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United States  
Environmental Protection  
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# Quality assurance and quality control workflow for the non-targeted analysis of de facto water reuse

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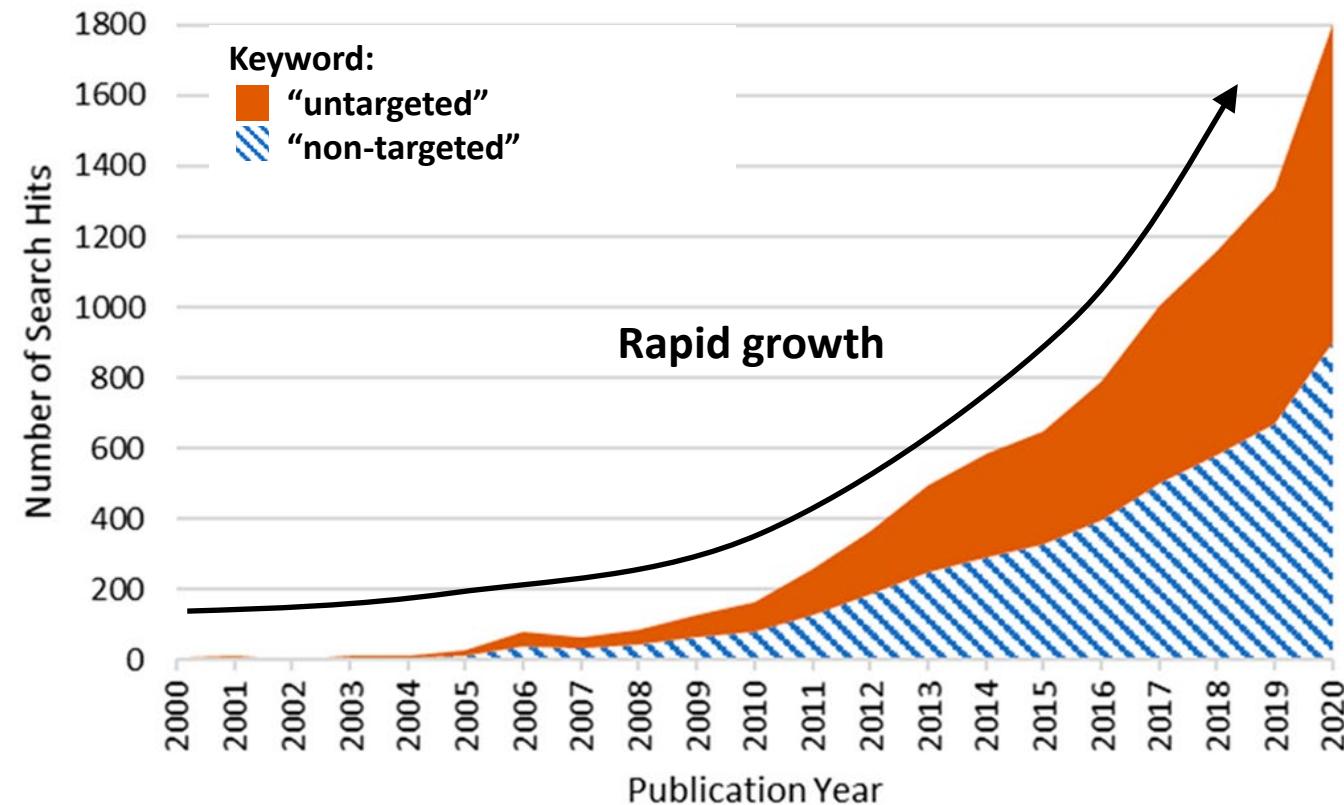
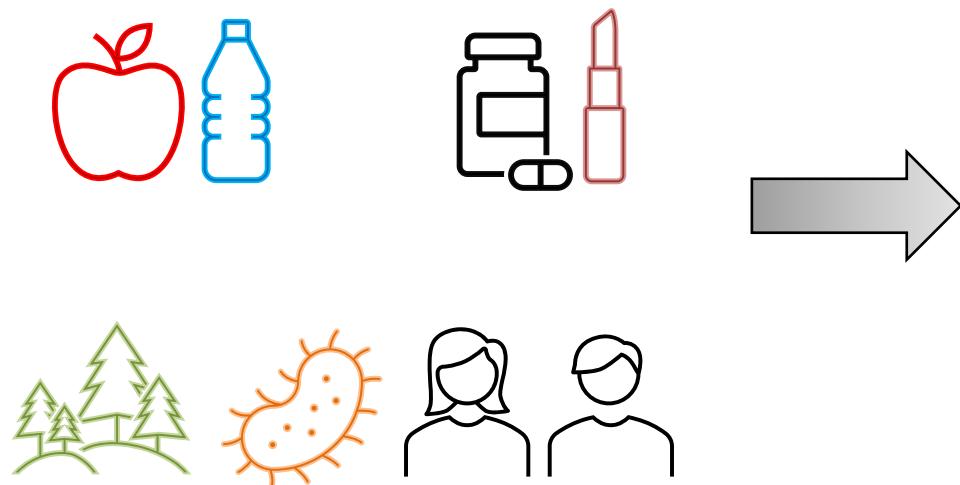
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# Non-Targeted Analysis (NTA): Definition and State-of-the-Science

