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Searching for LINCS to Stress

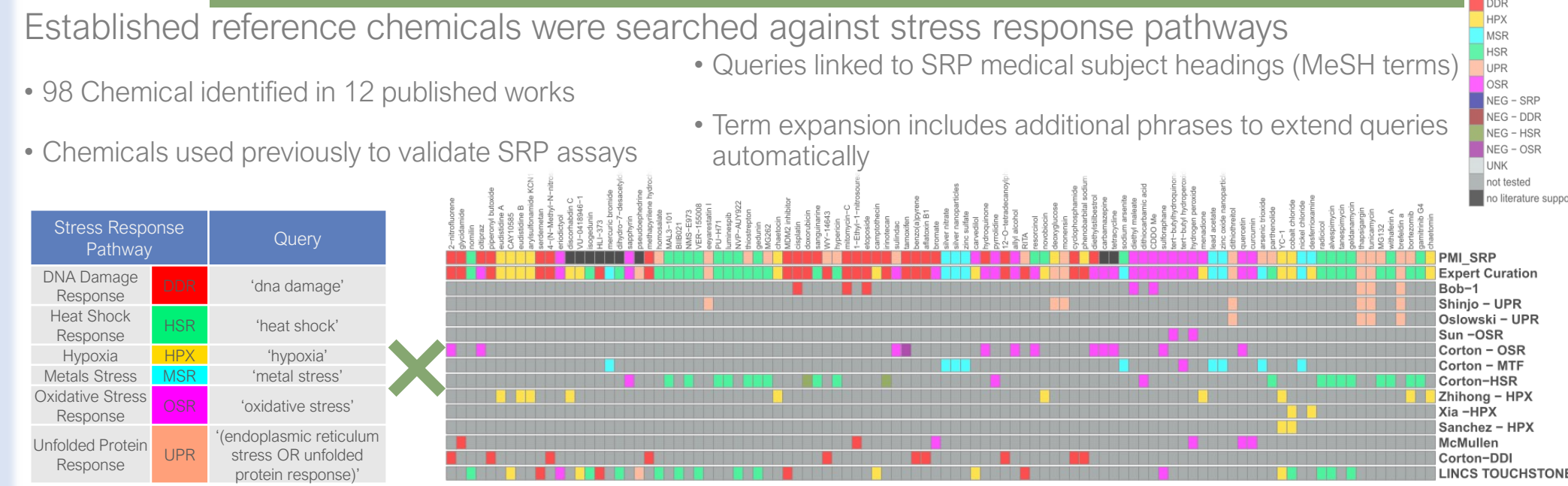
Using text-mining to automate reference chemical curation

