



NUTRIOME

NUTRIOME workshop1

Large-scale data handling and using tools to visualise multi-layered data from meal studies



Funded by
the European Union



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NUTRIOME

Techniques to measure metabolomics

Overview

- Introduction
- Approaches
- Study Design
- Quality Control
- Applications

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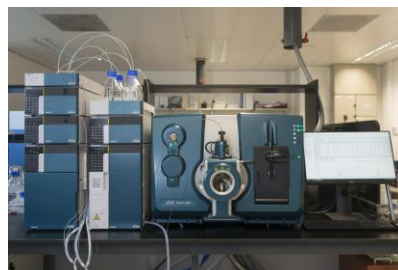


Approaches

Study of small molecules called metabolites: alterations in metabolic pathways under different conditions



NMR



LC-MS
GC-MS

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Targeted and non-targeted approach

Targeted: prior knowledge of metabolites to be measured

Non-targeted: no prior selection of metabolites

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Advantages of targeted data

- Quantitative
- Cross cohort comparisons
- Reproducibility
- Use as diagnostic biomarkers
- Re-use of data is easier

Advantages of un-targeted data

- Broader coverage of metabolome
- New discoveries possible
- Hypothesis generating

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Data Format

Targeted

Concentration [µM]																		
Sample Identification	C0	C2	C3	C4	C14	C16	C18:1	Trigonellin	TMAO	Ala	Arg	Asn	Asp	Cys	Gln	Glu	Gly	
	Acylcarniti	Acylcarniti	Acylcarniti	Acylcarniti	Acylcarniti	Acylcarniti	Acylcarniti	Alkaloids	Amine Ox	Aminoacid	Aminoacid	Aminoacid	Aminoacid	Aminoacid	Aminoacid	Aminoacid	Aminoacid	
P_11	21.9	13.7	0.539	0.792	0.058	0.114	0.106	3.125	18.9	609	158	82	9.954	46.3	931	49	440	
P_12	23.1	16.2	0.734	0.779	0.043	0.103	0.137	1.366	9.654	672	80.6	145	13.4	30.2	1075	84.3	458	
P_13	24.9	8.466	0.206	0.171	0.03	0.095	0.06	1.387	9.097	483	116	49.7	7.034	35.1	724	42.5	269	
P_14	29.1	14.2	0.428	0.362	0.063	0.114	0.128	0.932	9.652	423	136	49	11.3	39.3	721	46	313	
P_2	25.9	9.573	0.427	0.399	0.037	0.076	0.092	0.916	4.274	718	85.6	107	13.5	29.5	842	81	389	
P_3	26.4	8.969	0.417	0.328	0.036	0.126	0.11	2.846	25.2	414	178	51.2	9.11	29.9	656	36.8	313	
P_30	26.1	10.9	0.407	0.587	0.024	0.133	0.105	5.068	88	624	181	66.9	10.7	30.8	722	38.2	317	
P_31	17.4	9.942	0.46	0.445	0.019	0.117	0.079	4.452	147	418	144	40.2	10.9	18.2	560	28.2	217	
P_34	16.1	6.566	0.469	0.44	0.023	0.11	0.06	4.485	175	633	235	73.7	11.8	28.2	770	35	297	
P_35	13.3	6.075	0.436	0.303	0.023	0.109	0.145	4.391	225	403	134	51.7	9.041	30.6	562	25.7	262	
P_36	18.2	6.508	0.385	0.382	0.013	0.068	0.06	3.645	53.5	379	159	43.9	6.527	34.8	503	26.4	201	

