



**CERTAINTY
DISCOVERY**

CERTARA[®] |  Chemaxon

Integrating Artificial Intelligence into the Drug Discovery Pipeline

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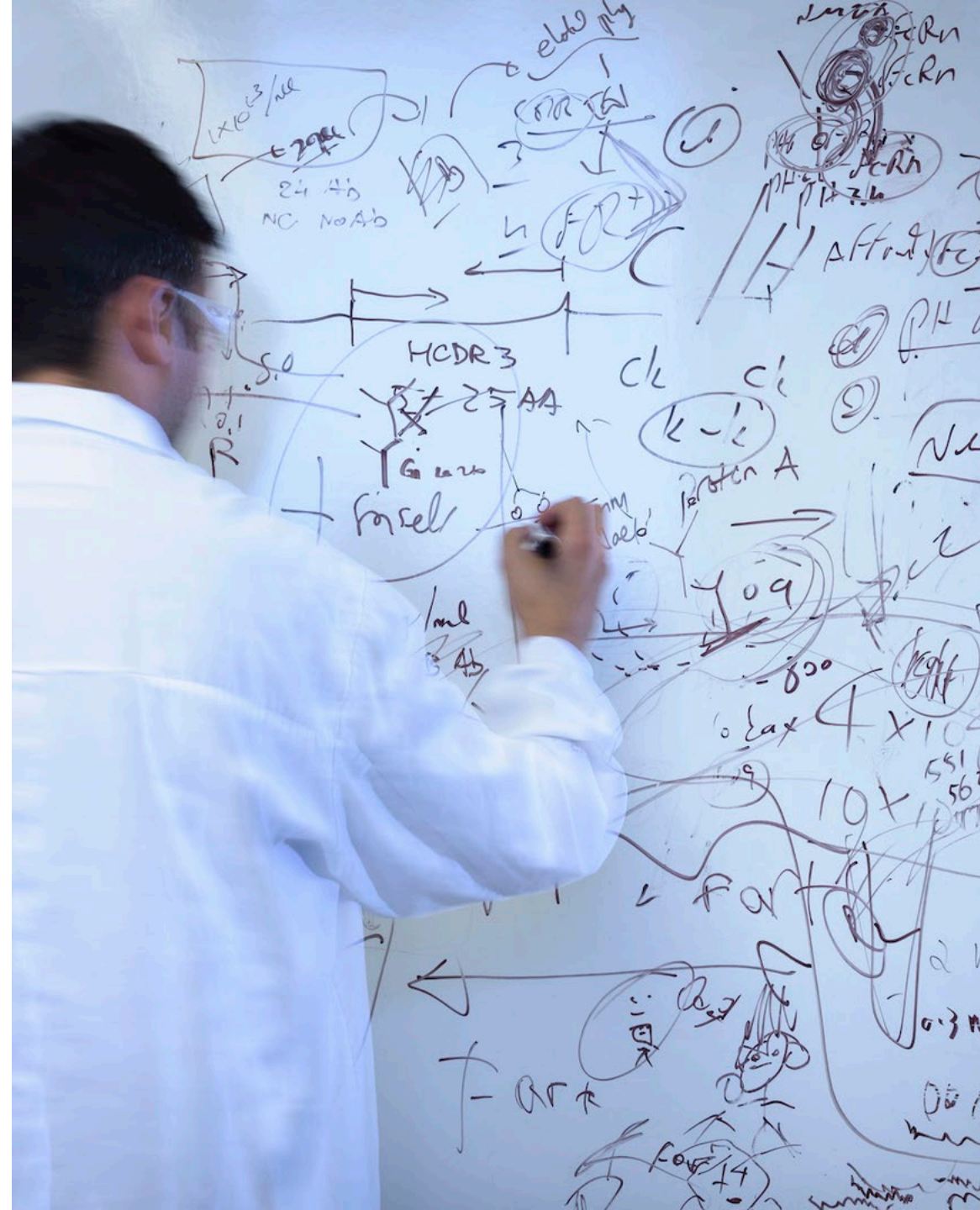
Scaled AI and Chemistry

(SAIC) Tech Lead

Integrating AI into the Drug Discovery Pipeline

Gian Marco Ghiandoni

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Certainty Discovery
Design Offices Frankfurt Wiesenhüttenplatz, Frankfurt, Germany



Myself

Gian Marco Ghiandoni (Giammy)

CheMLOps Lead | Associate Principal Engineer

- 6 years at AstraZeneca R&D IT
- Currently within the Augmented DMTA platform (ADMTA)
- Leading a team of scientific developers and chemistry/ML engineers
- Side-by-side with the business – we create capabilities for the scientists
- Disclaimer - ask Bill if you want to know why we run so many calculations in D360!



Contents:

- Theory vs. Practice, DMTA
- Predictive Insight Platform (PIP)
- PIP-D360 interaction
- Extended PIP functionalities in D360
- Vision

