

Cell Response Discovery

Drug Repositioning

Novel Drug Targets

Mechanism Of Action

TAHOE Tahoe 100M

xaira Atlas-X/Orion

Virtual Cell Challenge

Jiang2024 H1 Nadig

96,189,749
cells

6,925
pathways

95,944
perturbations

379
chemicals

58
cell lines

69,716
genes

18
diseases

16
tissues

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Cell Response Discovery Software

Explore, compare, and interpret perturbation data across experiments, pathways, and diseases without pipelines, infrastructure, complexity, or specialized expertise.

CHALLENGES

From Perturbation Data to Understanding is Hard



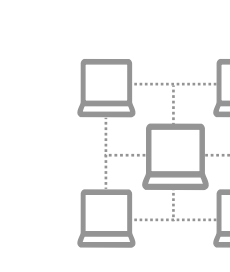
Data fragmented across experiments, modalities, and teams

Perturbation datasets spanning gene targets, compounds, and disease models are disconnected, limiting cross-study comparison and integrative analysis.



Interpreting results requires specialized computational biology expertise

Extracting insights requires coding skills and deep understanding of data structures, statistical models, and algorithms.



Infrastructure complexity slows analysis

Large-scale perturbation data requires sophisticated, compute-intensive pipelines that are difficult to scale across cloud and HPC environments.



Connecting results to mechanisms and literature is time-consuming

Linking computational findings to molecular pathways and prior studies requires extensive manual curation and domain expertise.

protoXell is a purpose-built scientific software designed to tackle these challenges by transforming perturbation data into interpretable biological insight.

VALUE PROPOSITION

protoXell: A Unified System for Mechanistic Insight

Unified Access

Explore perturbation data across studies, conditions, and datasets—no fragmentation

Comparative Insight

Uncover shared and distinct molecular mechanisms across biological responses

AI-Powered Interpretation

Interpret results with AI & support virtual cell modelling, facilitating mechanism-driven hypotheses

Speed at Scale

Move from raw data to actionable insights in minutes, not months, & eliminate technical bottlenecks.

