# What is a semiquantitative non-targeted method?

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#### **Outline**

This presentation applies primarily to MS & LC/MS

- What is a semi-quantitative non-targeted method?
- Some definitions where does a semi-quantitative targeted method fit into analysis?
- Characteristics of a non-targeted semi-quantitative method
- How do we ensure that untargeted semi-quantitative methods deliver "actionable" data?
- Examples based on metabolic phenotyping





# **Definitions – Quantitative Methods**

- Quantitative methods provide absolute concentrations and are usually targeted to known analytes
- Are validated, over defined ranges, for a wide range of "figures of merit"
- These include accuracy, precision, LOD, LOQ, ULOQ, stability etc.

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### **Qualitative Methods**

- Qualitative targeted methods usually targeted to known analytes but are there to detect but not quantify them
- Fit for purpose give yes/no answers
- Can be validated in terms of LOD, stability & robustness and specificity are very important





# **Semi-quantitative Targeted-methods**

- •Semi-quantitative methods are usually targeted to known analytes but do not provide absolute concentrations
- They are often used over a defined concentration range
- They can be subject to some validation for e.g., LOD, linear range etc.
- •Often designed to "trigger" a specific analysis

# Semi-quantitative Un-targeted methods

- Semi-quantitative untargeted methods are not targeted to particular analytes but are aimed a characterizing sample
- •Often "Class-based" & generic methods are used
- Analytes of interest are not known before analysis
- They do not provide absolute concentrations but <u>relative</u> ones
- Results usually expressed as <u>fold changes</u>
- limited validation for e.g., precision, "linear range" etc.
- These assays are usually used in "discovery mode"





# Semi-quantitative Methods Examples: "Omics" Methods Transcriptomics, Proteomics & Metabolomics

- In "discovery" mode transcriptomics, proteomics and metabolomics methods provide semi-quantitative "fold change" data.
- But, in order to be useful these semi-quantitative untargeted methods must provide reproducible results that are good enough to identify potential biomarkers.

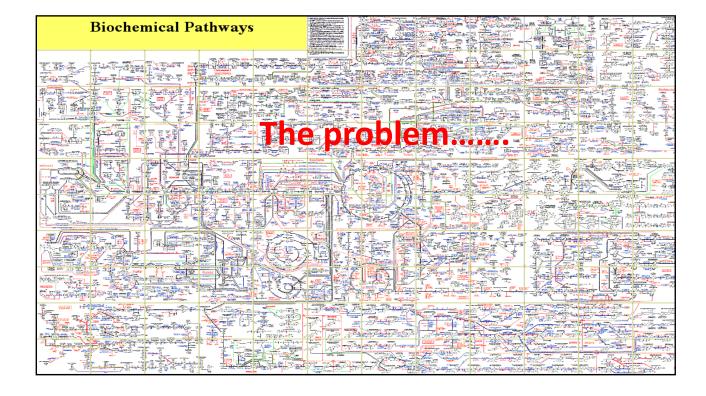
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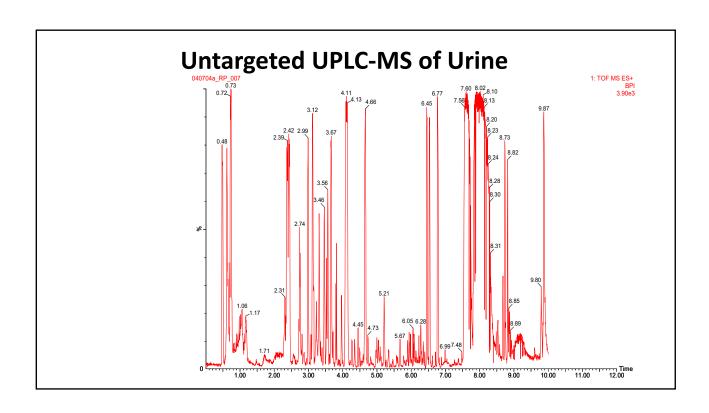
### **An Example: Untargeted Metabolomics**

- Metabonomics/metabolomics (metabolic phenotyping) untargeted analysis in its purest form.
- Intended to be unbiased, hypothesis free, but hypothesis generating.
- The aim is to find metabolites, or patterns of metabolites, that define a phenotype, in specific areas of basic biology, disease, toxicity etc.
- Ideally these "biomarkers" should be mechanistic and specific for the condition under investigation
- In the absence of knowing what they are the quantitative measurement is not an absolute concentration but a relative amount or fold change