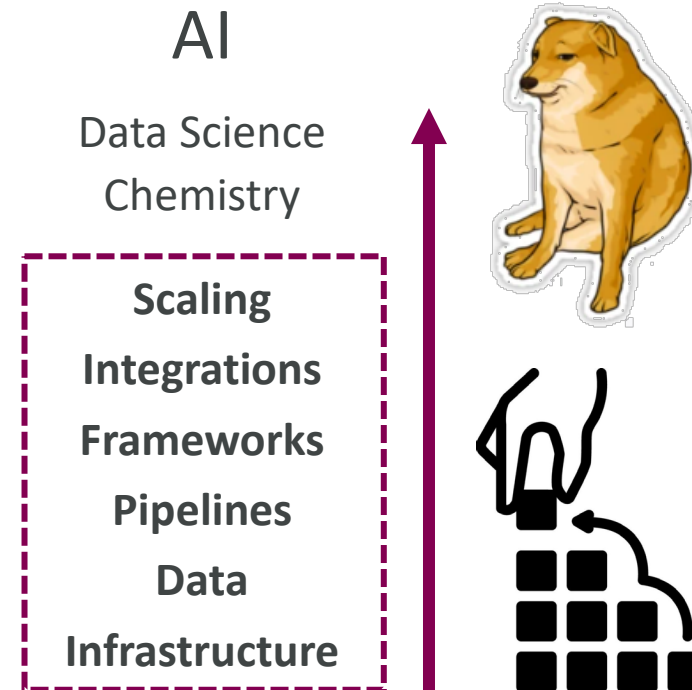


AI in Drug Discovery: Theory vs. Practice

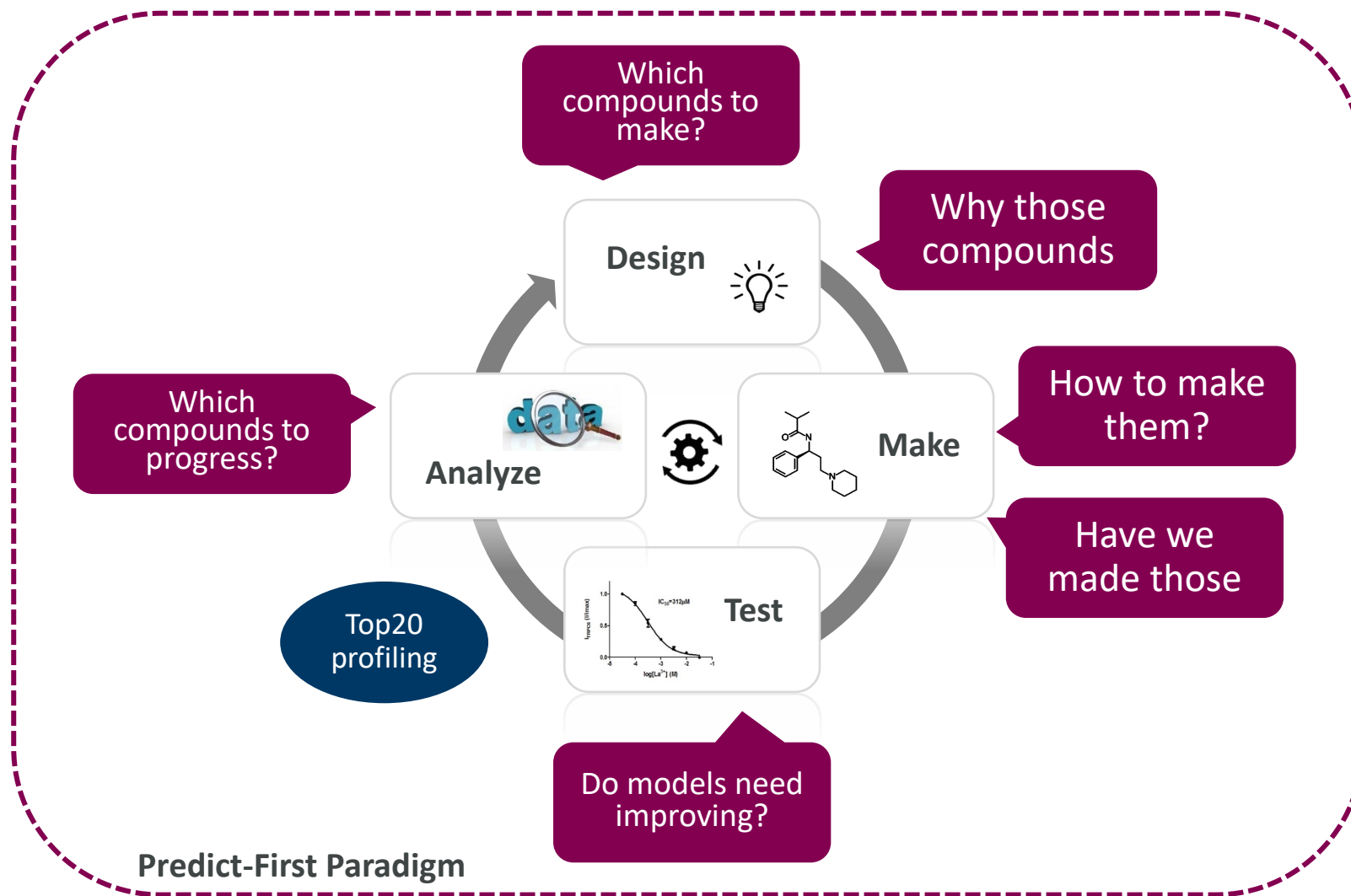
Theory: AI revolution



Practice: There is a lot of work to do...