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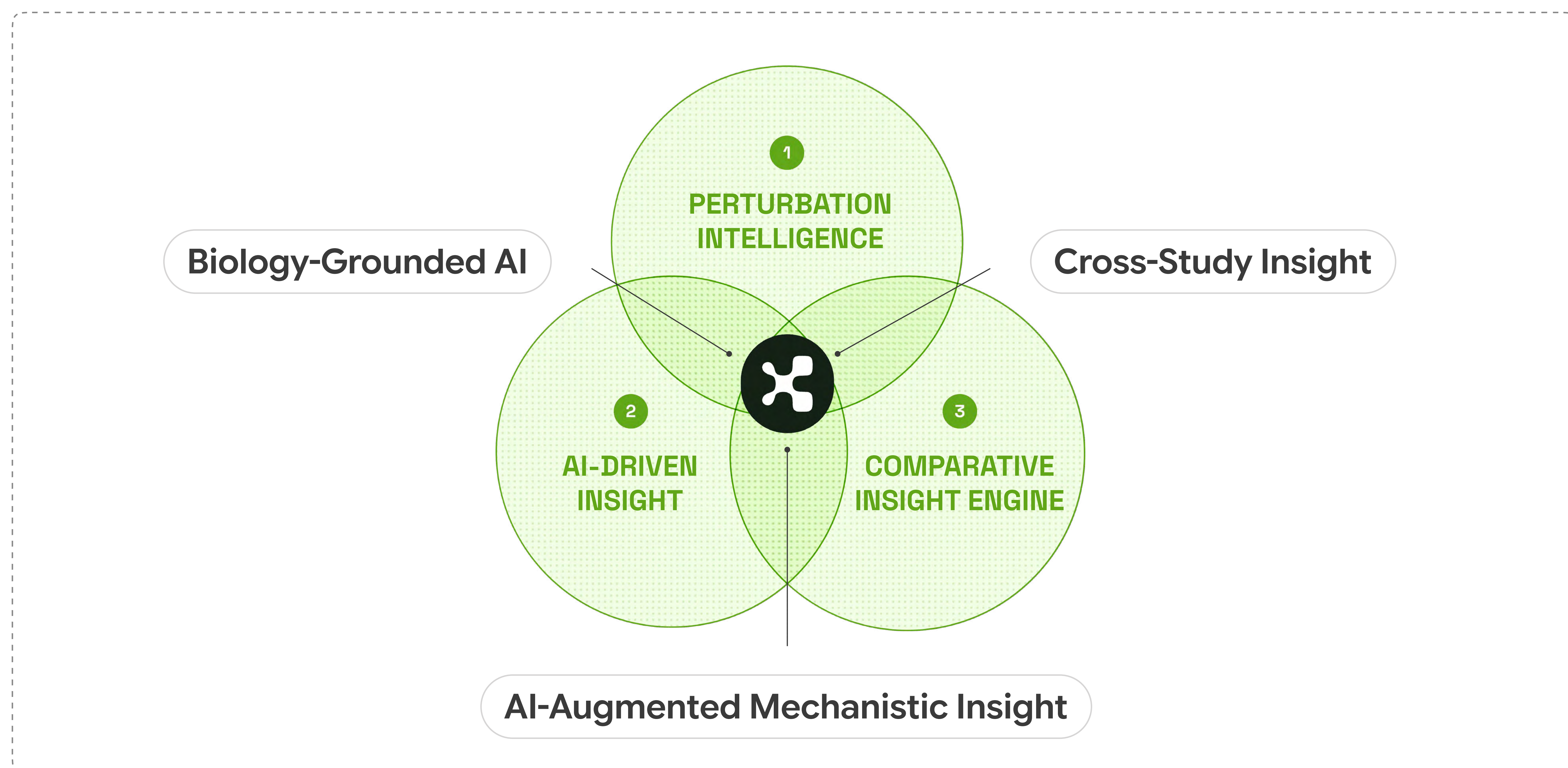
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HOW IT WORKS

protoXell's three core capabilities—**Perturbation Intelligence**, **Comparative Insight Engine**, and **AI-Driven Insight**—converge at their intersection to deliver primary values.

Perturbation Intelligence gives you unified access across studies and conditions. **Comparative Insight Engine** uncovers shared and distinct mechanisms. **AI-Driven Insight** translates those connections into actionable mechanistic hypotheses.



1 PERTURBATION INTELLIGENCE

- Access curated perturbation catalog
- Integrate public + proprietary data
- Query across experiments at scale

2 AI-DRIVEN INSIGHT

- Interpret results with AI
- Support virtual cell modeling
- Power LLM-driven agents

3 COMPARATIVE INSIGHT ENGINE

- Compare perturbations
- Uncover biological relationships
- Reveal mechanisms of action

Together, they compress your discovery timeline from months to minutes, eliminating fragmentation and technical bottlenecks.

EXAMPLE INSIGHT

Unexpected Drug Relationships

The Discovery:

Saquinavir (HIV protease inhibitor) and β -adrenoceptor agonists—Norepinephrine and Vilanterol—exhibit similar transcriptional signatures, despite distinct pharmacological mechanisms.

Why This Matters:

This counterintuitive connection reveals previously masked biological pathways shared across different therapeutic classes.

What This Enables:

- **Mechanism Insight:** Uncover non-obvious pharmacological effects
- **Drug Repurposing:** Identify promising candidates for clinical repositioning
- **Therapeutic Innovation:** Accelerate discovery of unexpected clinical applications

Validation:

Independent confirmation by researchers at Tahoe demonstrates the robustness of this finding—showcasing protoXell's capacity to detect complex biological relationships beyond traditional pharmacological frameworks.