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Data Format

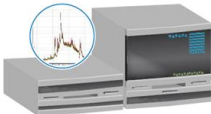
Un-targeted

Compound Name	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
RT	0.543	0.551	0.586	0.586	0.59	0.591	0.592	0.595	0.597	0.604	0.605	0.611	0.616	0.623	0.624
Mass	155.0692	103.9641	196.0581	171.9075	166.0476	155.9339	218.0551	246.0502	216.0396	125.9988	186.0292	113.0589	180.0631	150.0527	301.0457
P100 V1 0h neg	3262	1541	119397	1063	3965	3396.5	4236	1856	6153.5	56552	5088	7109	9009	12818.5	1134
P100 V1 2h neg	3262	1541	90628	14178	3965	3396.5	4236	1856	6153.5	1764.5	5088	52467	9009	12818.5	1134
P100 V1 4h neg	3262	1541	178767	23173	3965	3396.5	4236	1856	6153.5	48314	5088	7109	9009	12818.5	1134
P100 V1 6h neg	3262	1541	10734	1063	3965	3396.5	4236	1856	6153.5	74181	5088	44811	9009	12818.5	1134
P100 V1 24h neg	3262	1541	10734	1063	3965	3396.5	4236	1856	6153.5	61569	5088	7109	9009	12818.5	15658
P102 V2 0h neg	34749	1541	77624	2126	104976	3396.5	4236	1856	69028	29558	5088	30851	120668	228586	12174
P102 V2 2h neg	22252	42764	24998	1063	20624	9740	18385	4484	32677	1764.5	23395	15908	18018	40522	2268
P102 V2 4h neg	12729	1541	32949	2328	28703	16898	21068	1856	40997	1764.5	5088	7109	9009	108444	1134
P102 V2 6h neg	10440	21988	72304	3322	57946	23795	30742	10753	58762	29674	5088	7109	67997	175683	4927
P102 V2 24h neg	17642	1541	111298	1063	76775	17374	4236	1856	6153.5	36856	5088	22362	191573	244794	12604
P105 V3 0h neg	34245	9329	10734	1063	3965	3396.5	4236	1856	48548	43415	10176	61865	62103	12818.5	1134

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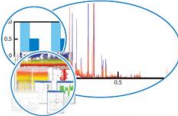


Study Design



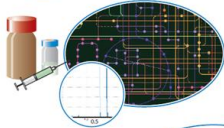
Sample treatment
Metabolite extraction

Data acquisition and conversion*
Feature detection
Generation of a reference database
Data import, compression, and matrix construction

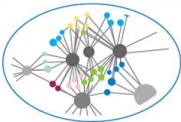


Data processing and statistical analysis⁵
Data alignment, filtering, normalization, transformation, scaling
Multivariate and univariate analyses

UNTARGETED



Metabolite identification⁷
Search in databases
MS/MS, isotopic pattern, standard injection

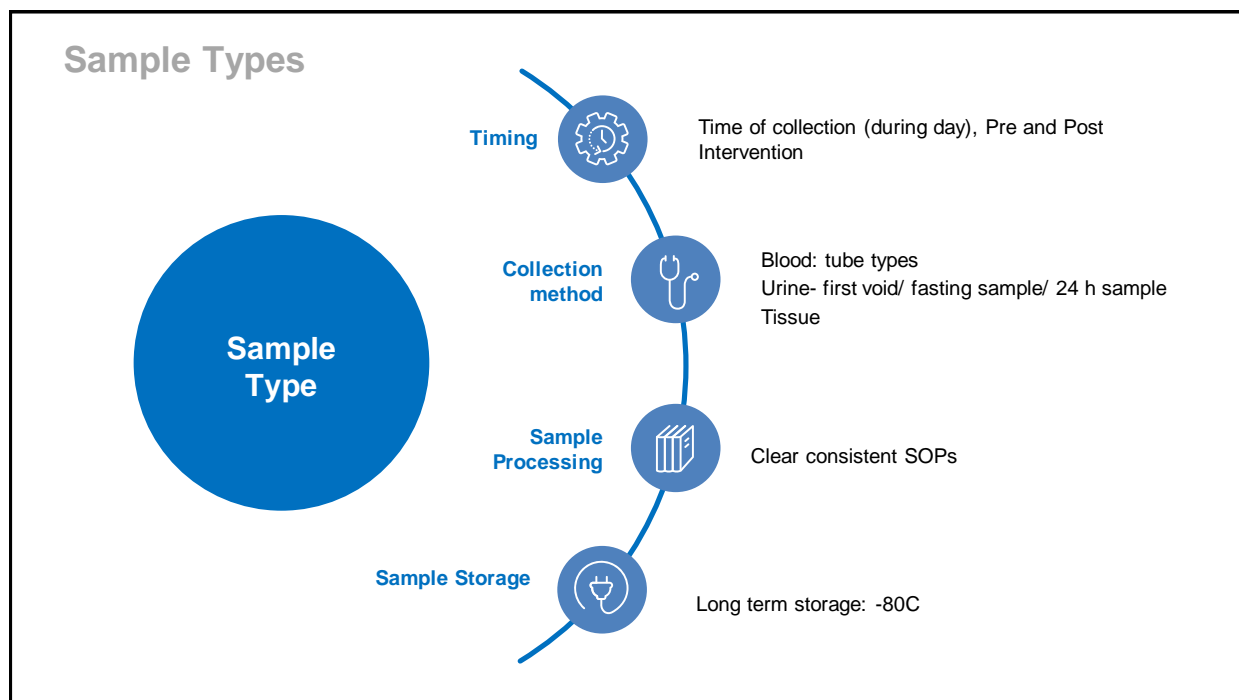


Biomarker identification and interpretation
Data validation and biochemical interpretation