- NTA – method for characterizing the chemical composition of a sample without *a priori* knowledge of the sample's chemical content
  - Whereas targeted analysis relies on pre-selected standards

Wide applicability and broad interest



# Non-Targeted Analysis (NTA): State-of-the-Science

- Still relatively nascent methodology
  - Limited guidance and standardization for study design and reporting (sample prep, data acquisition, QA/QC metrics)
    - NTA Study Reporting Tool (SRT) helping to address challenges

**A FRAMEWORK FOR CONSISTENT PEER REVIEW**

Section	Category	Sub-Category	Example Information to Report	Score	Rationale
Methods	Study Design	Objectives & Scope	• Study goals, hypotheses, scope • Expected chemical coverage	1	
		Sample Info & Preparation	• Sampling collection, processing • Description, intended use of blanks	2	
		QC Spikes & Samples	• Description of spike/controls	2	
	Data Acquisition	Analytical Sequence	• Sample run order, analytical batch(es)	NA	
		Chromatography		0	
		Mass Spectrometry		1	
	Data Processing & Analysis	Data Processing		2	Space for reviewer to explain assigned score (i.e., typical peer review rationale)
		Statistical & Chemometric Analysis		3	
		Annotation & Identification	• 3-4 examples of representative information to report for each of the 13 sub-categories. • Not an exhaustive list – intended to guide researcher/reviewer and relies on expertise/discretion.		
Results	Data Outputs	Statistical & Chemometric Outputs	• Basic statistical outputs & results of chemometric analyses • Visuals/plots, new statistical metrics, algorithms, etc.	3	
		ID & Confidence Levels	• Reported IDs and confidence levels & supporting data • (Semi)-quant data, exported MS/MS spectra		
	QA/QC Metrics	Data Acquisition QA/QC	• Method impacts on observable chemical space • Accuracy & precision of chromatography, mass error, abundance	1	
		Data Processing & Analysis QA/QC	• Method impacts on observable chemical space • Accuracy measures, fit accuracy, reproducibility of results	0	

