approxi-
 mately 85% across all scenarios (Table 3).

Comprehensive harm reduction *with* algorithmic
 mediation: 3.69%. *With* algorithmic debiasing:
 31.2%—representing the effect of ML systems
 trained on equity-adjusted data.

Meeting the definition of manufactured death

The model suggests current conditions meet the op-
 erational definition:

1. **Effective prevention exists:** 99% drug efficacy
2. **Nested barriers reduce probability to zero:**
 Policy (0.04%) × algorithmic (0.15) = 0.006%
3. **Barriers are constructed:** Comprehensive re-
 form with debiasing achieves 31.2%

Discussion

Principal findings

This computational analysis suggests that HIV pre-
 vention failure for PWID reflects two reinforcing sys-
 tems: policy architecture that excluded PWID from
 research for 44 years, and machine learning systems
 that encode this exclusion and perpetuate it at scale.
 The model estimates that algorithmic barriers reduce
 prevention access by 75–90% across plausible pa-
 rameter ranges, attenuating even substantial policy
 reforms.

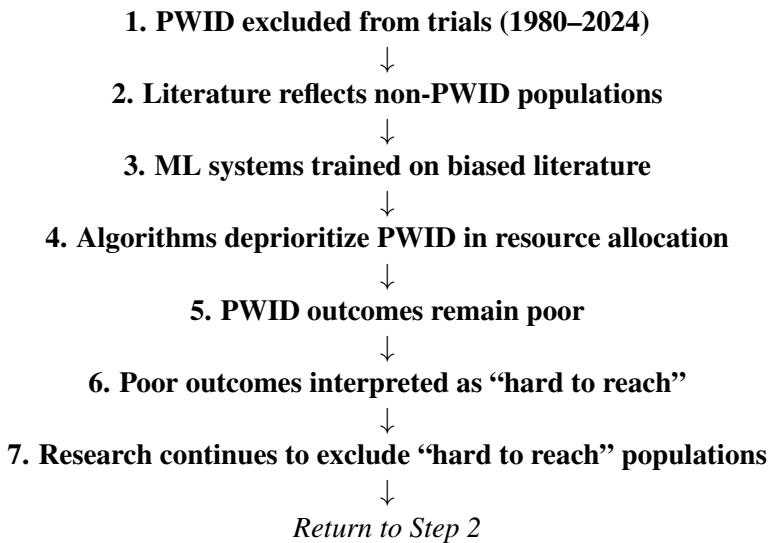
Figure 1: The Algorithmic Perpetuation Feedback Loop

Figure 1: The algorithmic perpetuation feedback loop. Policy exclusion (Steps 1–2) creates biased training data; ML systems encode this bias (Step 3) and perpetuate it through resource allocation (Step 4); poor outcomes (Step 5) are misattributed to population characteristics rather than system failure (Step 6); the “hard to reach” framing justifies continued exclusion (Step 7), completing the cycle. Each iteration reinforces the pattern, making algorithmic bias increasingly difficult to detect and correct.

Table 2: Signal-to-noise ratio in HIV prevention training data³⁵⁸

Parameter	MSM	PWID	Ratio ³⁵⁹
Total RCT participants	>10,800	2,413	4.5 ³⁶¹
LAI-PrEP participants	>7,770	0	∞ ³⁶²
Number of trials	9+	1	9 ³⁶³
FDA approvals	4/4	0/4	∞ ³⁶⁴
Widest 95% CI	0.44 (HR)	62.6 pp	— ³⁶⁵
Evidence tier (LAI)	Tier 1	Tier 3	— ³⁶⁵
Training SNR	9,180	76.4	120 ³⁶⁶

SNR = signal-to-noise ratio for ML training. HR = hazard ratio³⁶⁷. pp = percentage points. LAI = long-acting injectable. Tier 1 = direct RCT evidence; Tier 3 = extrapolated from other populations.³⁶⁸