Preparation of standards
and calibration curves

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Biofluids



Blood: plasma, and serum

Plasma – need to decide on the anti coagulant and be consistent

Serum – clotting time and temperature needs to be consistent

Strict SOPs should be in place for collection of samples
 some key items: time of collection
 fasting state
 consistent centrifugal speeds and temperature to be used

serum: clotting time
 plasma: time from collection to processing

Storage: -80C and minimal freeze thaw cycles

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Blood: plasma, and serum



Key recommendations

- Design – decide on collection type (serum/ plasma)
- SOP for collection (clotting times, processing times, temperature, centrifugal speed)
- Storage: -80C
- Minimise Freeze Thaw cycles

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SERUM
Clot for 30 min at room temperature, centrifuge 10 min at 4°C and 2,500 × g

Tips & Tricks

- ☹️ Serum samples can show features of polymeric material, peptides, and xanthenes (the latter ones probably from clot).
- ☹️ Higher content of peptides and protein fragments
- 😊 Incubation affects analyte peak area less in serum than in plasma, what may result in reduced peak areas of plasma amino acids, and carbohydrates with GC-MS detection
- 😊 Metabolite concentrations were found generally higher in serum, yet still highly correlated with plasma

PLASMA
Mix with anticoagulant, centrifuge 10 min at 4°C and 2,500 × g

Anticoagulants: L/ Na Heparin, K-EDTA, Na Citrate

- ☹️ Anticoagulants may interfere with NMR signals and MS analysis
- ☹️ Presence of anticoagulant cations can cause problems in metabolomic and lipidomic analysis by binding to negatively charged phospholipids and causing ion enhancement.
- ☹️ Lithium ions from heparin can exacerbate matrix effects by increasing the signals of plastic polymers from vacutainer container
- ☹️ EDTA was poorly suited for the analysis of polar metabolites. Sodium citrate can cause problems in determining citric acid and its derivatives
- ☹️ Sodium and potassium formate ion clusters from K-EDTA, Na Citrate creates adducts in MS spectra
- ☹️ Presence of anticoagulant residues may affect further extraction processes including derivatization efficiency in case of GC-MS analysis
- 😊 Isolation of plasma yields a greater sample volume per volume of whole blood drawn
- 😊 Absence of platelet microparticles and postcoagulation protein fragments

HEMOLYSIS PROBLEM:
The breakdown of blood cells strongly alters metabolic profiles of blood-derived samples, by increasing the concentrations of numerous metabolites coming from the intracellular space as well as by inducing the degradation of some compounds by the action of released enzymes

NORMAL SAMPLE

~~HEMOLYZED SAMPLES~~

HEMOLYZED SAMPLES SHOULD BE AVOIDED IN METABOLOMIC STUDIES



Mol. Nutr. Food Res. 2018, 1800384

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Urine

- Urine is composed of endogenous and exogenous metabolites that have been filtered from the bloodstream by the kidneys
- Collected at home by participants (keep chilled)
- Issues to consider: first void/ mid stream/ time of day/ fasting
24 h urine collection
- Processing: centrifugation before freezing
- Storage: -80C. Minimise freeze thaw cycles

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Urine

Recommendations

- SOP – for collection – clear instructions to participants
- Processing prior to storage
- Storage: -80C
- Limit freeze thaw cycles

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Feces

- Feces are considered a non-invasive proxy for the study of the intestinal microbiome and metabolome.
- The faecal metabolome- representation of host metabolism, microbial metabolism and host-microbial co metabolism


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Feces


- Sample collection: (1) spot sample
(2) bulk collection
- Specialised collection kit recommended
- Recent dietary intake recorded
- Clear instructions to volunteers
- Site of sampling needs to be consistent across the study
- Multiple sites if possible

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NUTRIOME

Tips & Tricks

Spot urine sample




24 h urine sample



Sarstedt®
MarketLab®


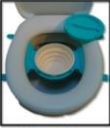
URINE COLLECTION

Wide-mouth plastic bag and a plastic container




FECES COLLECTION

Stool specimen collection units






Fecotainer®

Freezing toilet at -30°C



Toilet type T-1970, Gisebo;
Privetti® Pikkuvihrea

 collection of 24h urine sample requires **an instruction for volunteer.**


 avoid stool contamination with water, urine or other materials (e.g. toilet paper). **An instruction for volunteer is required.**

Samples should be transferred/delivered to laboratory as soon as possible for further storage (< 2h).