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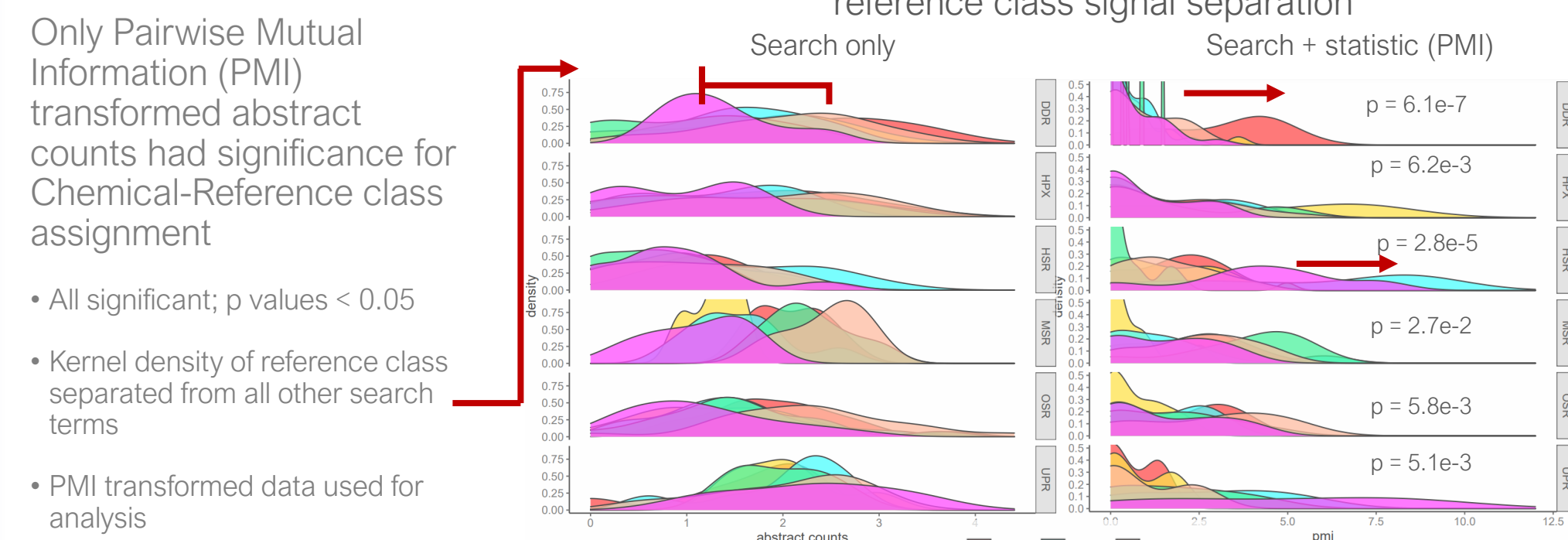
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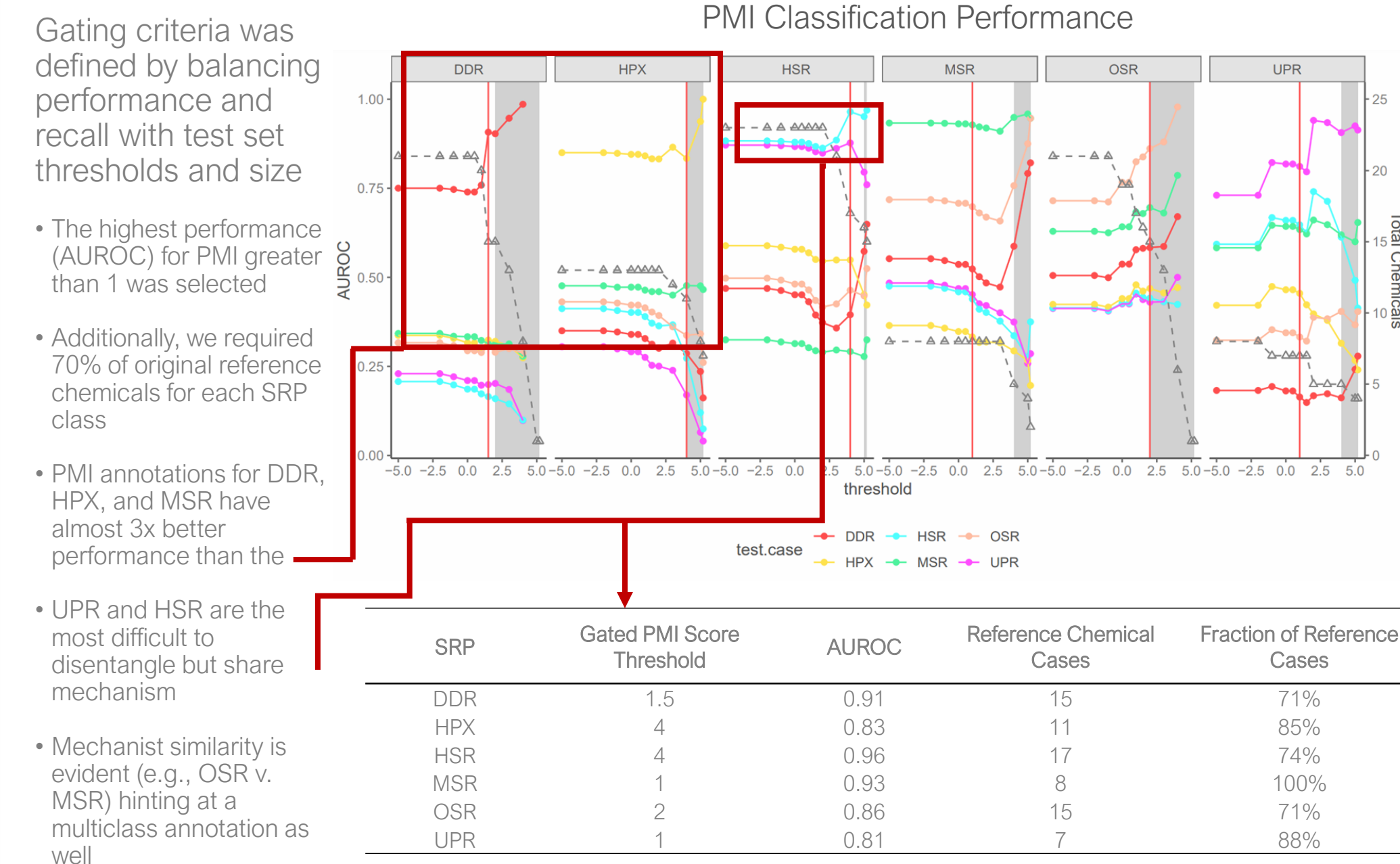
1a Reference Chemicals and Queries were taken from key studies