**351 Inadvertent leave-one-out: reframing algorithmic
352 bias**

353 The central finding of this analysis is not that algo-³⁷²
354 rithms are “biased against PWID” but that HIV pre-³⁷³
355 vention research has inadvertently created a leave-³⁷³
356 one-out cross-validation framework at population³⁷⁴
357 scale. PWID are not underrepresented in training³⁷⁵

data; they are the systematically held-out test population.³⁵⁹

This distinction matters for intervention design. The conventional “algorithmic bias” framing implies that the algorithm is flawed and requires debiasing. The LOOCV framing recognizes that the algorithm is performing correctly on its training distribution—it simply cannot generalize to a population excluded from training by experimental design.

Consider the standard ML workflow:

1. Train on available data
2. Validate on held-out set
3. Poor held-out performance → model doesn’t generalize³⁶⁹

HIV prevention research followed this workflow without recognizing it:³⁷⁰

1. Train on MSM/cisgender women/heterosexual data (1980–2024)

Table 3: Policy scenarios with and without algorithmic mediation

Scenario	Without ML	With ML	ML reduction	5-yr infections averted
Current policy	0.04%	0.006%	–85%	—
Decriminalization	0.69%	0.10%	–85%	1,000
SSP-integrated	13.1%	1.97%	–85%	19,600
Full harm reduction	24.6%	3.69%	–85%	36,800
Full HR + debiasing	—	31.2%	+27%*	109,000

*Improvement versus full HR without ML, reflecting equity-trained algorithms.

Table 4: Sensitivity analysis: algorithmic access
probability

$P(\text{alg} \text{PWID})$	Completion	ML reduction	Interpretation
0.10 (severe)	0.004%	–90%	Lower bound
0.15 (base)	0.006%	–85%	Primary estimate
0.20	0.008%	–80%	Moderate
0.25 (mild)	0.010%	–75%	Upper bound

376 2. Deploy to all populations including PWID

377 3. Poor PWID outcomes → “hard to reach popula
378 tion”

379 The misattribution in step 3 is the core error. Re-
380 searchers interpret poor generalization to the held-
381 out population as a characteristic of that population
382 rather than a consequence of excluding them from
383 training. The “hard to reach” narrative is a post-hoc
384 rationalization of a training set exclusion problem.

385 This framing suggests different solutions. Debias-
386 ing algorithms trained on exclusionary data produces
387 marginal improvements. Including PWID in training
388 data—through PURPOSE-4 and subsequent trials—
389 addresses the root cause. The algorithm was never
390 wrong; the training data was incomplete by design.

391 Human-AI collaboration as methodological re- 392 quirement

393 This study employed AI assistance not merely as
394 convenience but as methodological necessity. The
395 central finding—that ML systems trained on biased
396 literature perpetuate that bias—could not be ade-
397 quately identified or quantified without AI-assisted
398 analysis. The 120-fold SNR disparity, the 0.2% Best

399 Practices rate, the systematic absence of PWID from
400 trial literature: these patterns emerge from synthesis

401 across thousands of sources that exceeds unaided hu-
402 man cognitive capacity.

403 Primary estimate
404 Moderate
405 This creates a recursive relationship. AI systems
406 are required to identify the bias problem (through pattern recognition
407 across large corpora); AI systems will be required to
408 monitor solutions to the bias problem (through ongoing
409 audits of healthcare AI). Human researchers pro-
410 vide the ethical framework, domain expertise, and ac-
411 countability that AI cannot—but cannot perform the
412 synthesis without AI assistance.

Recent evidence suggests that approximately one-fifth of computer science papers and one-seventh of biomedical abstracts now contain AI-modified content.(29; 32) Detection tools achieve variable accuracy (54–99% depending on context), with consistent bias toward classifying AI-generated content as human-written.(33) This asymmetry means that AI-assisted research is already pervasive but inadequately disclosed, making transparent collaboration frameworks essential.

The ICMJE 2024 guidelines recognize this reality by requiring disclosure of AI assistance in both methods (for data analysis) and acknowledgments (for writing assistance).(25) We have implemented these guidelines comprehensively, providing a model for transparent human-AI collaboration in health services research.

