





# Ratisser plutôt que balayer



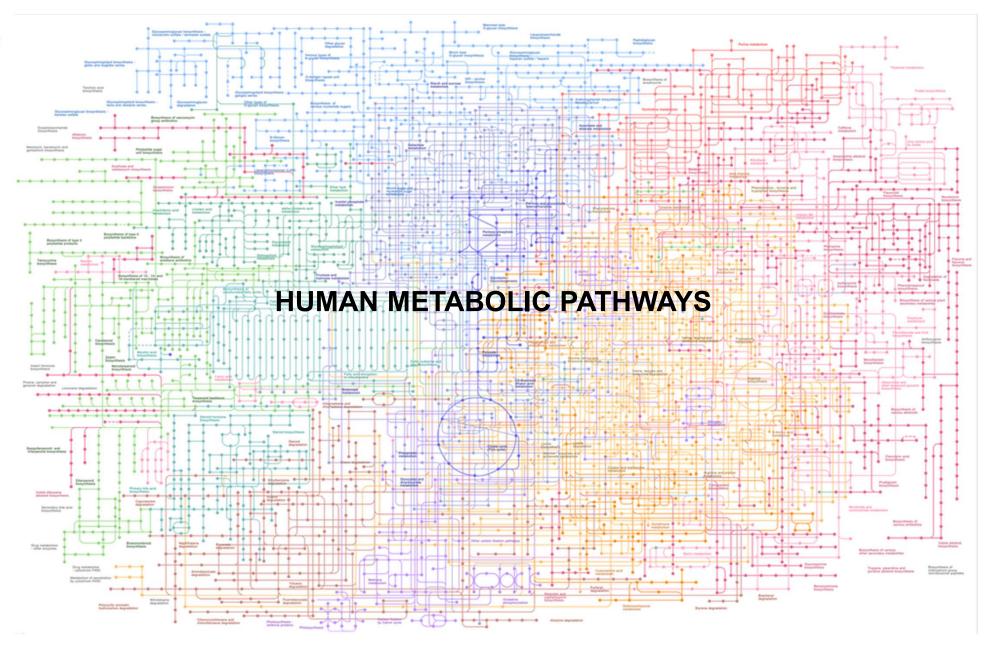
L'analyse multi-ciblée comme alternative de choix à l'analyse non-ciblée pour le profilage étendu des stéroïdes

#### Dr. Mathieu Galmiche

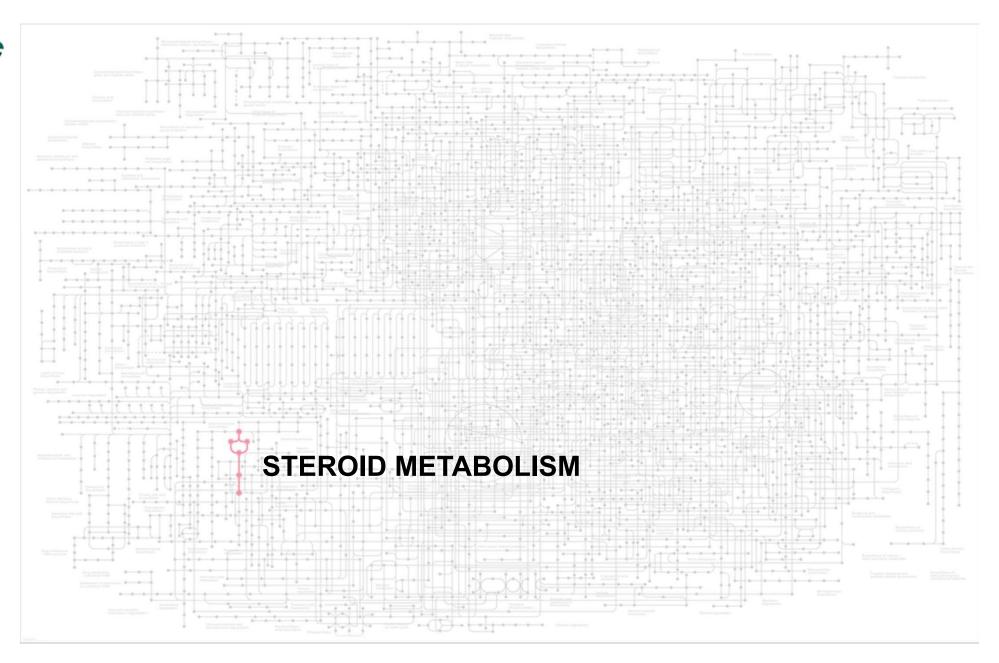
Post-doctorant
Université de Genève
Section des sciences pharmaceutiques
Analyse biomédicale et métabolomique



