

TruTYPE

Dynamic Pharmacokinetic Intelligence

Scientific Rationale, Patented-Process Framework, and Clinical Application

SCIENTIFIC WHITE PAPER

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Scope of this paper

This document describes the scientific rationale for a proprietary, patented TruTYPE process as represented by the product concept supplied for this paper. It does not reproduce patent claims or confidential implementation details, and it does not independently verify patent scope or validity. The literature cited supports the underlying pharmacology—especially genotype-to-phenotype translation, phenoconversion, drug-drug-gene interactions, and exposure changes—not the proprietary algorithm itself.

Executive Summary

Pharmacogenomics can identify inherited variation in drug-metabolizing enzymes, but germline genotype is only one determinant of a patient's functional metabolic state. Concomitant inhibitors and inducers, disease and inflammatory states, age, smoking, and other factors can create genotype–phenotype discordance—phenoconversion. A systematic review found phenoconversion associated with both extrinsic and patient/disease factors, while clinical pharmacogenetics literature specifically recommends incorporating CYP2D6 inhibitor effects when interpreting genotype in practice [1–4].

TruTYPE is proposed as an automated pharmacokinetic intelligence process that begins with available inherited metabolic information and then evaluates current regimen-related modifiers to produce a dynamic representation of functional drug-processing capacity. The intended clinical concept is simple: genotype is relatively stable, but functional phenotype can change as the medication regimen and patient context change.

Core scientific proposition

A patient's genetically predicted metabolizer phenotype may not equal the patient's current functional phenotype. Therefore, medication review and PGx interpretation can be strengthened by reassessing clinically supported phenoconversion whenever the regimen changes.

The scientific foundation is well established for selected pathways, particularly CYP2D6. University of Florida investigators have published a clinical tutorial describing a standardized phenoconversion calculator, and recent literature continues to emphasize phenoconversion assessment in polypharmacy [2,5]. FDA also states that CYP- and transporter-mediated interactions can change systemic exposure, including AUC and Cmax, potentially causing adverse reactions when exposure rises or loss of efficacy when it falls [6].

The distinctive TruTYPE proposition is automation across the medication regimen: repeatedly converting static genetic and drug information into an updated, patient-specific pharmacokinetic map that can feed medication reconciliation, PGx interpretation, TruRISK risk stratification, and prospective medication evaluation. That proprietary integration should be clinically validated independently from the individual pharmacologic rules on which it relies.

1. Clinical Need: Genotype Is Not the Whole Phenotype

PGx testing answers an important question: what metabolic function is predicted from inherited genetic variation? It does not, by itself, guarantee that the predicted phenotype represents enzyme activity under the patient's present medication and physiologic conditions. Phenoconversion describes a clinically important mismatch between genotype-predicted and functional phenotype. CYP inhibition can reduce functional activity; induction and other factors can shift activity in the opposite direction [1–5].

This distinction becomes increasingly important in polypharmacy. Malki and Pearson describe drug-drug-gene interactions as combined genetic and medication effects capable of markedly altering drug concentrations. Their framework includes inhibitory, induction, and phenoconversion interactions and argues that conventional DDI assessment can miss genetic variation that modifies interaction severity [7].

Static vs. dynamic information

Genotype: inherited and generally stable.

Medication regimen: changeable.
Enzyme inhibition/induction: changeable.
Functional metabolic phenotype: therefore potentially changeable.
TruTYPE: intended to represent this current, dynamic pharmacokinetic state.

2. Scientific Foundation

2.1 Cytochrome P450 activity and drug exposure

Drug exposure depends on absorption, distribution, metabolism, and elimination. CYP enzymes metabolize many medications, and inhibitors or inducers can alter the clearance of substrate drugs. FDA's current clinical interaction resources explicitly connect CYP/transporter interactions with changes in AUC, Cmax, and steady-state concentration and with potential toxicity or reduced efficacy [6].

2.2 Genotype-to-phenotype translation

PGx frameworks translate alleles into activity values and predicted phenotypes. For CYP2D6, consensus work from CPIC and the Dutch Pharmacogenetics Working Group standardized activity-score translation to improve consistency across laboratories and clinical implementation [8]. That genotype-derived phenotype is an essential starting point—but it can require modification when a clinically meaningful inhibitor is present.