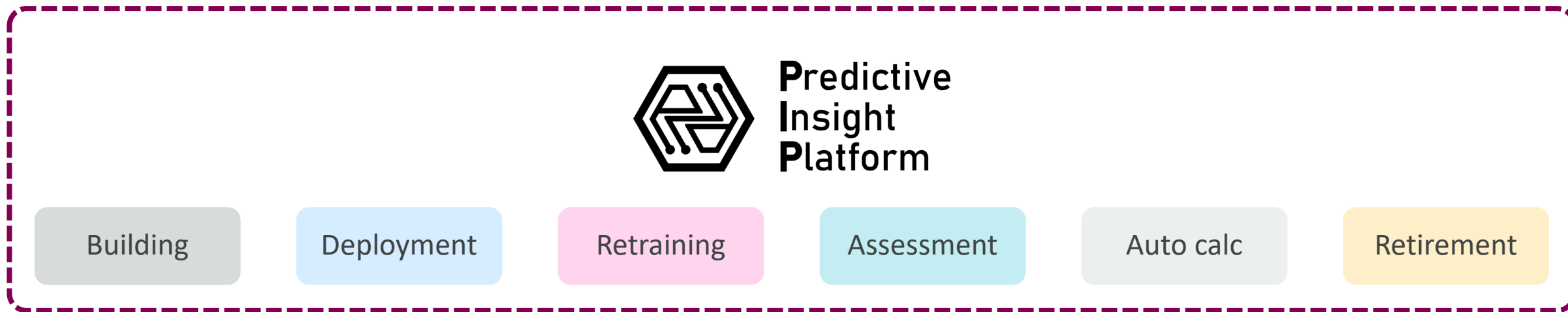


Predictive AI in the DMTA cycle

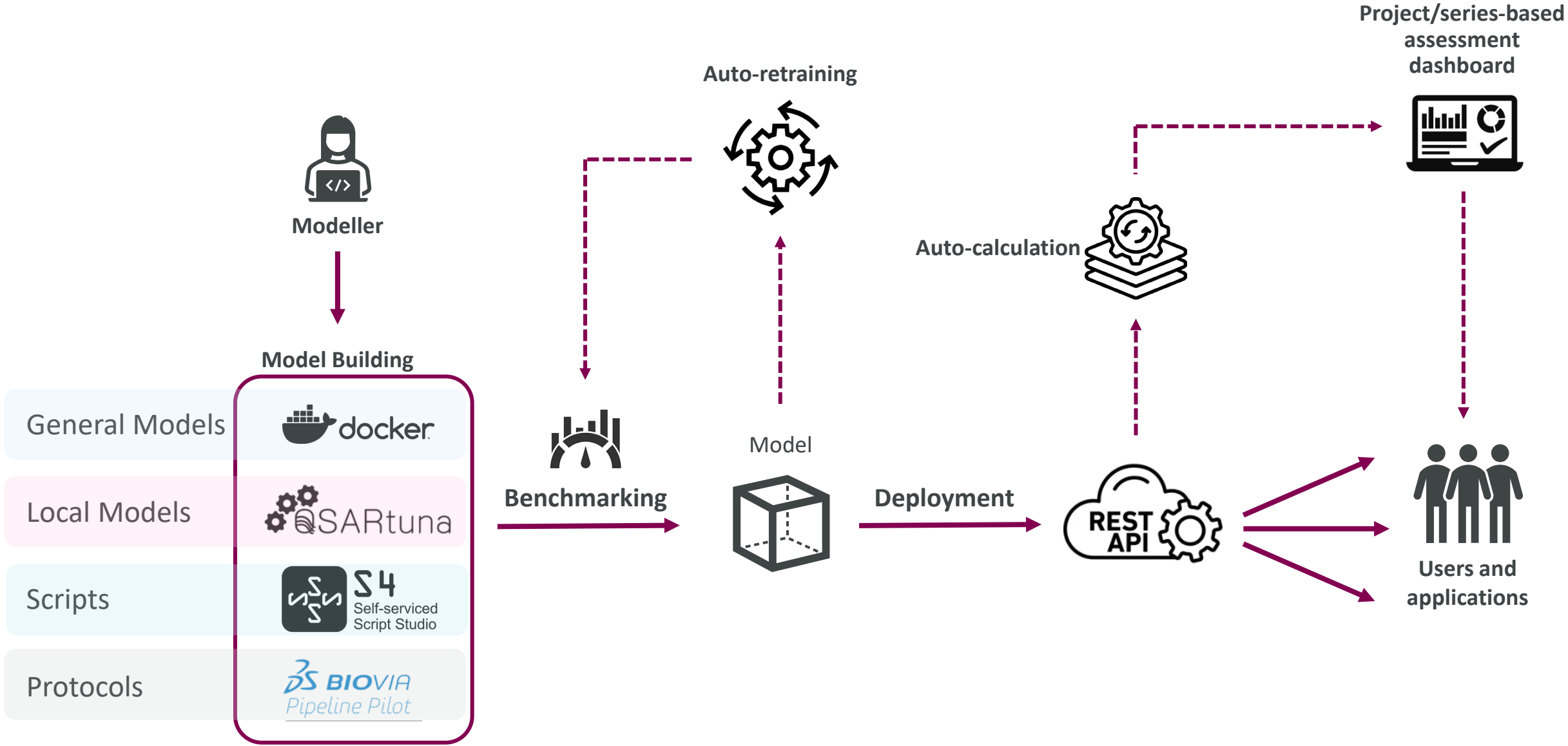


The Predictive Insight Platform (PIP)

- The Predictive Insight Platform (PIP) is a cloud-native platform for AI/ML drug discovery at AZ
- Hosting more than 400 models for small-molecule and new modality property prediction
- Integrated with 15+ chemistry applications
- Critical for operational systems - sample management and compound registration
- Enables “Predict-First” at AZ with almost 500M calculations being run every month



How PIP works



PIP augments all aspects of the discovery pipeline



De novo generation

PhysChem, in vitro
ADME, synthetic
accessibility



Hit-to-lead

Loose MPO, in
vivo ADMET
predictions

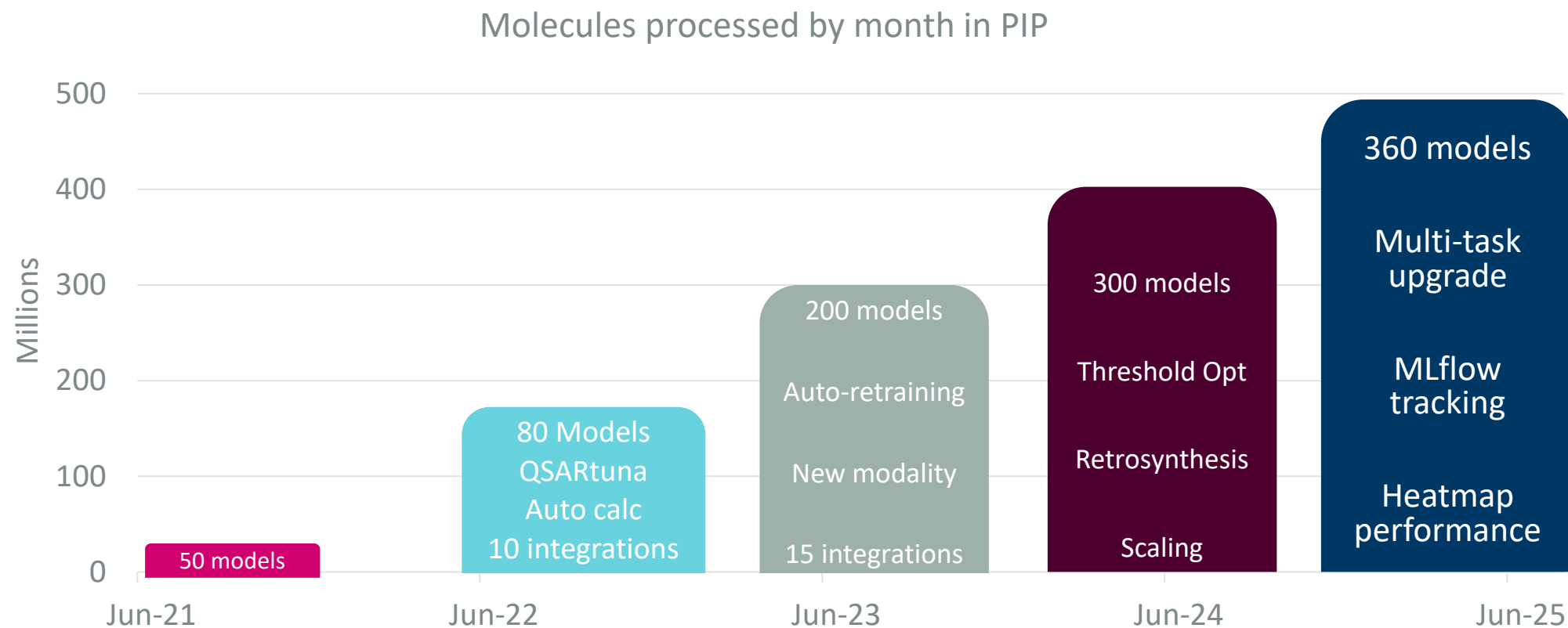


Lead optimisation

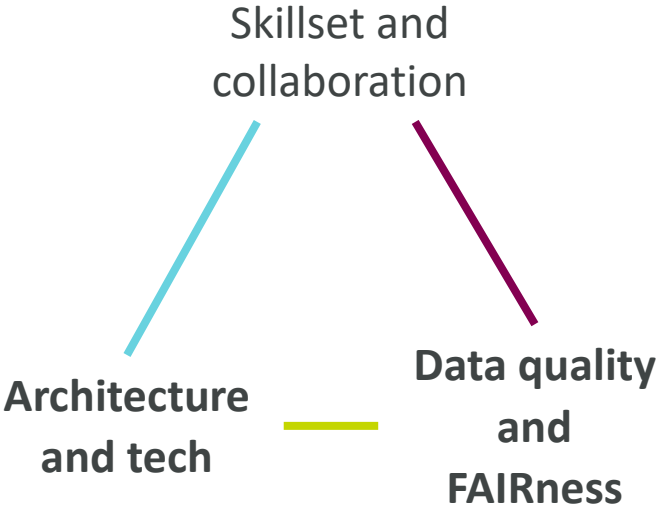
Strict MPO, safety,
translation into
human