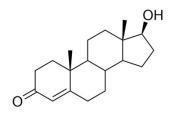




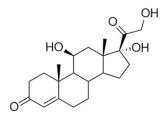




### Several hundreds (thousands?) of steroid metabolites in humans



**Androgens** 



**Corticosteroids** 

**Progestogens** 

Bile acids

**Estrogens** 

**Glucuronides** 

**Sulfates** 

### Several hundreds (thousands?) of steroid metabolites in humans : SteroidOMICS



2019



Article

## DynaStI: A Dynamic Retention Time Database for Steroidomics

Santiago Codesido <sup>1,\*</sup> , Giuseppe Marco Randazzo <sup>1,2</sup>, Fabio Lehmann <sup>3</sup>, Víctor González-Ruiz <sup>1,4</sup> , Arnaud García <sup>1</sup>, Ioannis Xenarios <sup>3,5</sup>, Robin Liechti <sup>3</sup> , Alan Bridge <sup>3</sup> , Julien Boccard <sup>1,4</sup> and Serge Rudaz <sup>1,4</sup>

**Androgens** 

HOOH

**Corticosteroids** 

**Progestogens** 

Bile acids

The current DynaStI database offers dynamic retention time generation for LC separations under the following conditions:

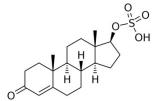
- Stationary phase: Kinetex<sup>TM</sup> (Phenomenex)  $C_{18}$  100 Å,  $2.1 \times 150 \times 1.7$  mm,
- Weak solvent: Water + 0.1% formic acid,

 $5\% B \rightarrow 95\% B : 14 \text{ minutes}$ 

- Strong solvent: Acetonitrile + 0.1% formic acid,
- Temperature: 30 °C.