430 ***The signal void***

431 The SNR analysis quantifies what 44 years of exclusion means for ML training: algorithms receive 120⁴⁷²
 432 fold more reliable signal about MSM than PWID. For LAI-PrEP—the modality with highest efficacy—the ratio is undefined because PWID data do not exist.⁴⁷³
 433 PURPOSE-4, if positive, will provide the first PWID⁴⁷⁴
 434 LAI-PrEP signal point; until then, ML systems have literally zero information about LAI-PrEP effectiveness⁴⁷⁵
 435 in this population.⁴⁷⁶

436 The Bangkok Tenofovir Study's wide confidence interval (9.6–72.2%) illustrates the precision problem.⁴⁷⁷
 437 An algorithm trained on this data learns that PWID PrEP efficacy could be anywhere from negligible⁴⁷⁸
 438 to excellent—a signal so noisy it provides minimal guidance.⁴⁷⁹ In contrast, HPTN 083's narrow CI (HR 0.18–0.62) provides precise information about MSM LAI-PrEP effectiveness.⁴⁸⁰

448 This asymmetry is not natural variation; it reflects research investment decisions. The same pharmaceutical companies that conducted multiple large⁴⁸¹
 449 MSM trials chose not to seek PWID indication after⁴⁸²
 450 Bangkok. The signal void was manufactured.⁴⁸³

453 ***Consistency with algorithmic bias literature***

454 These findings align with documented patterns of algorithmic bias in healthcare. Obermeyer and colleagues demonstrated that a widely-used algorithm reduced Black patient enrollment in care management by 62% (from 46.5% to 17.7%) because historical healthcare disparities were encoded in training data.⁴⁵⁵ Our model estimates a comparable magnitude of effect (85% reduction) for PWID.⁴⁵⁶

462 The mechanism is analogous: just as Obermeyer's algorithm learned that Black patients “need” less care because they historically received less care, HIV prevention algorithms learn that PWID are not candidates for prevention because they were excluded from the trials that defined “evidence-based” intervention.⁴⁶³ The bias is not in the algorithm's logic but in its training data—and the training data reflects⁴⁶⁴

470 years of policy decisions.

Chen and colleagues' systematic review of algorithmic bias in electronic health record models found that marginalized populations face compounded disadvantage when multiple bias sources interact.⁴⁷¹ Our nested barrier model operationalizes this insight: PWID face policy barriers, implementation barriers, and algorithmic barriers, each multiplying the effect of the others.

Substance use disorder populations are specifically identified as vulnerable to algorithmic bias. Butt and colleagues note that “people who use drugs are particularly vulnerable to algorithmic bias” given structural healthcare inequalities and societal stigma.⁴⁷² Guerrero and colleagues documented that ML models for substance use treatment exhibit racial disparities that compound existing inequities.⁴⁷³ Our model extends this analysis to HIV prevention, demonstrating how algorithmic bias creates an additional barrier layer beyond those traditionally considered.

The 0.2% problem

Kamitani's finding that 0.2% of HIV prevention literature meets Best Practices criteria has profound implications for healthcare AI.⁴⁷⁴ ML systems trained on this literature learn from 3,965 studies that did not meet quality standards—studies with methodological limitations, null findings, or population-specific results generalized inappropriately.

The Lancet Digital Health's STANDING Together consensus recommendations explicitly address this concern, calling for “proactive evaluation” of AI effects across population groups and transparency regarding dataset limitations.⁴⁷⁵ Our model suggests that for PWID, such evaluation would reveal systematic deprioritization encoded in the statistical patterns of training data.

Implications for healthcare AI governance

The model identifies a governance gap. Current frameworks for healthcare AI focus on algorithmic

510 fairness within deployed systems but do not address
 511 bias embedded in training data at the literature level.
 512 An algorithm can be “fair” by standard metrics while
 513 systematically disadvantaging populations excluded
 514 from the evidence base that defines its training corpora
 515 plus.