2.3 Phenoconversion

A systematic review of 27 studies reported lower-metabolizer phenoconversion with CYP-inhibiting drugs and with factors including age, cancer, and inflammation; higher-metabolizer shifts were reported with inducers and smoking. The authors emphasized that genotype-phenotype discrepancies are real while also noting that the magnitude and clinical outcome consequences require further study [1].

2.4 Clinical implementation is feasible

Cicali and colleagues published a tutorial describing how a health-system precision medicine program incorporated CYP2D6 phenoconversion into clinical pharmacogenetics. Their method begins with a genotype-based activity score, evaluates concomitant CYP2D6 inhibitors, adjusts the score according to inhibitor strength, and then derives a clinical phenotype [2]. This is important evidence that automated or semi-automated phenoconversion assessment is not merely theoretical.

2.5 Polypharmacy and drug-drug-gene interactions

Polypharmacy can create multiple simultaneous effects on metabolic pathways. A 2025 review specifically addresses models for estimating joint drug-interaction and genetic effects and concludes that phenoconversion assessment is especially important for personalized therapy under polypharmacy conditions [5]. Drug-drug-gene literature similarly supports considering genetic variation and interacting medications together rather than as independent silos [7,9].

3. Proposed TruTYPE Process Framework

The following framework describes the intended clinical logic without disclosing proprietary implementation details. Each automated rule should be traceable to a defined evidence source and should distinguish established rules from product-specific inference.

Step 1 — Build the patient's medication map

Identify the active regimen, dose and relevant route when available, and map each medication to clinically supported metabolic enzymes and transport pathways.

Step 2 — Establish inherited function when PGx is available

Translate genotype into guideline-consistent predicted activity/phenotype. If PGx is unavailable, the system should explicitly distinguish unknown inherited function from normal function rather than assume equivalence.

Step 3 — Identify functional modifiers

Evaluate the regimen for clinically recognized inhibitors and inducers and, where validated, other patient or disease factors capable of modifying pathway activity.

Step 4 — Reconcile genotype with current modifiers

Apply evidence-based phenoconversion logic to derive an adjusted or functional phenotype. The evidence source and assumptions should remain auditable.

Step 5 — Map affected drugs to the functional pathways

Determine which current medications depend materially on pathways whose functional activity has changed, recognizing that substrate fraction, alternative pathways, active metabolites, and therapeutic index influence clinical importance.

Step 6 — Generate a current pharmacokinetic map

Present the likely direction of altered processing—such as reduced, expected, or increased functional activity—without representing inferred exposure as a measured plasma concentration.

Step 7 — Recalculate when the regimen changes

Adding, stopping, or changing a medication can change inhibition/induction and therefore the functional map. The defining clinical concept is continual reassessment rather than a one-time static report.

4. TruTYPE With and Without PGx Testing

Clinical state	What TruTYPE can evaluate	Important limitation
PGx available	Inherited activity plus current medication-related phenoconversion	Accuracy depends on genotype quality, translation rules, inhibitor/inducer evidence, and pathway relevance.
PGx not available	Medication-driven inhibition/induction and known pathway traffic can still identify acquired PK pressure	Inherited baseline activity is unknown and should not be represented as genetically normal.
Regimen changes	Reassess functional pathway state and affected substrates	The new map is an inference until supported by clinical response or measured concentrations where

		appropriate.
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5. Clinical Applications

Medication reconciliation

A medication list can be transformed from a static inventory into a pathway-level review. Clinicians can see not only which drugs are present, but which metabolic routes may be under inhibition or induction and which substrates may consequently deserve closer attention.

PGx interpretation

TruTYPE can place a genetic result into current medication context. This is especially relevant when a genotype-predicted normal or intermediate phenotype is functionally altered by an inhibitor.

New medication evaluation

Before adding a drug, the clinician can evaluate whether the proposed medication uses a pathway already affected by the regimen and whether the new drug itself could alter processing of existing medications.

Longitudinal medication management

Because the functional phenotype can change when drugs are added or removed, TruTYPE can be recalculated over time. This supports the concept of PGx as reusable biological information rather than a one-time report.

Transitions of care and polypharmacy

Admission, discharge, specialist prescribing, and pharmacy reconciliation are periods when regimens change quickly. A dynamic pathway map may help organize medication-review attention, subject to prospective validation.

Foundation for TruRISK and TruSELECT

TruTYPE can serve as the pharmacokinetic layer for downstream processes: TruRISK can use current PK context when prioritizing established medication risks, while TruSELECT can compare prospective alternatives against the patient's current regimen.