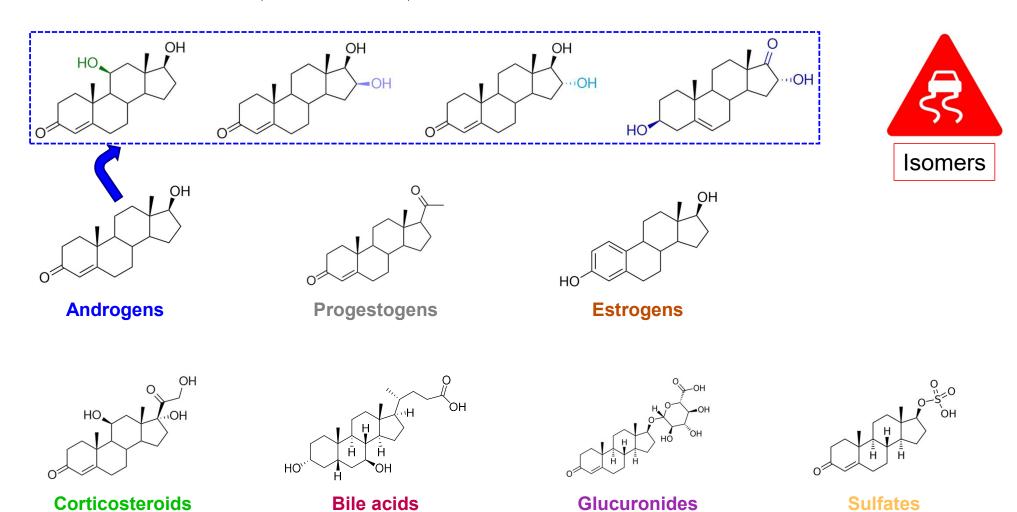
**Estrogens** 

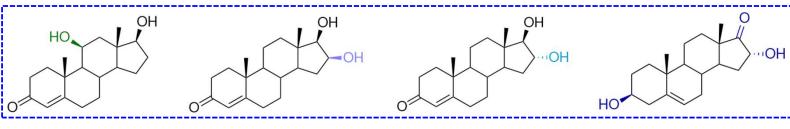
**Glucuronides** 



**Sulfates** 

### Several hundreds (thousands?) of steroid metabolites in humans

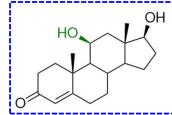




Produced in the adrenal. Precursor of potent '11-keto' androgens Produced in the liver. Inactive metabolite (elimination product) Produced in the liver. Inactive metabolite (elimination product) Produced in the liver, ovaries and placenta. Estrogen precursor

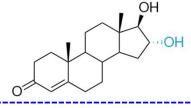


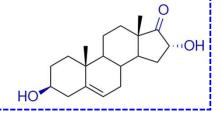
m/z = 305.2112



Produced in the liver.

Inactive metabolite





Isomers

Produced in the adrenal.
Precursor of potent

'11-keto' androgens (elimination product)

RT = 8.3 min

Produced in the liver. Inactive metabolite (elimination product)

 $RT = 7.55 \, min$ 

Produced in the liver, ovaries and placenta. Estrogen precursor

RT = 8.3 min

m/z = 305.2112



 $RT = 8.25 \, min$ 



Article

# DynaStI: A Dynamic Retention Time Database for Steroidomics

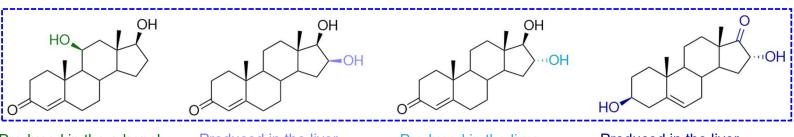
Santiago Codesido <sup>1,\*</sup>, Giuseppe Marco Randazzo <sup>1,2</sup>, Fabio Lehmann <sup>3</sup>, Víctor González-Ruiz <sup>1,4</sup>, Arnaud García <sup>1</sup>, Ioannis Xenarios <sup>3,5</sup>, Robin Liechti <sup>3</sup>, Alan Bridge <sup>3</sup>, Julien Boccard <sup>1,4</sup> and Serge Rudaz <sup>1,4</sup>

The current DynaStI database offers dynamic retention time generation for LC separations under the following conditions:

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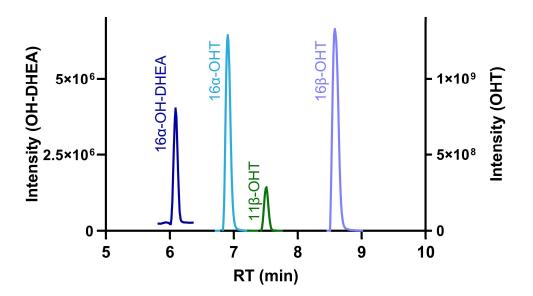
- Strong solvent: Acetonitrile + 0.1% formic acid,
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Produced in the adrenal. Precursor of potent '11-keto' androgens Produced in the liver. Inactive metabolite (elimination product) Produced in the liver. Inactive metabolite (elimination product) Produced in the liver, ovaries and placenta. Estrogen precursor



m/z = 305.2112



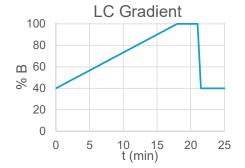
Column: Restek Inert **Biphenyl** 100 x 2.1 mm, 1.8 μm Guard: Inert **Biphenyl** 5 x 2.1 mm, 2.7 μm

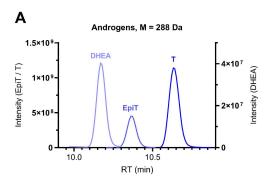
A: H<sub>2</sub>O + 0.01 % FA B: MeOH + 0.01 % FA