Evolution of PIP



Recipe for success



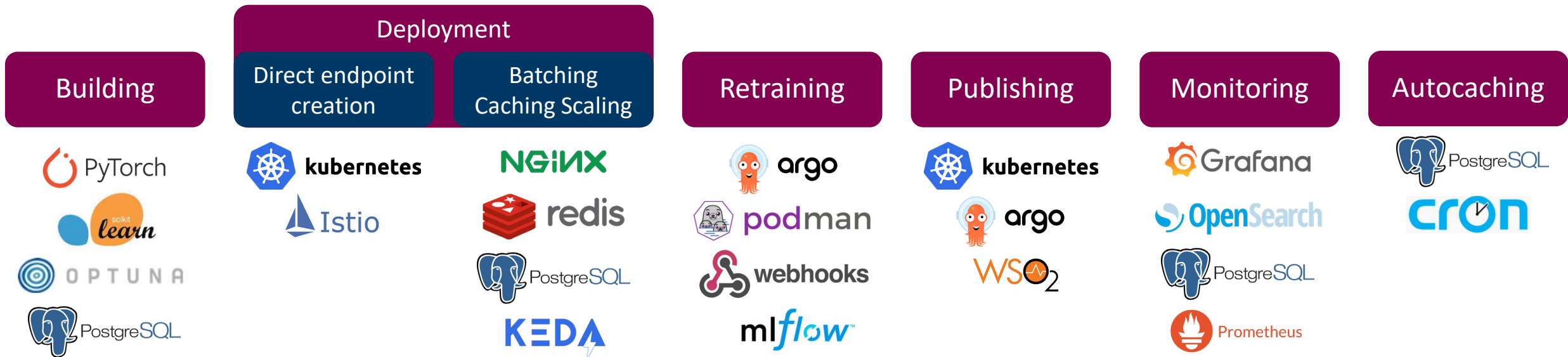
Architecture and tech



 Sustainable development



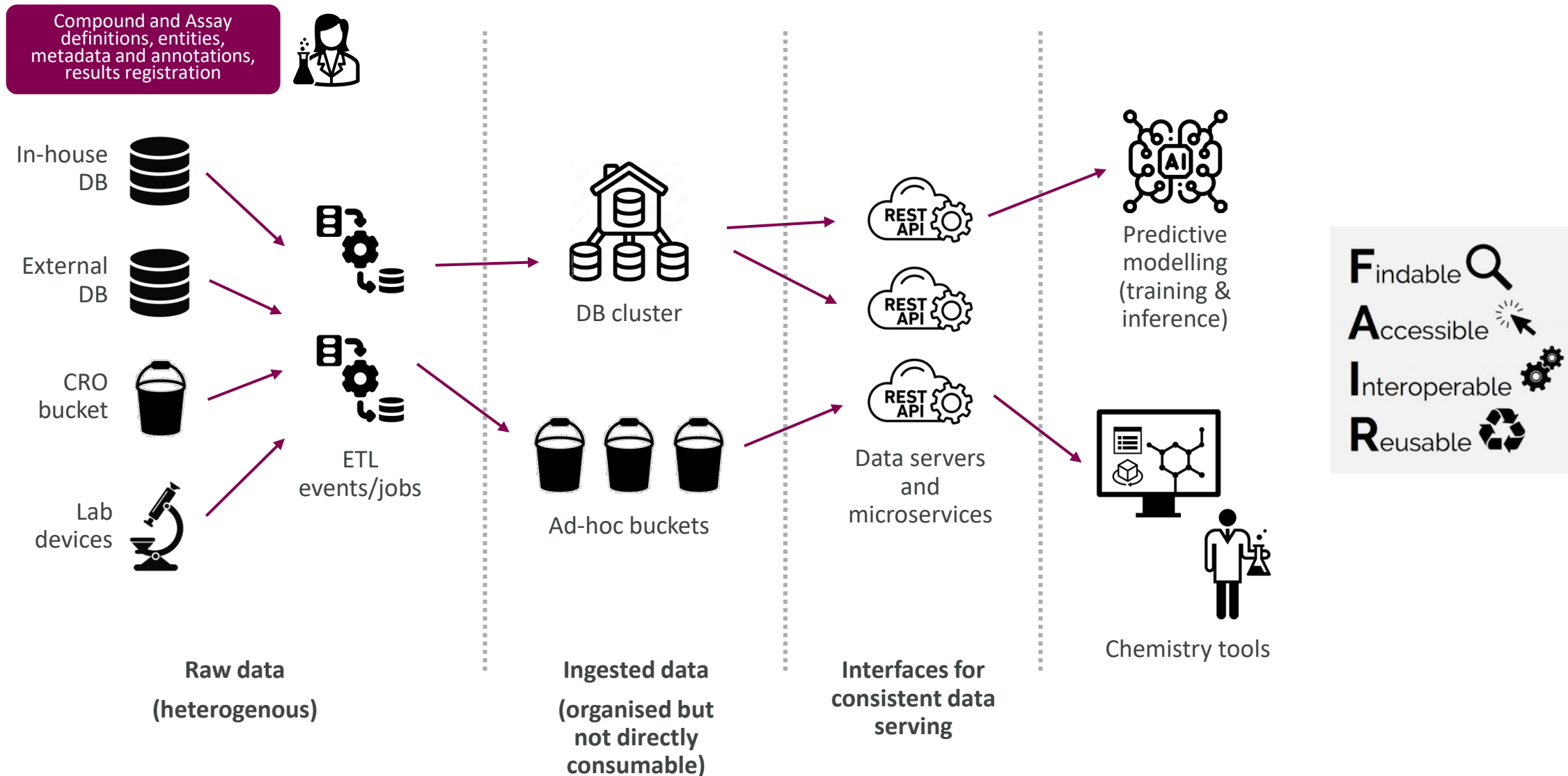
Architecture and tech: Hybrid technologies



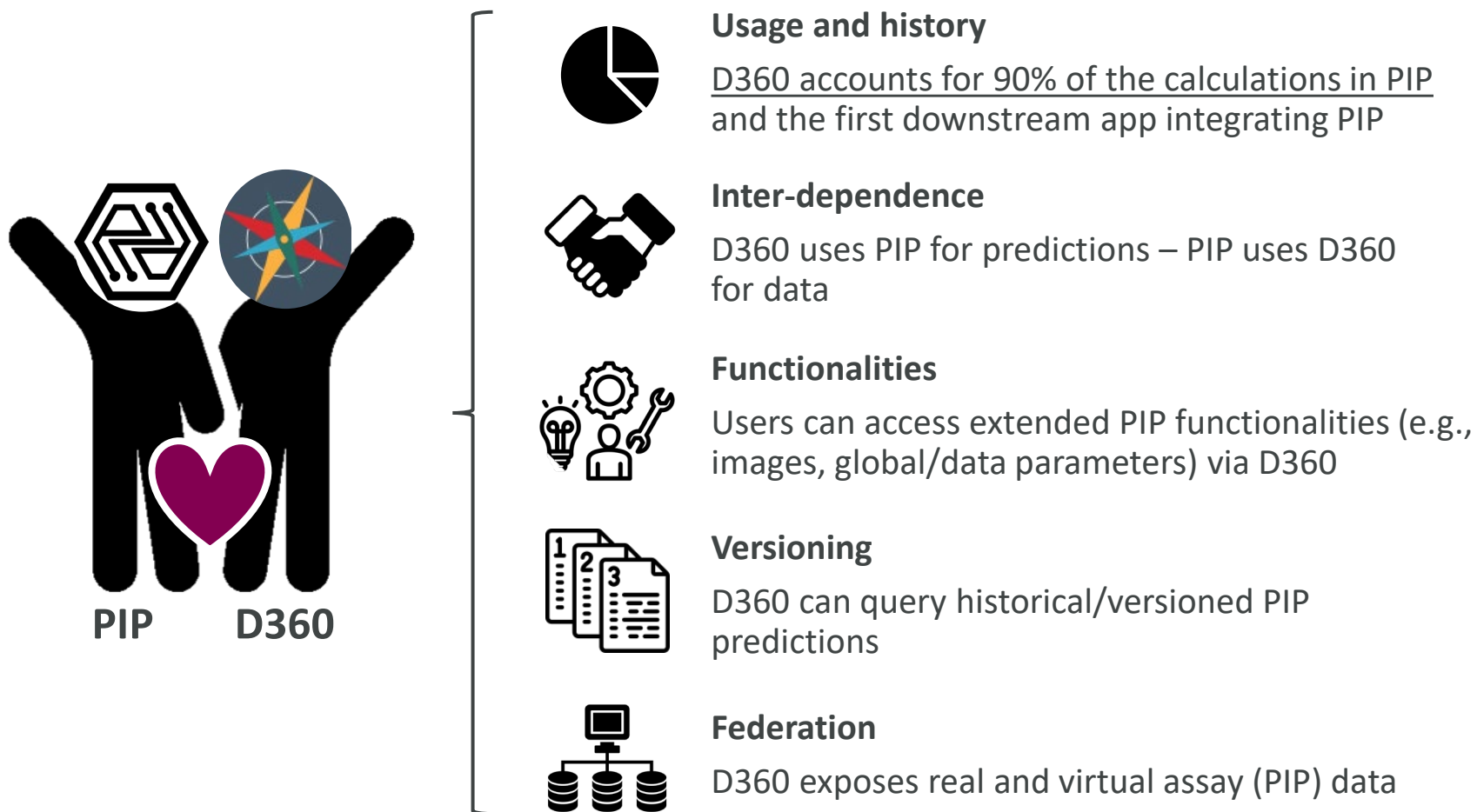
The platform is implemented using a blend of proprietary and open-source technologies