1b Mutual information identifies reference class better than search



2 Maximizing performance by chemical gating defines inclusion criteria



Problem

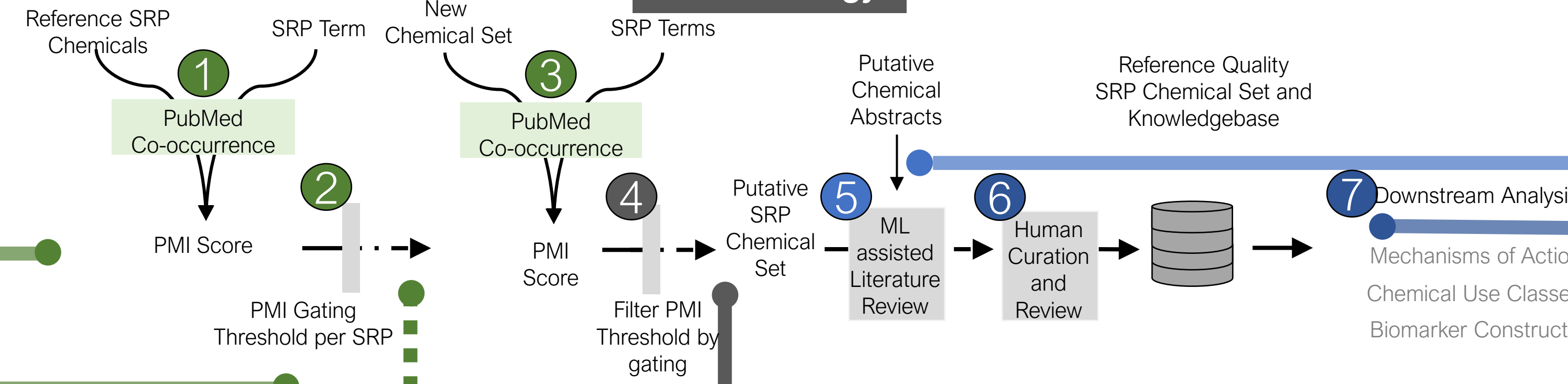
- Stress Response Pathways (SRPs) are hypothesized to be a key part of non-specific toxicity routes and play a role in disease.
- Chemical annotations for Stress Response Pathways (SRPs) activity are unevenly represented and no formal database exists.
- A database of SRP-chemical associations is needed to inform and support SRP assay development for non-specific toxicity.