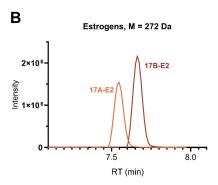
0.4 mL/min

25 minutes

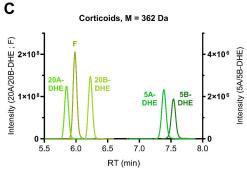


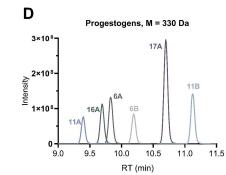


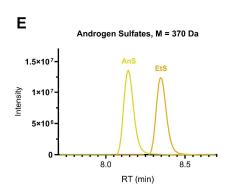


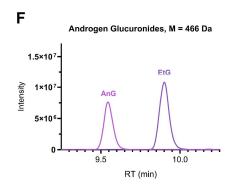












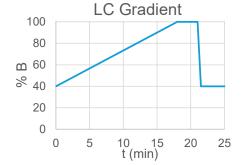
M.Galmiche et al., *Journal of Separation Science*, **2024**, 47(16), 2400436 M.Galmiche et al., *Journal of Separation Science*, **2025**, 48(4), e70147

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A: H<sub>2</sub>O + 0.01 % FA B: MeOH + 0.01 % FA

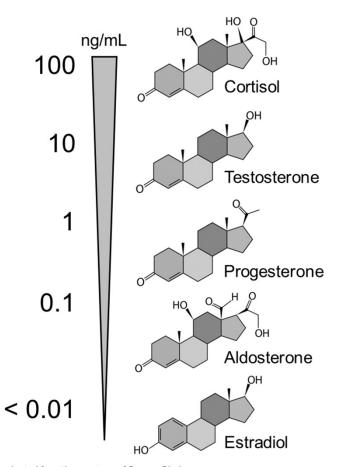
0.4 mL/min 25 minutes





### Are you sure there is no 'David' peak hidden under the 'Goliaths'?

### **Endogenous concentrations**



\*

#### **Ionization efficiencies**

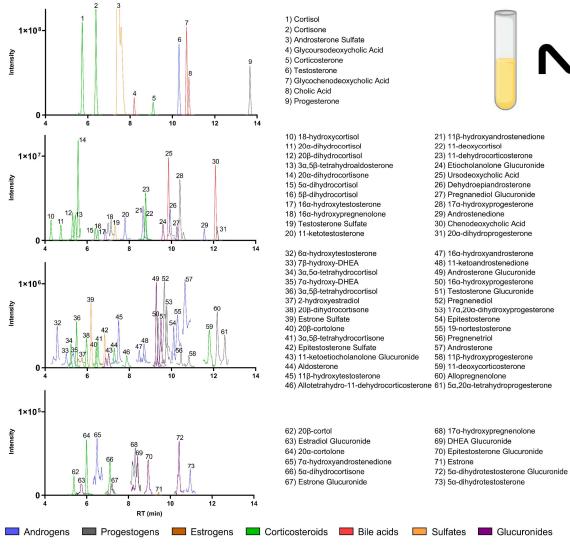


T. Higashi et al. / Journal of Pharmaceutical and Biomedical Analysis 39 (2005) 718–723

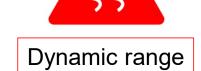
$$\begin{array}{c} \\ \text{HO} \\ \\ \Delta^{5}\text{-steroid} \end{array} \xrightarrow{\text{Protonation}} \\ \\ \text{H.} \\ \\ \\ \frac{}{\oplus} \end{array} \xrightarrow{\text{Protonation}} \\ \\ \text{H.} \\ \\ \frac{}{\oplus} \end{array} \xrightarrow{\text{H.} \\ 0} \xrightarrow{\text{H.} \\ 0}$$

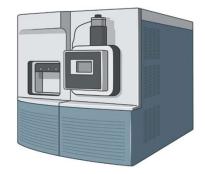
adapted from the courtesy of Sergey Girel