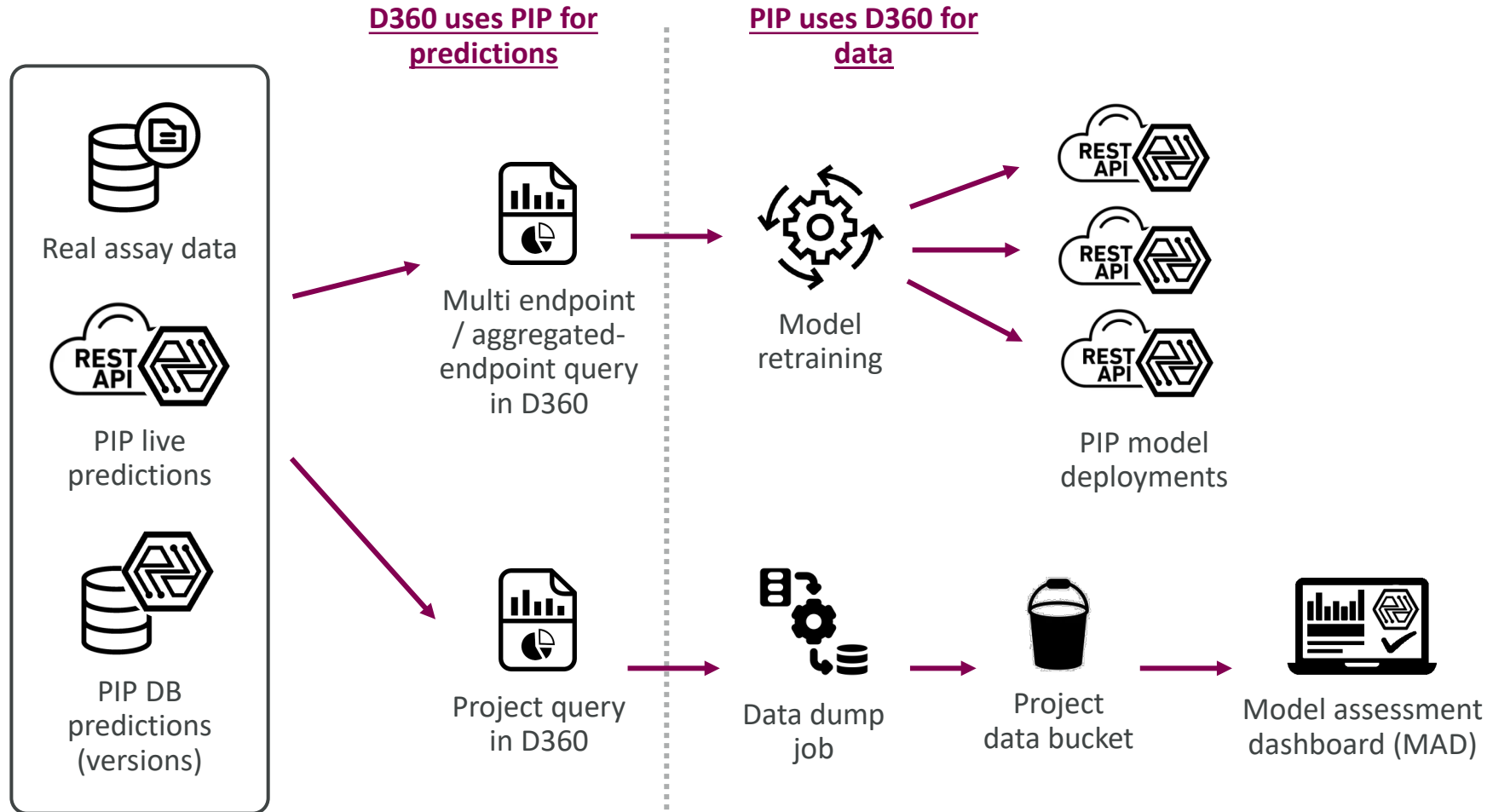
Data quality and FAIRness



Interaction between PIP and D360

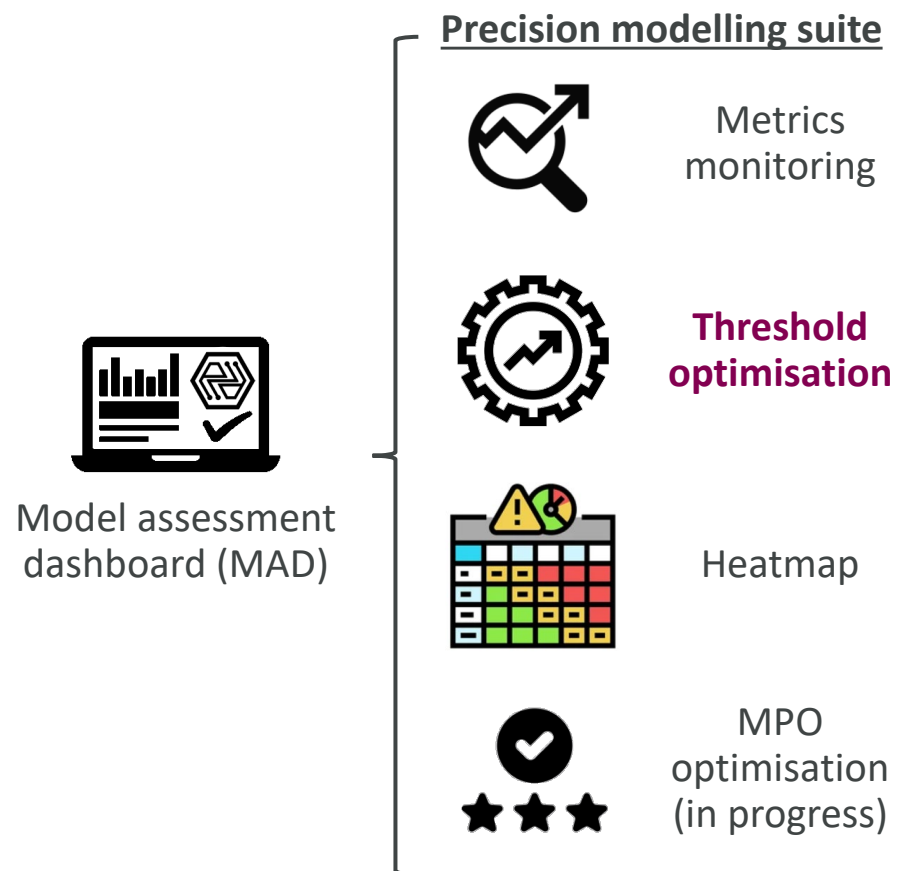


Inter-dependence, Federation, and Versioning



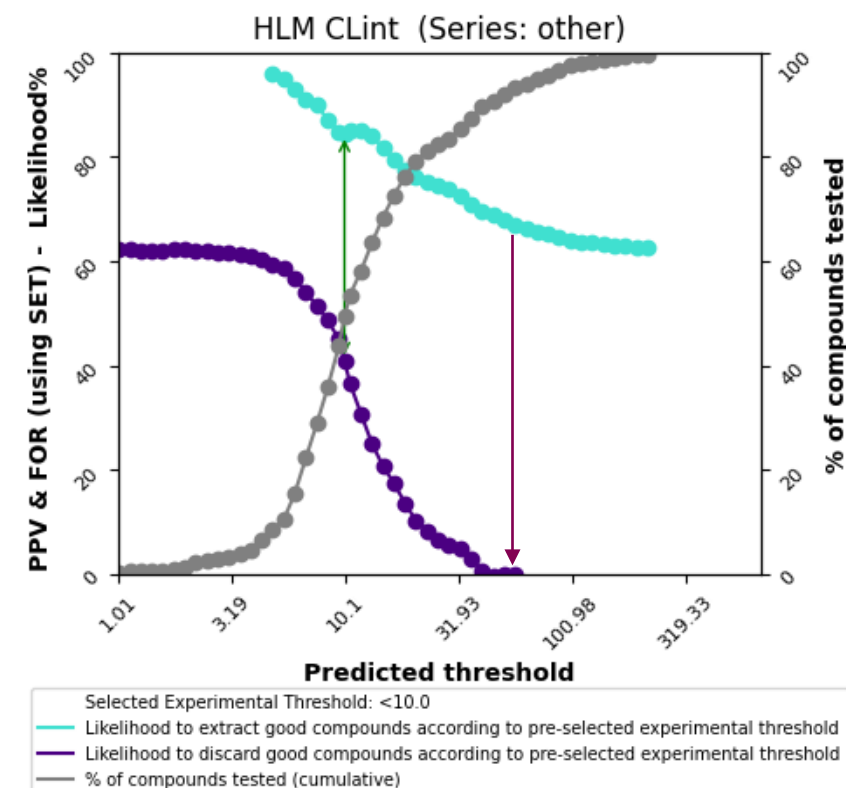
Model assessment dashboard:

Built outside D360 but uses it as a data source



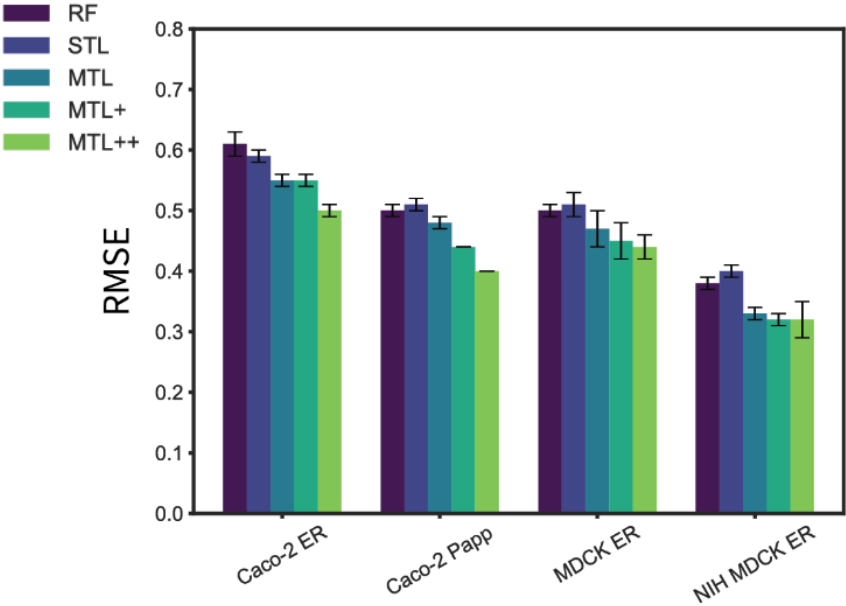
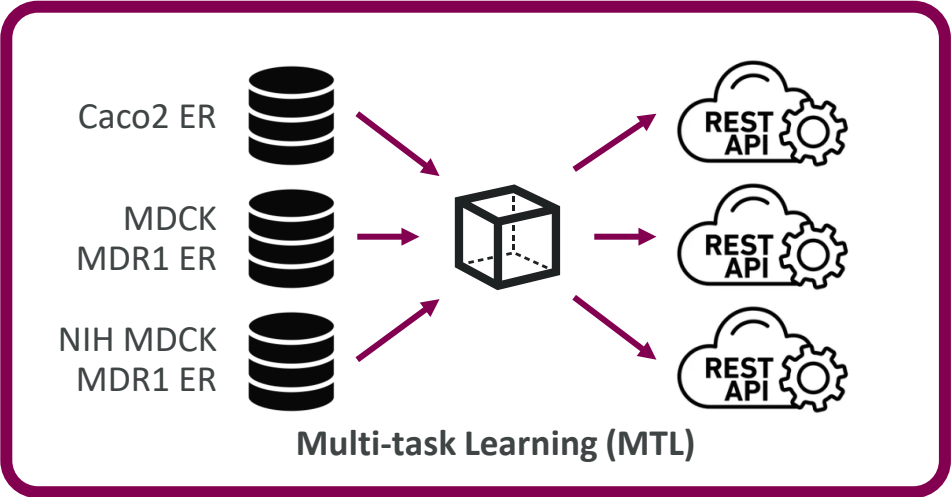
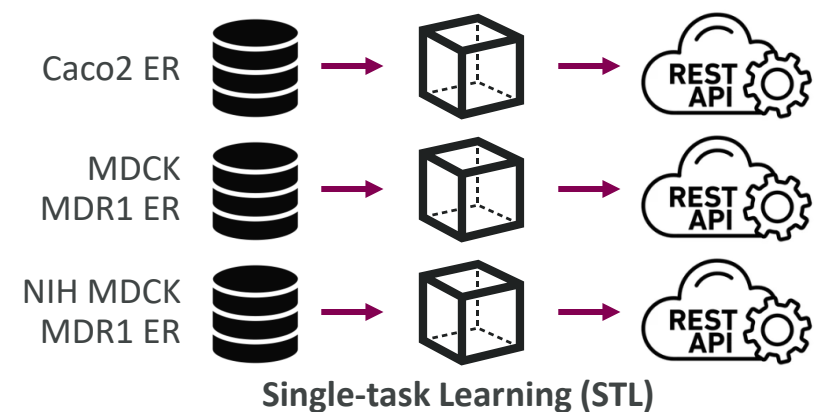
What predicted threshold gives best enrichment for Series: other

	Predicted Threshold	PPV %	FOR %
Selected Experimental Threshold	10.0	84	41
Recommended Threshold	45	68	0



Extended functionalities:

Making better predictions: Multi-task modelling pipeline



1. 20% overall increase of accuracy across 15 global ADME-Safety endpoints
2. Enhancement of low-data endpoint accuracy



Extended functionalities:

Understanding predictions: Image explanations

Atomic-level explanation

PIP Images

Available Models
☒ Jazzy Descriptors

Selected Compounds
☒ CHEMBL453920
☒ CHEMBL2377854

Fetching Images... Clear

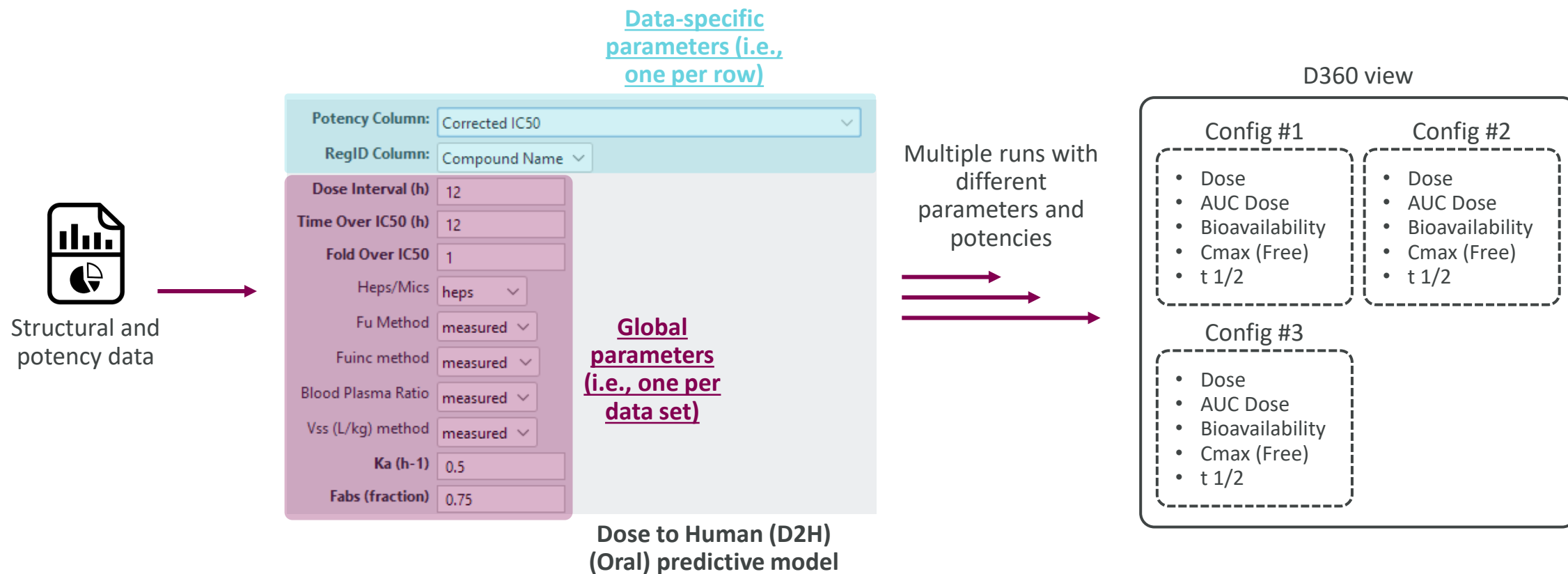
Molecular-level prediction

Spreadsheet Details									
		Structure	Header	pIC50	SMILES_ISOMERIC	Jazzy Descriptors HB Acceptor Strength	Jazzy Descriptors HB Donor Strength	Jazzy Descriptors HB Carbon Donor Strength	Jazzy Descriptors HB Hetero Donor Strength
1:	<input checked="" type="checkbox"/>		CHEMBL453920	4.022		2.640	5.140	3.630	1.510
2:	<input checked="" type="checkbox"/>		CHEMBL2377854	4.000		2.990	7.000	5.630	1.370



Extended functionalities:

Augmenting predictions: Global and data-specific parameters



Vision – What are we missing?

- 1. Efficient interaction with slow & non-cacheable & non-batch-able calculations, e.g.,**
 - Calculations that heavily rely on freshly measured data (D2H)
- 2. Improved prediction DB search also allowing multi-type IDs, e.g.,**
 - Optimisation of federated queries between Virtual (remote) and Registered (local) compound DBs
- 3. Visualisation of structure-processing calculations, e.g.,**
 - Calculations using sequence inputs
 - Enumerations (one-to-many outputs)
- 4. Better management of resources, e.g.,**
 - Identification of queries that run unnecessary calculations
 - Better UX for breaking events in queries (e.g., effect of schema changes to equations)



Acknowledgements

Augmented DMTA Platform

- Nagarajan PS
- David Riley
- Evgenii Maksimov
- Vladimir Chugunov
- Nick Tomkinson
- Susan Leung
- Arthur Garon
- Prakash Rathi
- Rajendra Kumar (ex AZ)

Stakeholders

(Oncology & BioPharma R&D)

- Emma Evertsson
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- Jenny Viklund
- Greg Kauffman
- Susanne Winiwarter
- Graeme Robb
- Graham Smith



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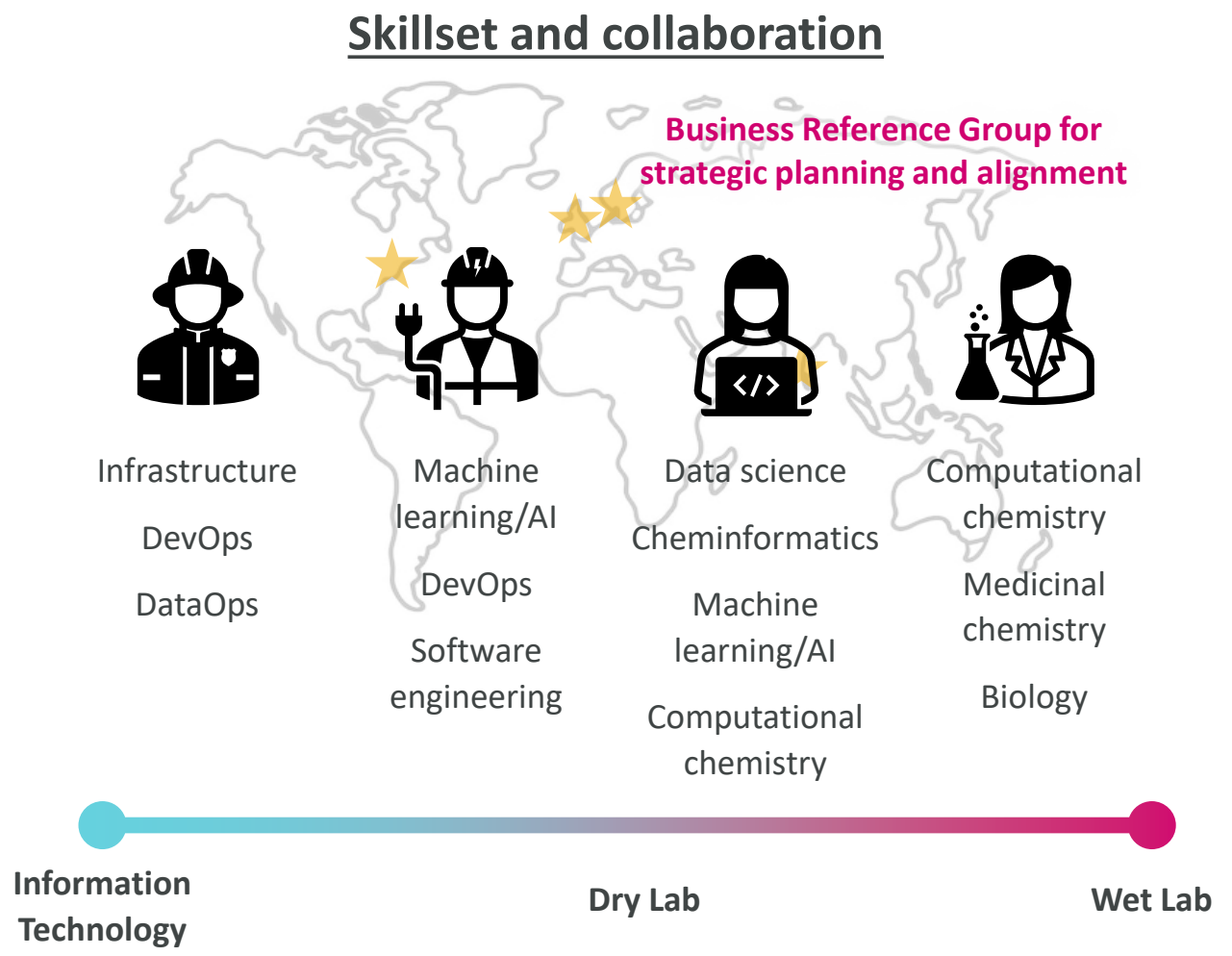
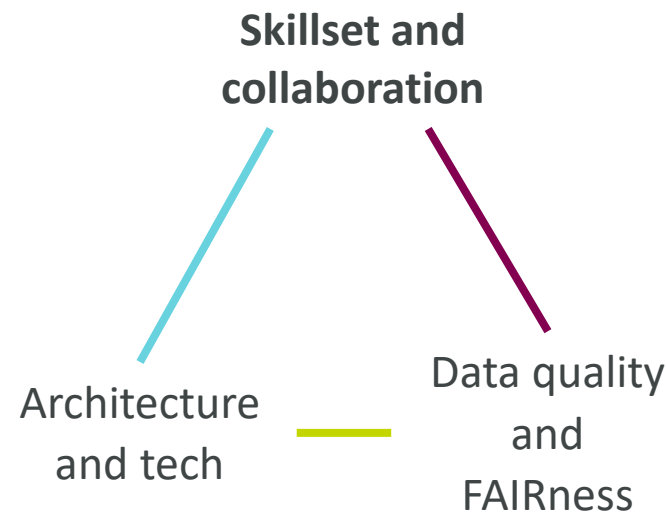
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Backup