Overview

Solution

- We developed an approach to automate the curation SRP active chemicals from literature linked to bioinformatics data
- Using an information statistic and machine learning we reduced human burden during curation and identified chemical use classes with significant SRP activity

Methodology

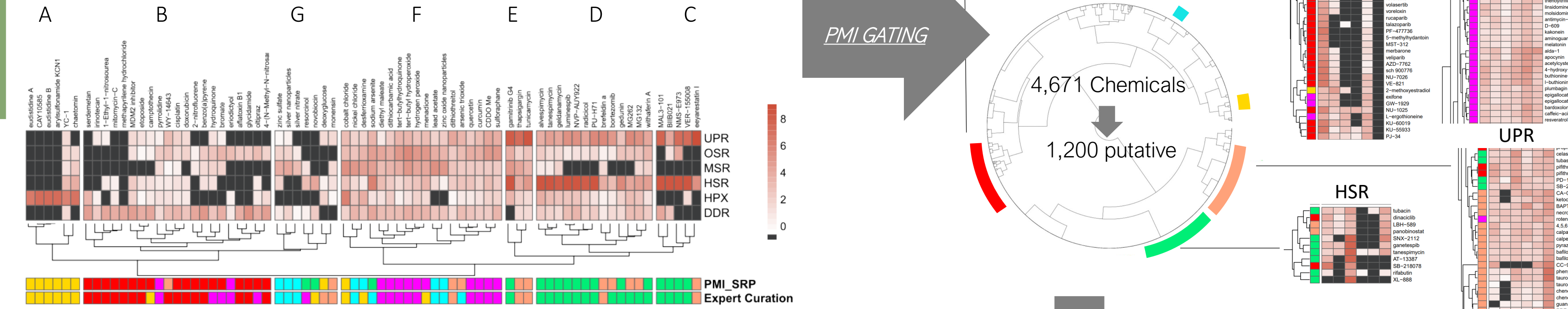


Key Outcome

- 3 & 4 Applying PMI thresholds to LINCS dataset increases chemical set for down stream analysis
- Hierarchical clustering of PMI score vectors exhibit seven activity group in literature data
- Single activity: B:DDR, A:HPX, D:HSR, E:UPR, F:OSR, G:MSR
- Dual activity and overlapping system: C: Mixed UPR/HSR G:Mixed MSR/OSR
- Some mixed OSR and DDR
- Mimics mechanistic induction observed in cross-activated and co-induced systems

Using gating criteria to identified 1,200 chemicals in the bioinformatics database with SRP literature support

- DDR, OSR, and HSR were the most represented classes
- MSR and HPX were the least represented classes
- IR identified almost 10x as many SRP active chemicals as are annotated in the database



Key Result

Among the same transcriptomic profiles targets and use classes were enriched by SRP