### Are you sure there is no 'David' peak hidden under the 'Goliaths'?



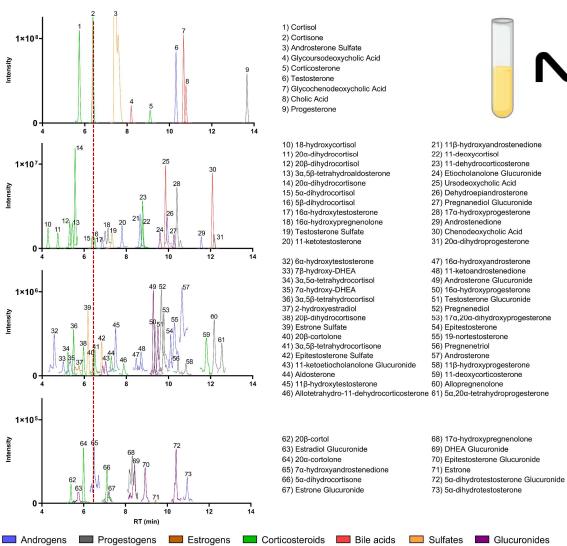








### Are you sure there is no 'David' peak hidden under the 'Goliaths'?



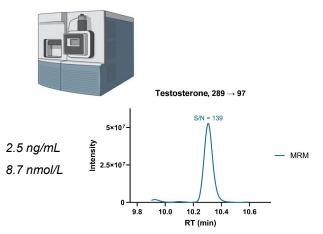


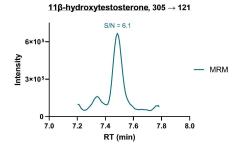


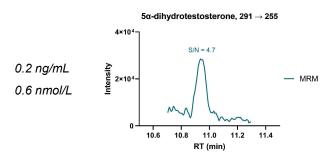


In data-dependent untargeted metabolomics, such low-intensity peaks will not be fragmented, hampering structural elucidation.

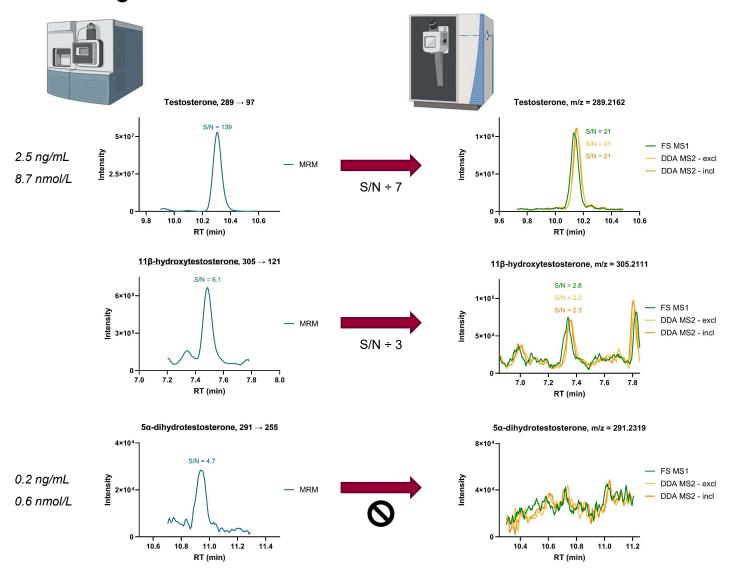
### Sniffing out the ultratraces ...



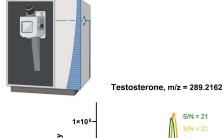




### Sniffing out the ultratraces ...



### Sniffing out the ultratraces ...



1×10<sup>6</sup>

S/N = 21

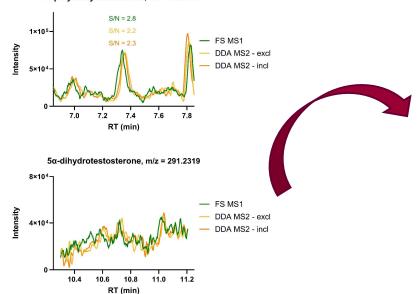
S/N = 21

DDA MS2 - excl

DDA MS2 - incl

PT (min)