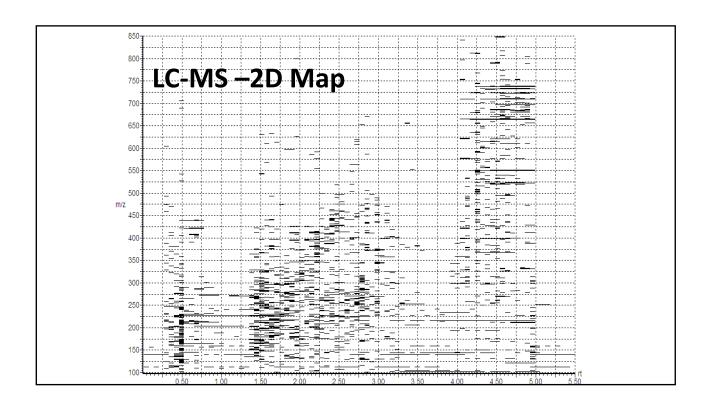












# Sources of variability in LC/MS-based methods

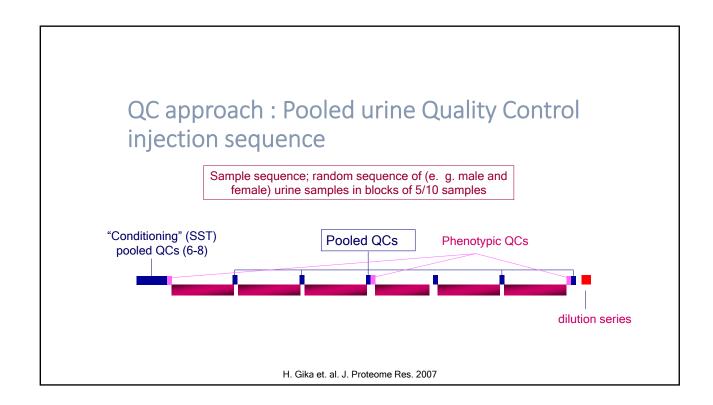
- Changes in chromatographic properties (retention, peak shape, resolution, selectivity).
- Changes in mass accuracy.
- Changes in sensitivity with time.





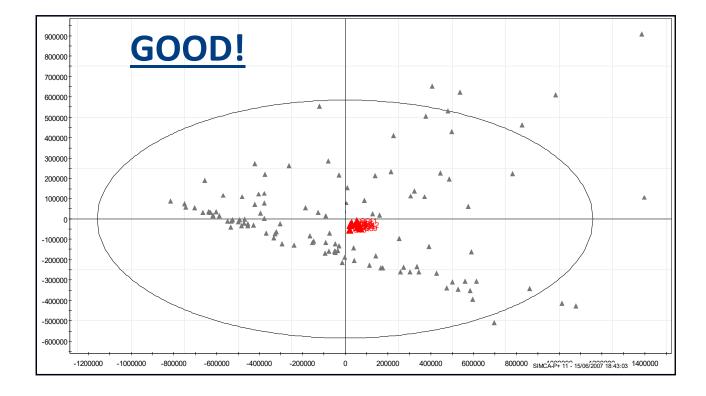
### **Showing Precision and Stability via Quality Control**

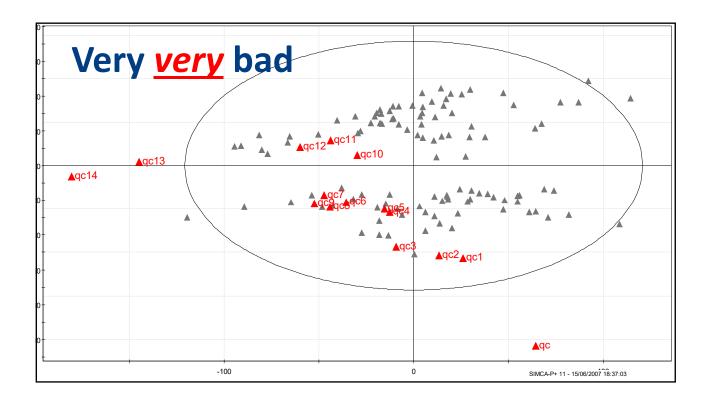
- How do you formulate a QC policy when you don't know what you want to measure?
- One approach is to use a standard/representative BIOLOGICAL sample, ideally by taking an aliquot of each sample to make a pooled sample.
- This pooled QC can also be used as a system suitability test, and via a
  "dilution series, to show the linear range of the system
- For long term studies may also want to use a reference sample/QC for inter-batch correction