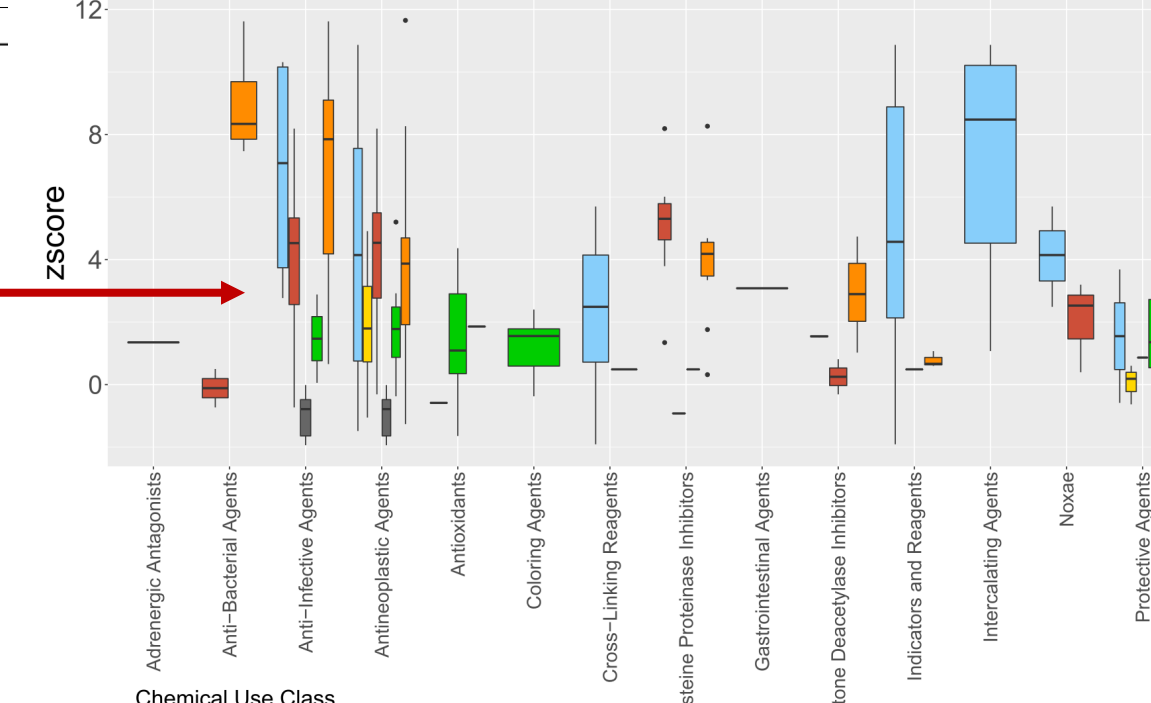
Most surprisingly, scoring with an orthogonal set of SRP biomarkers indicated use-pathway matching

Process identified predicted activities in chemical and automated activity annotation

Literature Enrichment

Use Class	p value
Neurotransmitter Agents	6.08E-16
Peripheral Nervous System Agents	5.44E-10
Central Nervous System Agents	3.94E-07
Depressants	1.01E-05
Anti-Infective Agents	1.05E-05
Antioxidants	2.89E-05
Psychotropic Drugs	4.26E-05
Anti-Bacterial Agents	5.95E-05
Agonistic Agents	3.71E-04
Sensory System Agents	4.53E-04
Gastrointestinal Agents	2.28E-03
Phosphatase Inhibitors	2.39E-03
Cysteine Protease Inhibitors	3.70E-03
Chemical Agents	3.76E-03
Sedating Agents	3.76E-03
Indicators and Reagents	4.10E-03
Antineoplastic Agents	4.26E-03