#### 11β-hydroxytestosterone, m/z = 305.2111





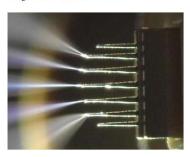
pubs.acs.org/ac

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Article

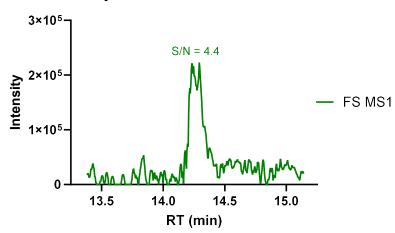
Microflow Liquid Chromatography Coupled to Multinozzle Electrospray Ionization for Improved Lipidomics Coverage of 3D Clear Cell Renal Cell Carcinoma

Sergey Girel, Mathieu Galmiche, Mathis Fiault, Valentin Mieville, Patrycja Nowak-Sliwinska, Serge Rudaz,\* and Isabel Meister\*



micro-flow chromatography: 2.0 μL/min multi-nozzle emitter: 0.4 μL/min per nozzle

 $5\alpha$ -dihydrotestosterone, m/z = 291.2319



### Multiplexing has its limits ...

185 compounds

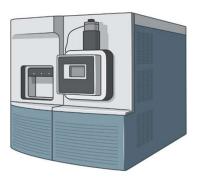
2 to 4 MRM transitions per compound

Positive / Negative polarity switching









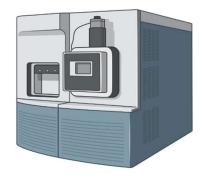
### Multiplexing has its limits ... that we can circumvent

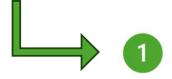
185 compounds

2 to 4 MRM transitions per compound

Positive / Negative polarity switching







Injection of group-pooled QCs

Separately in positive and negative ionization modes

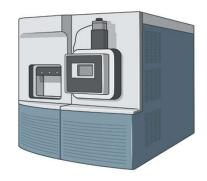
### Multiplexing has its limits ... that we can circumvent

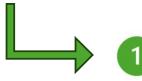
185 compounds

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Injection of group-pooled QCs

Separately in positive and negative ionization modes

Construction of a cohort-tailored MRM database with tentative identifications
POS 45 31 18 NEG 94 total hits

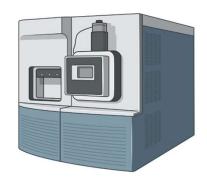
### Multiplexing has its limits ... that we can circumvent

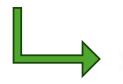
185 compounds

2 to 4 MRM transitions per compound

Positive / Negative polarity switching



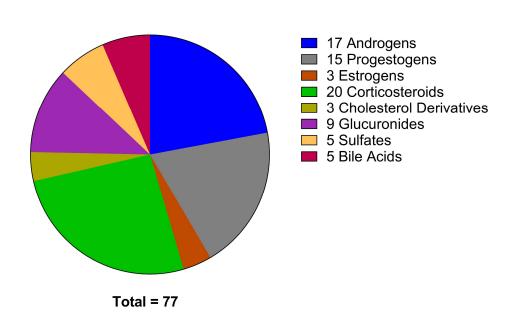


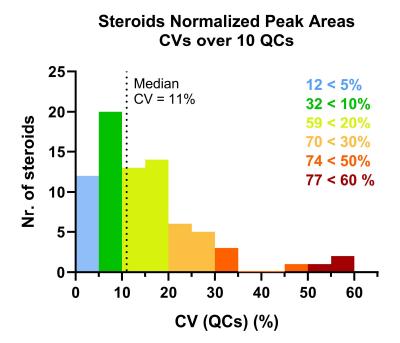


- Injection of group-pooled QCsSeparately in positive and negative ionization modes
- Construction of a cohort-tailored MRM database with tentative identifications
  POS 45 31 18 NEG 94 total hits
- Acquisition of the entire cohort with the specific list of MRM transitions for the 94 tentative identifications, with polarity switching