In contrast to serum/plasma, urine and feces require sample specific normalization.
Volume and weight of urine and feces and thus the overall concentration of metabolites may vary drastically.
Information such as volume and weight for both matrices should be collected at sample arrival to the laboratory, before samples aliquotation.

Mol. Nutr. Food Res. **2018**, 1800384

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NUTRIOME

Feces

Recommendations

- Bulk stool if possible (collection device consistent throughout study)
- Spot sampling may introduce variation
- Minimise freeze thaw
- Storage – at -80C recommended

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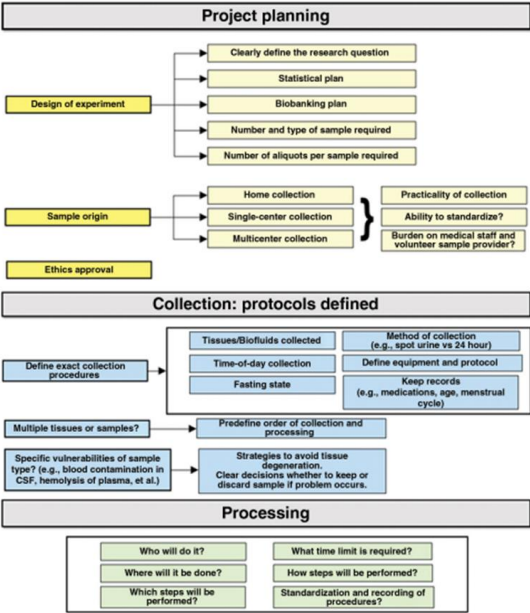
Clinical Chemistry 64:8
1158-1182 (2018)

Review

Preanalytical Processing and Biobanking Procedures of Biological Samples for Metabolomics Research: A White Paper, Community Perspective (for "Precision Medicine and Pharmacometabolomics Task Group"–The Metabolomics Society Initiative)

Jennifer A. Kirwan,^{1,2*} Lorraine Brennan,³ David Broadhurst,⁴ Oliver Fiehn,⁵ Marta Cascante,⁶ Warwick B. Dunn,⁷ Michael A. Schmidt,^{8,9} and Vidya Velagapudi^{10*}

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Kirwan et al. 2018

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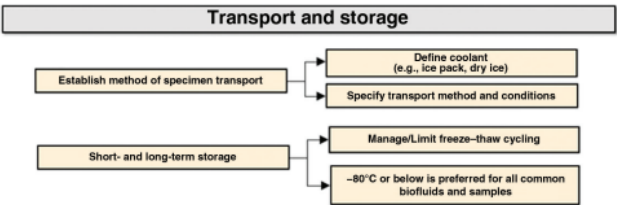


Fig. 1. Schematic of standard stages in planning tissue or body fluid collection for a biobank or tissue repository.

Kirwan et al. 2018

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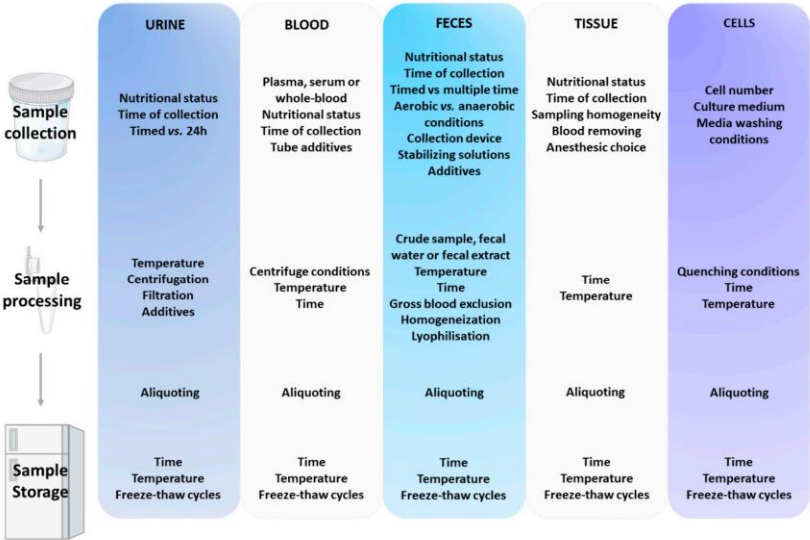


Figure 1. Summary of pre-analytical factors that can affect metabolite profiles in various matrices.