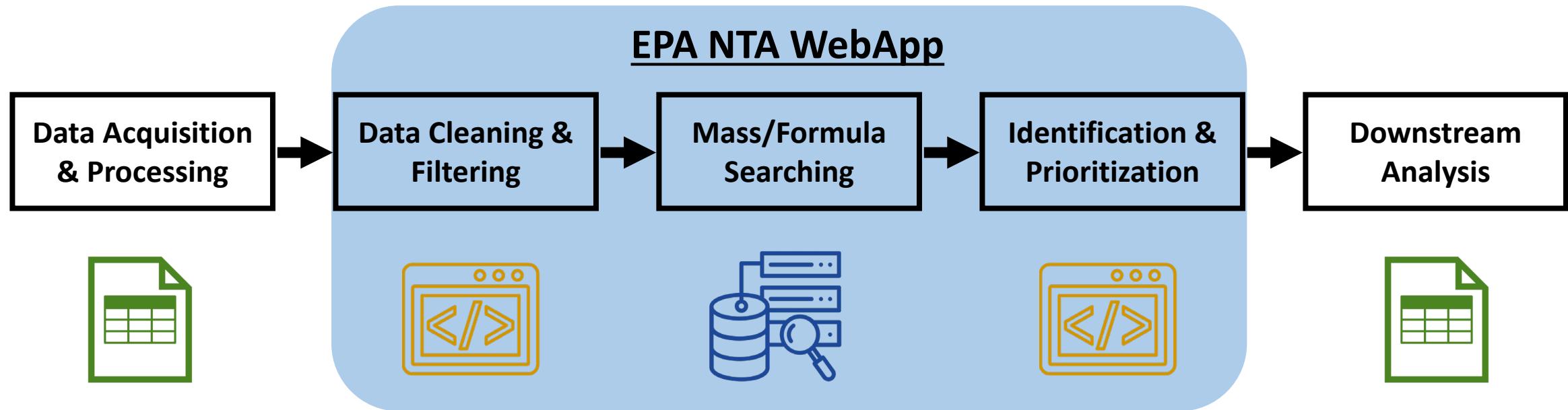
Enables rigorous evaluation of reporting quality in NTA studies



<https://nontargetedanalysis.org/>

<https://doi.org/10.1021/acs.analchem.1c02621>

# Typical NTA Data Workflow, Common Issues, and NTA WebApp



## Common Issues:

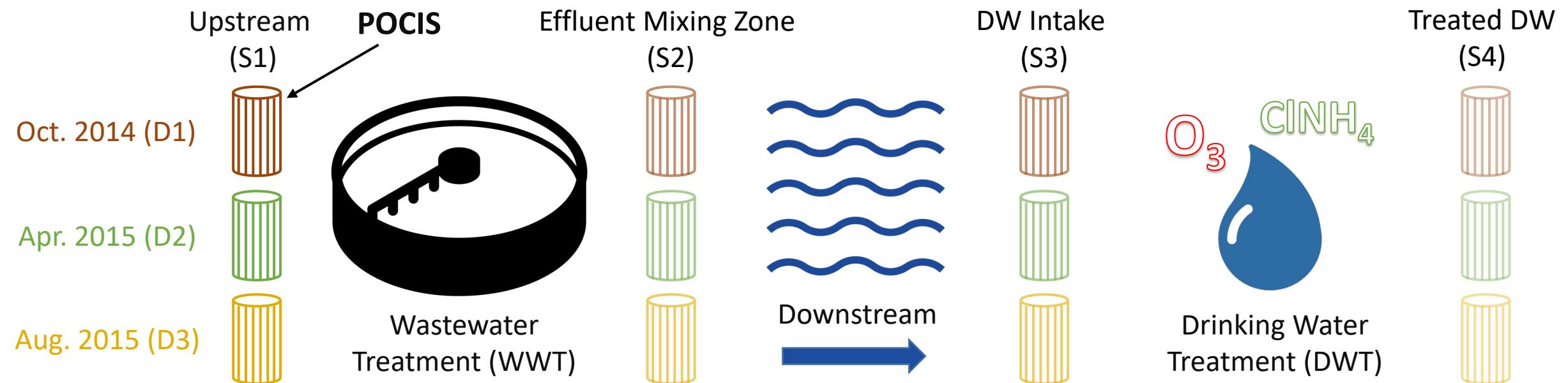
- Individualized methodologies and/or custom code lead to
  - High variability between practitioners
  - Opaque processes
    - Difficult to reproduce and communicate
  - User burden and slow adoption