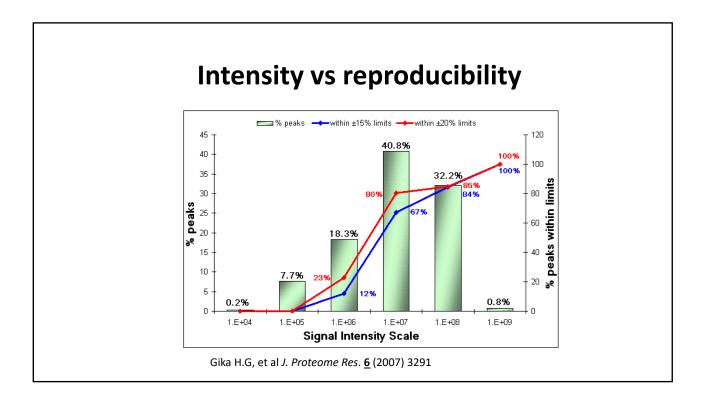


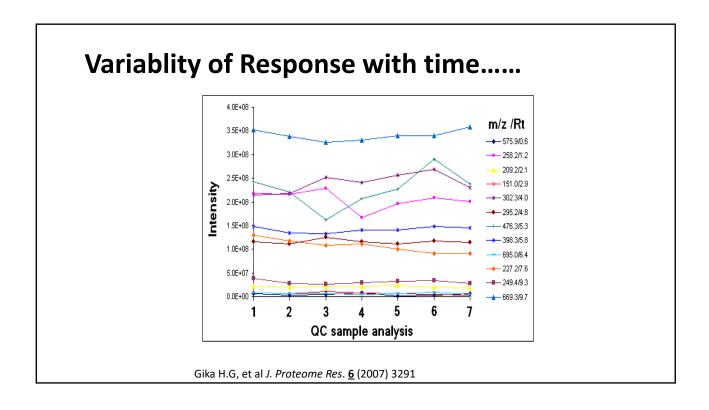






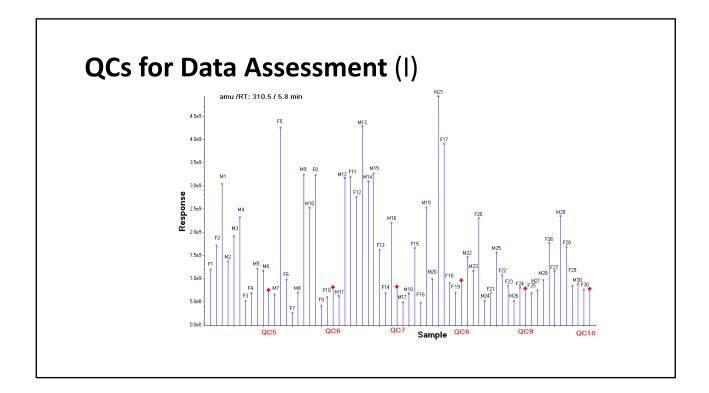


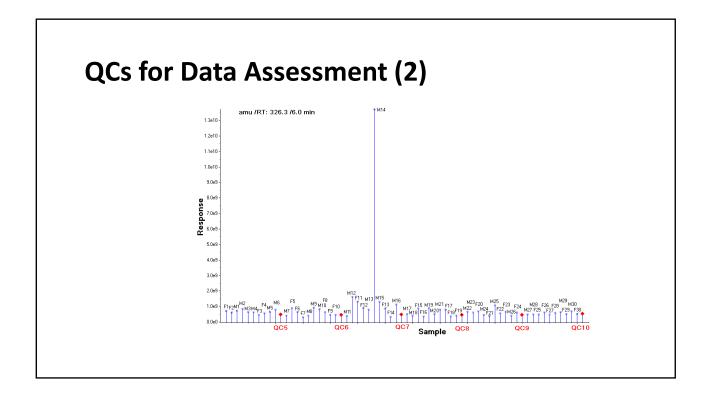






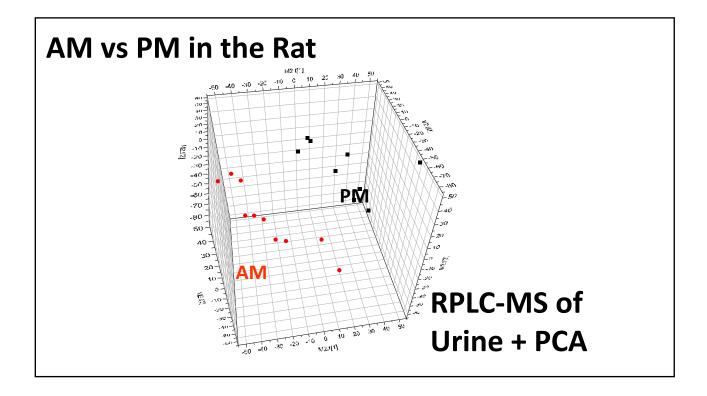


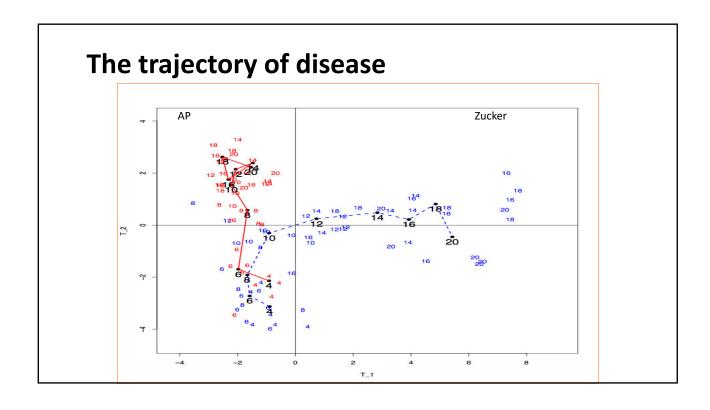






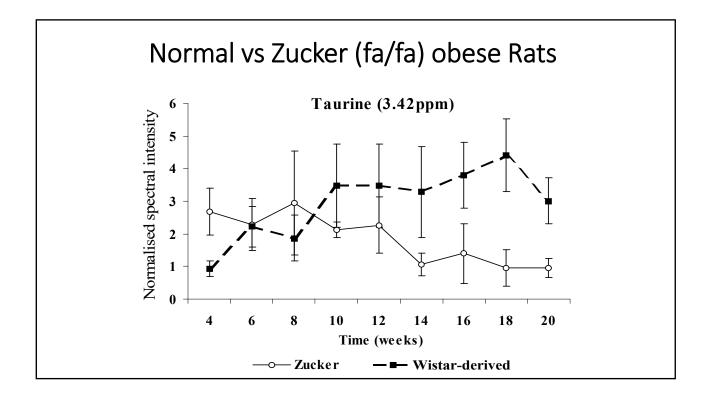


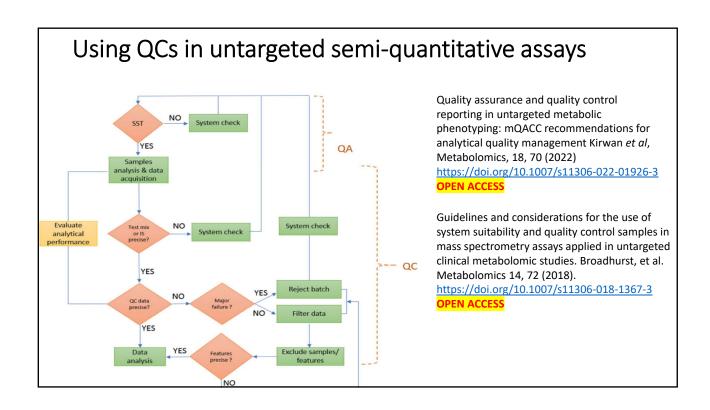
















### **Conclusions**

- Untargeted semi-quantitative methods can provide repeatable and robust fold change data to identify potential biomarkers
- Instrument performance, analyte precision, repeatability, robustness can be demonstrated, even when the identity of the analyte has yet to be determined, via pooled (and other) QCs
- Having identified the biomarkers develop quantitative targeted methods

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