Gene Set Enrichment



Conclusion

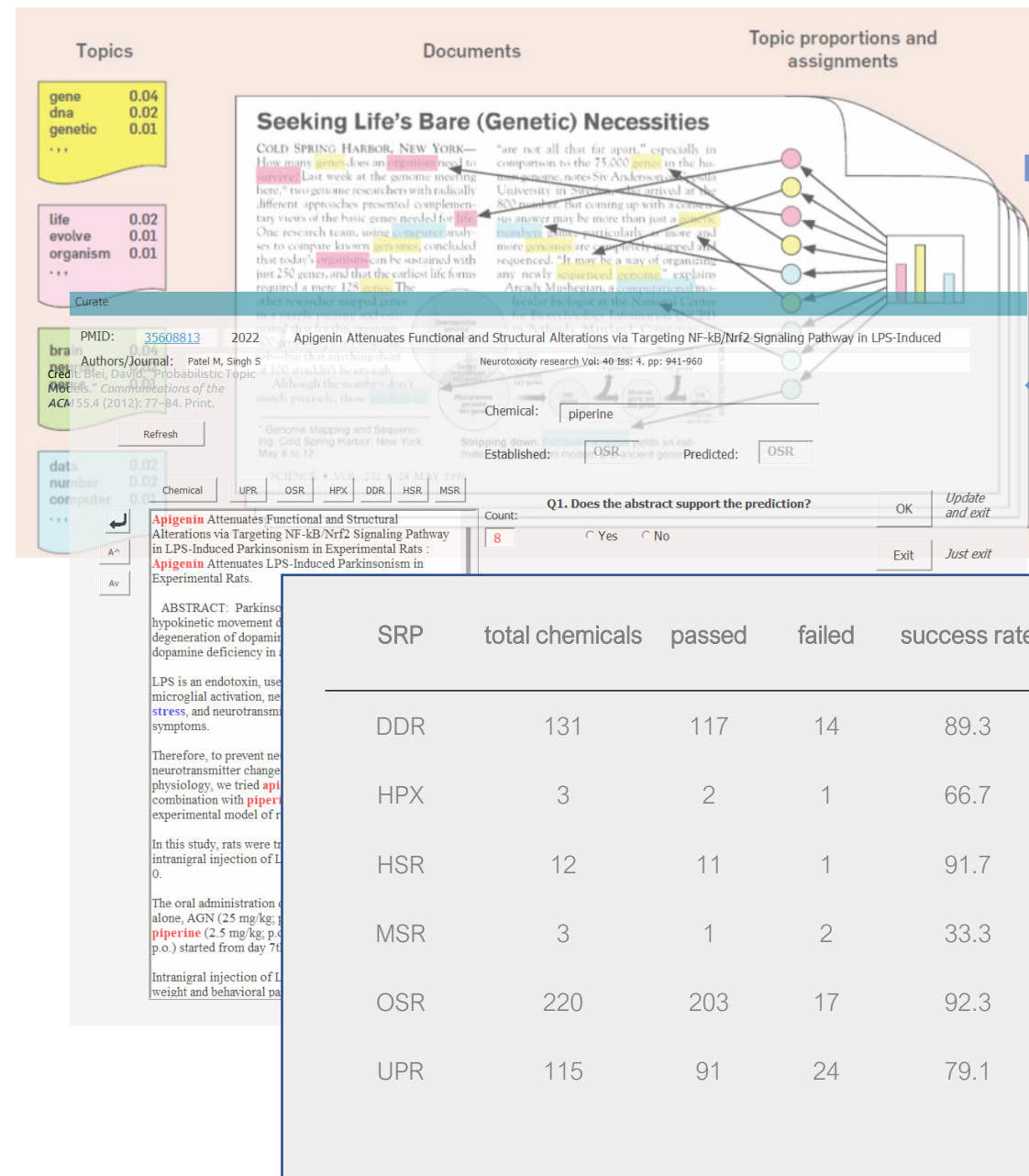
- We annotated 480 additional SRP active chemicals in LINCS
- Literature mining reduces effort in hazard assay development
- Transcriptomic space mirrored literature
- New chemical use group were associated with SRP activity and that activity was validated orthogonally with transcriptomic data
- The process is generalizable beyond SRPs and can build validation and test sets for a variety of problems

The views expressed in this presentation are those of the author(s) and do not necessarily represent the views or policies of the U.S. Environmental Protection Agency

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ML assisted systematic review prioritizes literature and identifies 480 new chemicals

Topic modeling – human curation overview



ML assisted review reduced human burden and prioritized evidence to confirm chemical-SRP relationships

- Multiclass-classifier used to predict topic and relationship between chemical and text
- Negative examples were confirmed using up to 5,000 abstracts per chemical negating SRP language
- 268,000 abstract were reduced to the 2,053 most essential
- Process save almost 240% of person-hours
- UPR and DDR best likely hood with high support rates down to 53% match probability
- OSR had greatest drop of support rate after 68% match probability

7a

PMI annotations exhibit unique transcriptomic signals

Transcriptomic profiles of SRP annotated chemicals classified by PMI only cluster by PMI SRP annotation which indicates that literature annotation maps to unique biological spaces

- Similar mechanistic annotations like UPR and HSR clustered together
- Clustering was cell specific indicating some potential differences in cell type SRP response

Transcriptomic profile clustering