## Goals of WebApp:

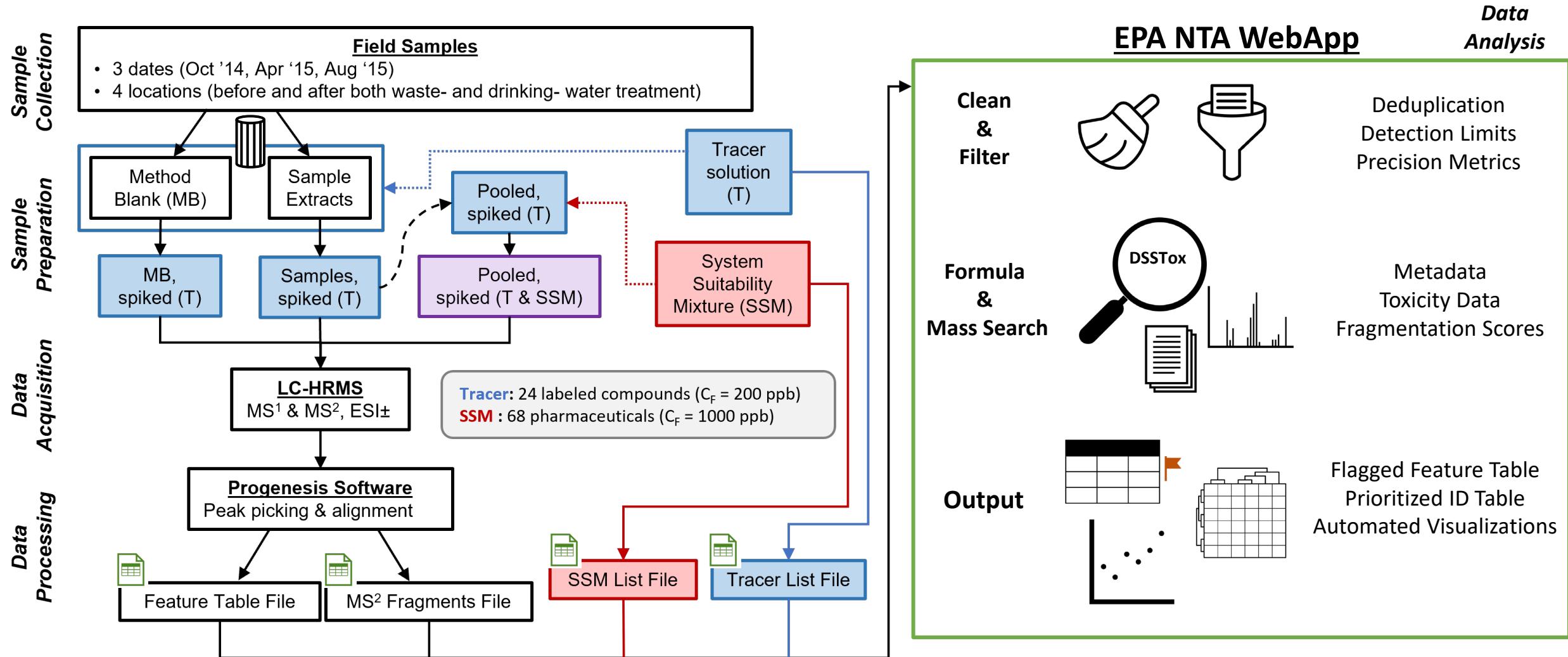
- **Standardize** by using statistically rigorous methodology and robust code
- **Elucidate** via guides and tool tips
- **Streamline** while maintaining user control