### Multi-targeted data can still be handled like untargeted data

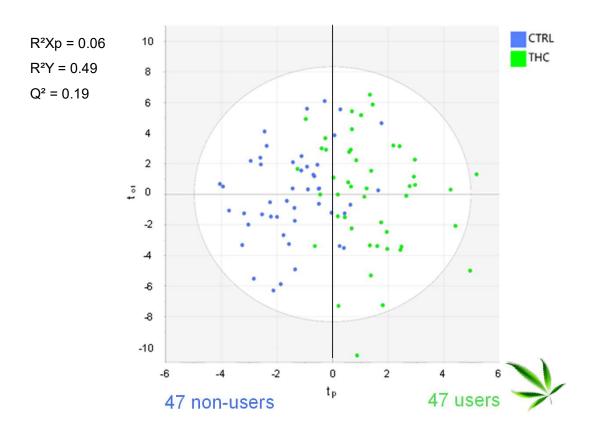
### 70 manually curated steroid detections





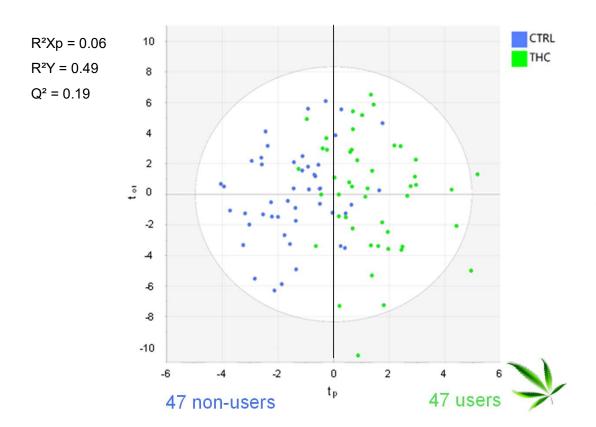
### Multi-targeted data can still be handled like untargeted data

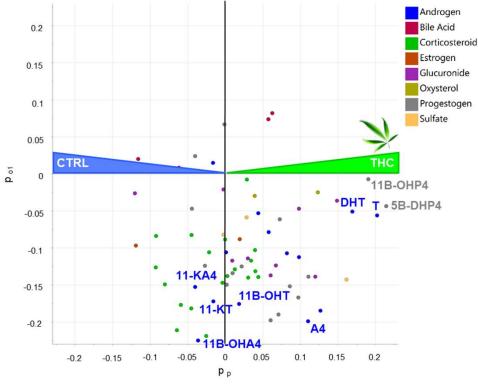
Multivariate Analysis: OPLS-DA



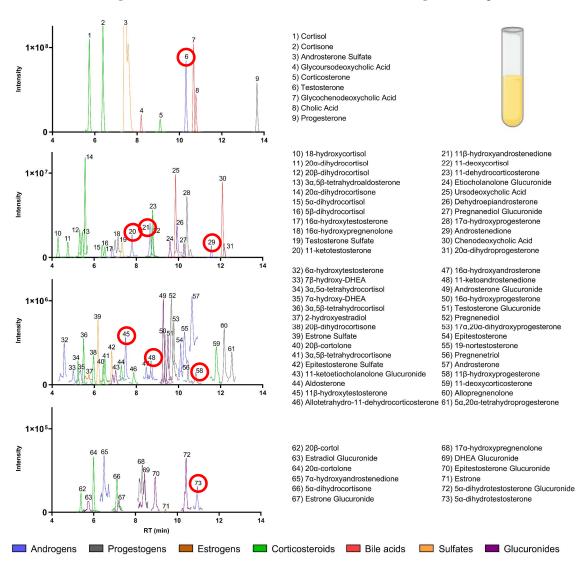
### Multi-targeted data can still be handled like untargeted data

Multivariate Analysis: OPLS-DA





### Which signals are the most biologically meaningful?



### Summary: Targeted 7 Untargeted metabolomics for human health

- ► Annotation is a critical bottleneck in HRMS-based metabolomics. It has been for years.
- Targeted approaches provide unequivocal compound identity, even without HRMS.
- ► Biological/biochemical interpretation of unidentified features for health applications is very tricky.

  Processing of untargeted HRMS data is frequently performed with a 'post-targeted' approach.
- ▶ If so, there is no information gain compared to targeted metabolomics, and even likely some information loss due to decreased sensitivity.
- ► Even in 'untargeted' setups, chromatography defines the breadth of chemical coverage.