516 Addressing this requires:

- 517 • Mandatory population representation audits before training data curation
- 519 • Prospective monitoring for population-level algorithmic discrimination
- 521 • Equity constraints that prevent systematic deprivatization of underrepresented groups
- 523 • Literature-level bias assessment as a precondition for training data inclusion

525 **Limitations**

526 This analysis establishes computational validity;
 527 clinical validity requires prospective validation. The
 528 algorithmic access parameter was derived from literature
 529 representation rather than direct measurement of ML system behaviour. Actual algorithmic discrimination may differ from modeled estimates.

532 Sensitivity analysis demonstrated robustness across plausible parameter ranges (75–90% ME₂ attributable reduction), but the true value is unknown.
 535 The model does not capture heterogeneity within PWID populations or regional variation in ML deployment.

538 **The path forward**

539 Ending manufactured death requires addressing both barrier systems:

541 **Policy reforms:** FDA approval for PWID indication; decriminalization; SSP-integrated delivery; integrated custody PrEP continuity.

544 **Algorithmic reforms:** Equity audits of healthcare AI; mandatory PWID representation in training data; algorithmic impact assessments; governance framework works for healthcare ML.

Policy alone is insufficient. Algorithms trained on 44 years of biased data will attenuate policy gains by 75–90%. Both systems must change.

Conclusion

Computational modeling suggests that HIV prevention failure for PWID reflects an inadvertent leave-one-out cross-validation framework operating at population scale. For 44 years, research systematically excluded PWID from trials; the resulting literature trained ML systems that cannot generalize to a population absent from their training manifold. The 120-fold SNR disparity quantifies this exclusion; the 0/9 Best Practices representation confirms PWID as the held-out test set.

We have named this *manufactured death* because precision matters. The deaths are manufactured not by algorithmic bias but by experimental design: PWID were excluded from the training data that defines “evidence-based” prevention. The algorithm performs correctly—it simply cannot generalize to populations it never encountered. Researchers misattribute this generalization failure to population characteristics (“hard to reach”) rather than training set composition.

The 8,833-fold disparity between PWID and MSM—using identical drug efficacy—is the mathematically inevitable consequence of leave-one-out structure. MSM are in-distribution; PWID are out-of-distribution. Drug efficacy is irrelevant when the deployment population was excluded from training.

These estimates require prospective validation. But the LOOCV structure is not speculative—it is documented in the trial record. Two of eleven trials included PWID. Zero of nine Best Practices studies included PWID. Zero LAI-PrEP participants were PWID. The held-out set is precisely defined.

PURPOSE-4, when complete, will provide the first PWID data point for LAI-PrEP. This is not “expanding access”—it is adding the excluded population to training data. The solution to a leave-one-out prob-

588 lem is including the left-out population, not debiasing
 589 models trained on their absence.

590 Effective prevention exists. Experimental design
 591 excluded PWID from evidence generation. Algorithms learned from that exclusion. The manufacturing of death continues until the training data changes!

594 Declarations

595 **Contributors:** ACD conceived the study, developed the nested barrier model, conducted analysis, and wrote the manuscript.

598 **Declaration of interests:** ACD was previously employed by Gilead Sciences. This manuscript was developed independently.

601 **AI assistance:** This manuscript was developed through structured human-AI collaboration using Claude (Anthropic, 2024–2025). AI assistance was used for: (1) systematic literature search and synthesis; (2) mathematical formalization and validation of probability equations; (3) signal-to-noise ratio calculations from trial data; (4) manuscript drafting with iterative human revision. All factual claims were verified against primary sources. The author (ACD) maintained full responsibility for study design, interpretation, and conclusions. This disclosure follows ICMJE 2024 recommendations.⁽²⁵⁾

613 **Data sharing:** Code available at [repository].⁶⁵¹ Supplementary Files S1–S2 provide AI Readiness assessment and sensitivity analyses.

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