# De Facto Water Reuse Study Summary

- **Goal** – examine the exposure and fate of contaminants of emerging concern (CECs) from before wastewater treatment to after drinking water treatment
- **Subgoal** – use passive sampling and NTA to broadly identify CECs
  - **POCIS** – polar organic chemical integrative samplers



# Study Design and WebApp



## NTA: non-targeted analysis of MS data (beta)

### Tools

#### MS1 Tool

Run MS1 Tool

MS1 Tool Algorithms

MS1 Tool QA/QC

MS1 Tool References

MS2 CFMID Tool

### Documentation

Source Code

## Run NTA MS1 Tool

Easy file inputs

Input	Value
Project name:	Example nta
Positive MPP file (csv):	<input type="button" value="Choose File"/> No file chosen
Negative MPP file (csv):	<input type="button" value="Choose File"/> No file chosen
Adduct mass accuracy units:	ppm
Adduct mass accuracy:	10
Adduct retention time accuracy (mins):	0.05
Tracer file (csv; optional):	<input type="button" value="Choose File"/> No file chosen
Tracer mass accuracy units:	ppm
Tracer mass accuracy:	5
Tracer retention time accuracy (mins):	0.1
Min sample:blank cutoff:	3
Min replicate hits:	<input type="range" value="2"/>
Max replicate CV:	0.8
Parent ion mass accuracy (ppm):	<input type="range" value="5"/>
Discard features below this retention time (mins):	0.0
Search dashboard by:	mass
Save top result only?	no
DSSTox search batch size (debugging):	150

User-defined parameters

Defaults

Clear

Save Metadata?

Submit

# Screenshots of NTA WebApp

## NTA: non-targeted analysis of MS data (beta)

### Tools

MS1 Tool

#### MS2 CFMID Tool

Run MS2 CFMID Tool

MS2 CFMID Tool Algorithms

MS2 CFMID Tool QA/QC

MS2 CFMID Tool References

Merge MS1 and MS2 Data

User-defined parameters

## Run MS2 CFMID Tool

Input	Value
Job ID:	DVE6FJR0
Neg Mode Data:	<input type="button" value="Choose File"/> No file chosen
Pos Mode Data:	<input type="button" value="Choose File"/> No file chosen
Project name:	Example nta
Precursor mass accuracy (ppm):	10
Fragment mass accuracy (Da):	0.02
Fragment Classifications (csv):	<input type="button" value="Choose File"/> No file chosen