  Although 'untargeted', the study will still be limited to RP-amenable molecules, for example.
- ► On the other hand, 'targeted' does not mean restricted! It can be extended to hundreds of metabolites.

# Combining untargeted screening and targeted absolute quantification: The future of metabolomics?



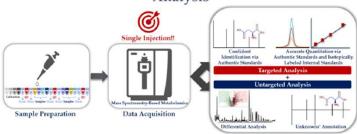


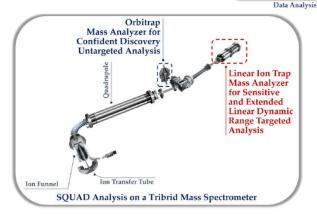
Review

Simultaneous Quantitation and Discovery (SQUAD) Analysis: Combining the Best of Targeted and Untargeted Mass Spectrometry-Based Metabolomics

Bashar Amer \*, Rahul R. Deshpande and Susan S. Bird

### Simultaneous Quantitation and Discovery (SQUAD) Analysis





Analytica Chimica Acta 1331 (2024) 343314

Triple acquisition mass spectrometry (TRAM) combining targeted and non-targeted metabolomics in a single run

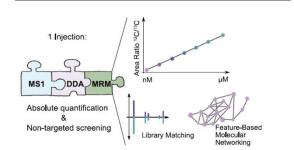


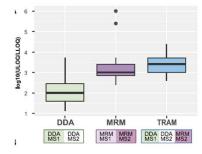
Lisa Panzenboeck  ${}^{a,b}$ , Harald Schoeny  ${}^a$ , Bruno Stelzer  ${}^a$ , Elisabeth Foels  ${}^{a,b,c}$ , Marvin Glas  ${}^a$ , Marlene Pühringer  ${}^{a,b}$ , Dorian Hirschmann  ${}^c$ , Daniela Loetsch  ${}^c$ , Christian Dorfer  ${}^c$ , Evelyn Rampler  ${}^{a,b}$ , Gunda Koellensperger  ${}^{a,d}$ , ${}^*$ 

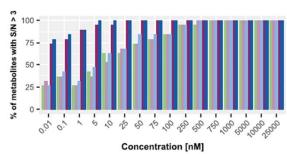
#### HIGHLIGHTS

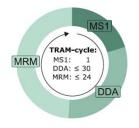
- High-speed triple acquisition strategy unifies targeted & non-targeted metabolomics.
- Absolute quantification & high number of DDA MS2 scans for individual samples.
   TRAM unites MS1, DDA-MS2 & MRM-
- TRAM unites MS1, DDA-MS2 & MRM-MS2 data acquisition within a single injection.
- TRAM was benchmarked using SRM 1950 & cerebrospinal fluid of meningioma patients.
- Optimized MRM parameters & HILIC retention times for more than 90 metabolites.





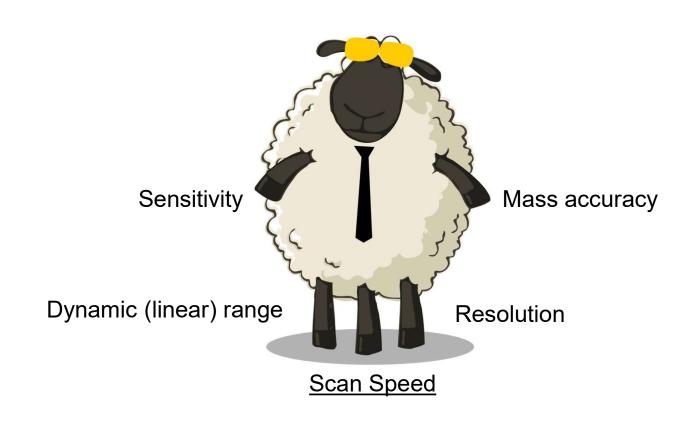








# Combining untargeted screening and targeted absolute quantification: The future of metabolomics?





## **CHEERS!**



Dr. Julien Boccard

Dr. Isabel Meister

**Mathis Fiault** 

Dr. Sergey Girel



Greta Galante

Célie Da Silva

Oriane Strassel

Dr. Mathieu Galmiche