6. What TruTYPE Should and Should Not Claim

Scientifically supportable positioning	Requires additional validation / caution
Integrates genotype and clinically supported non-genetic modifiers of metabolism.	Does not directly measure enzyme activity or plasma drug concentration.
Can identify circumstances consistent with phenoconversion.	Should not imply that every inhibitor produces the same effect for every substrate or patient.
Can dynamically reassess the regimen when medications change.	Should not equate an inferred functional phenotype with a guaranteed clinical outcome.
Can provide PK context for medication review and PGx interpretation.	Absolute exposure changes or adverse-event probabilities require drug-specific quantitative

	evidence and validation.
Can operate with PGx information when available and still map medication-driven pathway effects without it.	Without PGx, inherited metabolic function remains unknown.

7. Proposed Clinical Validation Program

A patented process and a scientifically plausible process are not automatically a clinically validated process. A staged program can establish the incremental value of TruTYPE.

- Analytical verification: confirm medication-to-pathway mapping, inhibitor/inducer classification, genotype translation, rule versioning, and reproducibility.
- Concordance validation: compare TruTYPE-adjusted phenotypes with expert manual phenoconversion assessment using guideline-based test cases.
- PK validation: where datasets permit, test whether TruTYPE classifications correlate with measured concentrations, AUC, clearance, or validated metabolic ratios.
- Retrospective outcomes: test associations with exposure-related adverse effects, dose changes, discontinuation, treatment failure, or healthcare utilization.
- Prospective observational study: generate TruTYPE outputs without directing therapy and measure whether altered functional states predict clinically meaningful outcomes.
- Clinical utility study: determine whether access to TruTYPE improves medication-review efficiency, PGx interpretation, medication selection, or preventable adverse-event rates.

8. Testable Scientific Hypotheses

- Genotype-only phenotype assignment will misclassify a clinically meaningful subset of patients receiving strong or moderate inhibitors compared with phenoconversion-adjusted phenotype.
- TruTYPE-adjusted functional phenotype will correlate more strongly with selected drug-exposure measures than genotype-predicted phenotype alone.
- The incremental value of dynamic phenoconversion assessment will increase with medication burden and the number of interacting metabolic pathways.
- Recalculation after medication addition or discontinuation will identify clinically meaningful changes in functional metabolic status that a static PGx report cannot represent.
- For selected exposure-sensitive drugs, TruTYPE-informed review will identify a higher-risk subgroup than conventional pairwise DDI screening alone.

9. Scientific and Clinical Guardrails

- Use authoritative, version-controlled sources for genotype translation and inhibitor/inducer classifications.
- Keep measured concentration, predicted exposure, and functional phenotype as distinct concepts.
- Do not assume that absence of a PGx result means normal inherited function.
- Account for substrate-specific pathway contribution and alternative clearance routes where evidence supports doing so.
- Clearly label uncertain or conflicting evidence.

- Preserve clinician interpretation; the output should provide pharmacokinetic context rather than imply certainty.
- Validate each expansion beyond well-characterized phenoconversion rules before assigning strong clinical weight.

10. Conclusion

TruTYPE is grounded in a clinically recognized problem: genetically predicted metabolic phenotype can be modified by the patient's current medications and other factors. Phenoconversion is supported by systematic review evidence, clinical implementation literature, CPIC-associated methods, FDA interaction science, and drug-drug-gene research [1–9].

The proposed TruTYPE innovation is to automate this reasoning across the medication regimen and update it whenever relevant inputs change, producing a dynamic pharmacokinetic map for clinical review. The strongest near-term scientific positioning is therefore not that TruTYPE measures drug levels or guarantees outcomes, but that it systematically integrates established pharmacogenetic and drug-interaction evidence to estimate current functional metabolic context.

Proposed scientific positioning statement

TruTYPE transforms static pharmacogenetic and medication information into a dynamic representation of the patient's current drug-processing environment—helping clinicians interpret how inherited function and the present medication regimen may jointly influence pharmacokinetic risk.

References

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Evidence Note

The references above support the underlying scientific principles. They should not be cited as independent validation of the proprietary TruTYPE process. Before publication, investor diligence, regulatory submission, or peer-reviewed use, the final implemented algorithm and patent claims should be reviewed against the exact wording of this paper and the reference list should undergo formal bibliographic verification.