Clear

Defaults

Submit

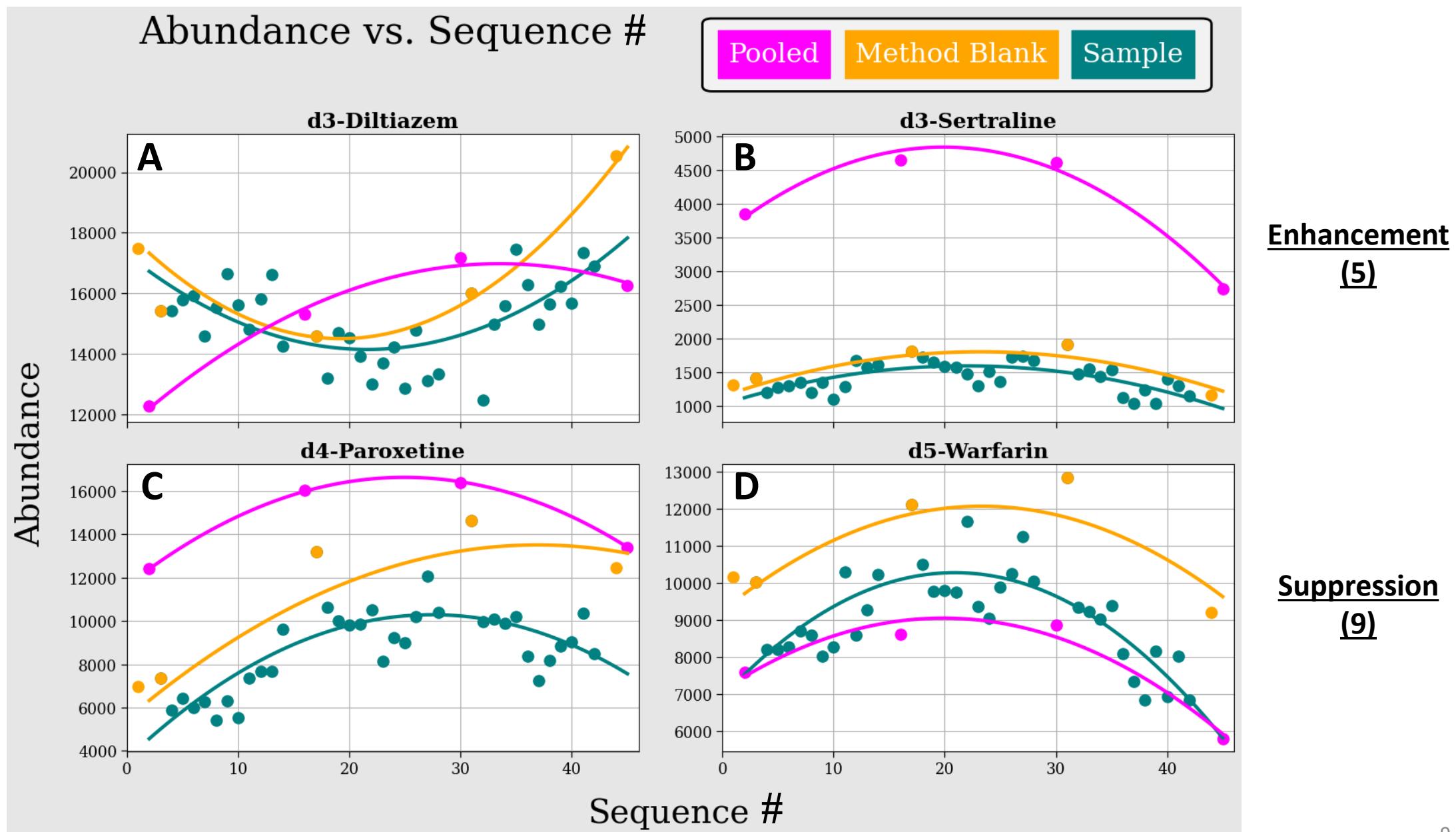
# Tracer Results Table

Chemical Name	DTXSID	Ionization Mode	Mass Error (ppm)	RT Drift (min)	Precision (max %CV)	Detection Frequency (%)
<b>User-defined settings</b>						
acetaminophen-d3	<a href="#">DTXSID50480414</a>	ESI+	3.20	0.06	12	100
albuterol-d9	<a href="#">DTXSID10675541</a>	ESI+	2.52	0.00	20	100
amitriptyline-d6	<a href="#">DTXSID501349824</a>	ESI+	2.14	0.09	18	100
amlodipine-d4	<a href="#">DTXSID50661983</a>	ESI+	8.59	0.09	35	97.8
atenolol-d7	<a href="#">DTXSID101027977</a>	ESI+	2.59	0.02	15	100
Caffeine-13C3	<a href="#">DTXSID20437172</a>	ESI+	2.45	0.02	17	100
carbamazepine-d8	<a href="#">DTXSID401349821</a>	ESI+	0.79	0.12	22	100
diltiazem-d3	<a href="#">DTXSID801016193</a>	ESI+	1.61	0.05	15	100
fluoxetine-d5	<a href="#">DTXSID50661983</a>	ESI+	0.41	0.10	18	100
glipizide-d11	<a href="#">DTXSID601349827</a>	ESI+	4.51	0.13	20	100
metoprolol-d7	<a href="#">DTXSID30648858</a>	ESI+	2.92	0.07	16	100