Recipe for success

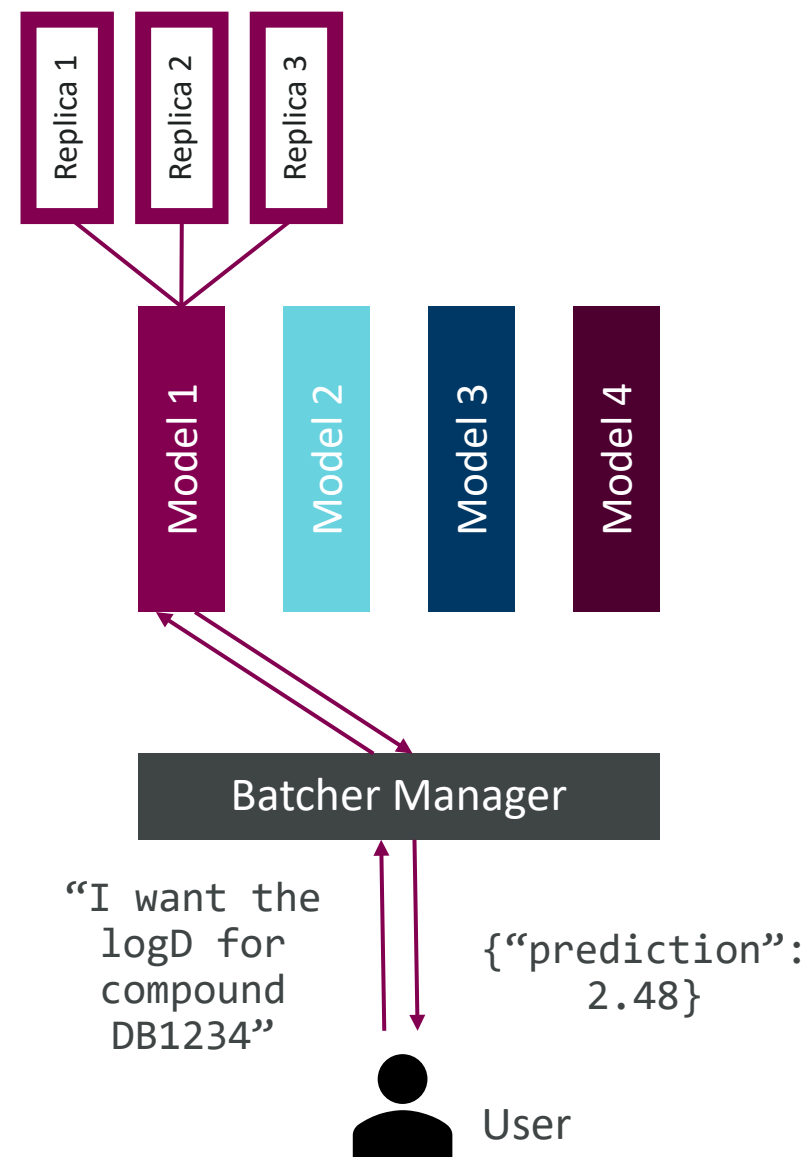


Architecture and tech: Consistent, augmented APIs

Users interact with a gateway called “Batcher Manager” (or Batman, for friends)

Batman provides many functionalities:

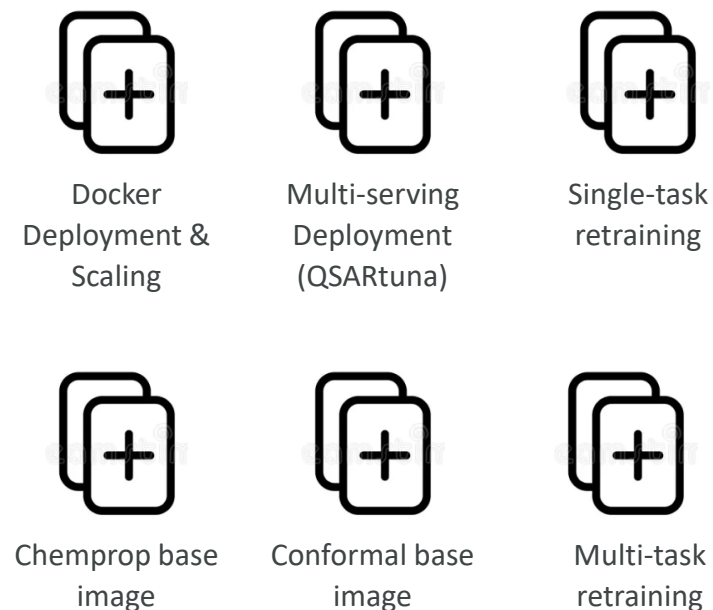
- Consistent interface for all models/calculations
- Asynchronous requests
- Batching & Queue management
- Caching
- Database ID lookup
- Chemistry (e.g. format conversion, R-group replacement)



Architecture and tech: Templates and versioning

Reusable templates

~10 templates to (mostly) rule them all



Source control

One, versioned, source of truth for all environments