norethindrone-d6	<a href="#">DTXSID401349857</a>	ESI+	0.48	0.11	14	100
paroxetine-d4	<a href="#">DTXSID101349822</a>	ESI+	1.58	0.05	32	100
sertraline-d3	<a href="#">DTXSID201349825</a>	ESI+	0.35	0.08	23	100
sulfamethoxazole-d4	<a href="#">DTXSID101016780</a>	ESI+	3.68	0.09	15	100
triamterene-d5	<a href="#">DTXSID701349820</a>	ESI+	1.25	0.05	29	100
trimethoprim-d9	<a href="#">DTXSID10662219</a>	ESI+	2.19	0.04	15	100
verapamil-d6	<a href="#">DTXSID801349823</a>	ESI+	0.39	0.08	28	100
warfarin-d5	<a href="#">DTXSID801016155</a>	ESI+	1.62	0.17	19	100
gemfibrozil-d6	<a href="#">DTXSID601028063</a>	ESI-	0.29	0.16	12	100
glipizide-d11	<a href="#">DTXSID601349827</a>	ESI-	1.19	0.04	22	100
hydrochlorothiazide-13C,d2	<a href="#">DTXSID00662001</a>	ESI-	0.92	0.06	8	100
ibuprofen-d3	<a href="#">DTXSID00481299</a>	ESI-	1.01	0.15	12	100
sucralose-d6	<a href="#">DTXSID301339960</a>	ESI-	1.62	0.01	12	100
warfarin-d5	<a href="#">DTXSID801016155</a>	ESI-	0.13	0.03	11	100

- Crucial first step for ensuring data integrity
- Provides hyperlinks to DSSTox database
- Summary statistics for each ionization mode
- Out-of-spec statistics prompt follow-up action
  - Doesn't necessarily invalidate whole study

\*most extreme

# Run Sequence Plot Demonstrating Sequence and Matrix Effects (ESI+)



# Nomenclature – features, samples, occurrences

## Sample-Replicates

Sample 1			Sample 2			Sample 3		
REP 1	REP 2	REP 3	REP 1	REP 2	REP 3	REP 1	REP 2	REP 3

**Sample-Replicate Occurrences**  
(abundances)

Input Table

Clean,  
Filter,  
Flag,  
&  
Blank Subtract



## Samples

median Sample 1	median Sample 2	median Sample 3

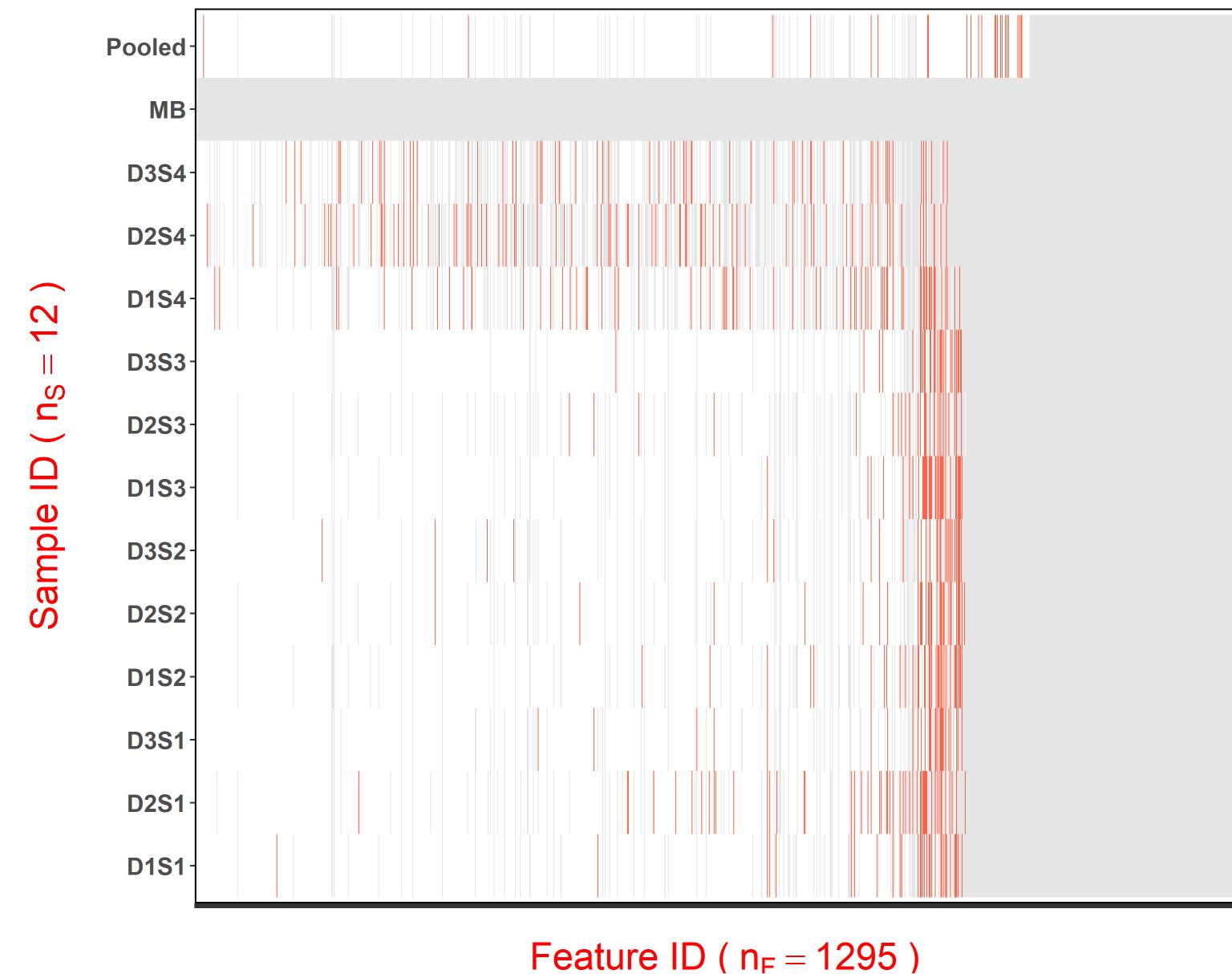
**Sample Occurrences**  
(Blank-subtracted  
median abundances)

Output File

# CV Heat Map: A Visualization of Flagged, Non-Detected, and Passing Occurrences

ESI+, post-blank subtraction (  $n_{Occ} = 15540$  )

Sorted by median sample abundance (highest [left] to lowest [right])



Occurrence Flag (samples only)

- ≤ 0.5 (8594, 55%), no flags
- > 0.5 (460, 3%), CV flag
- non-detect (6486, 42%)

Includes:

- missing all replicates
- < replicate threshold
- < MDL

### Upstream

### Effluent Mixing Zone

### DW Intake

### Treated DW

Features

1000

800

600

400

200

0

Oct 2014   Apr 2015   Aug 2015

-SD    +SD

## Cluster Heat Map (k-means)

- Differences across time?
  - Seasonality and stream flow conditions
- Differences across location?
  - Before vs after wastewater treatment
  - Before vs after drinking water treatment
    - Disinfection byproducts

# Summary

- NTA is a rapidly growing methodology → standardized QA/QC procedures still under development
- The NTA WebApp is being designed to:
  - Help practitioners more quickly and easily analyze their NTA data
  - Standardize NTA workflows with robust statistical analyses and helpful visualizations
  - Consolidate QC procedures, database querying, and feature identification/prioritization
  - Provide transparency and reproducibility
- De Facto Water Reuse Study data indicate that:
  - Tracers have acceptable mass errors, retention time drift, and CVs
  - 55% of blank-subtracted sample-occurrences present no flags
  - Heat map elucidates spatiotemporal trends and provides guidance for compound ID prioritization

Questions?