Smith et al 2020

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Statistical Plan

- Plan for analysis documented
- Data treatment
- Engage with statistician

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Quality Control



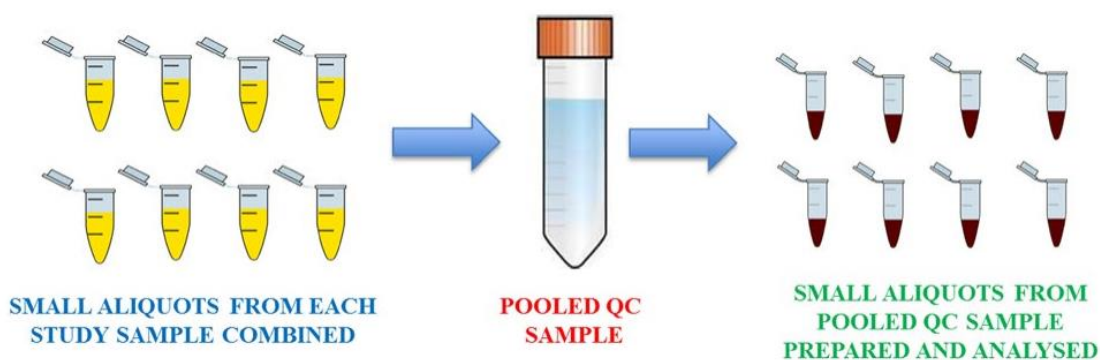
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Quality Control

- Safeguards to be incorporated into a successful metabolomics study
- All samples that are to be directly compared to one another must be collected, processed, measured and statistically analysed in exactly the same way.
- Randomisation: samples should be extracted processed and measured in a random order.

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Broadhurst et al. 2018 Metabolomics, 14, 72

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Standard Reference Material

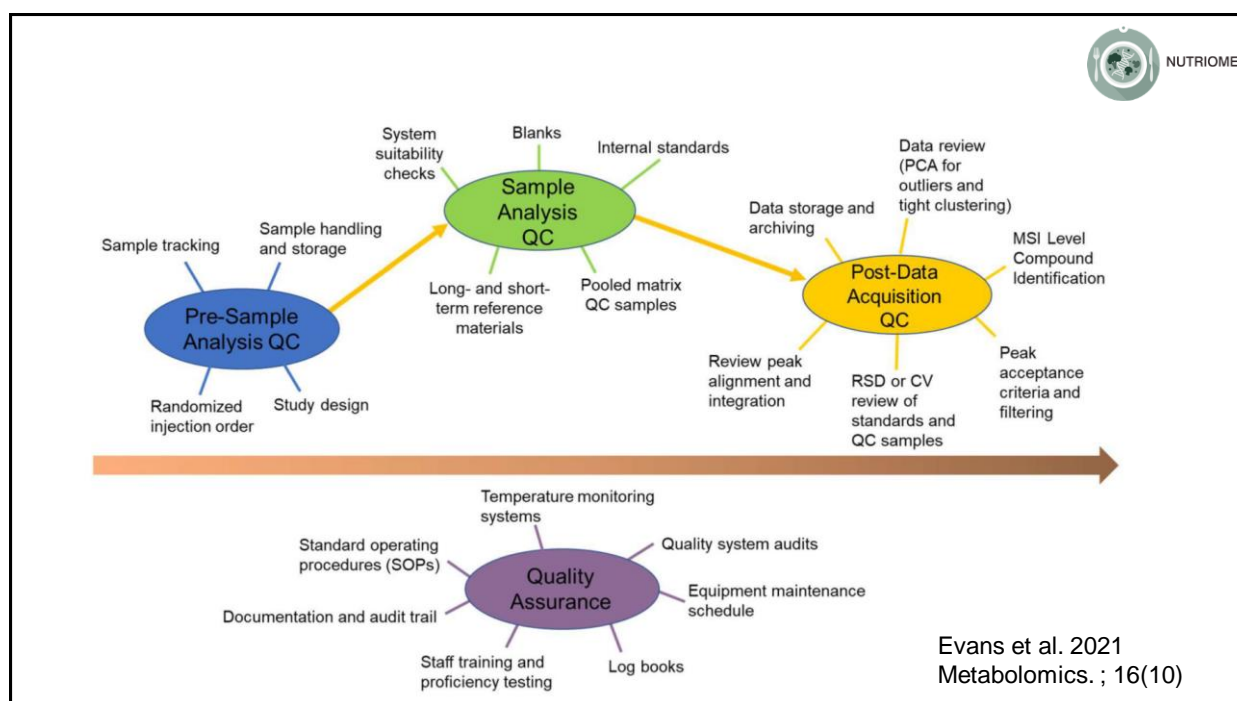
a method to allow quality assessment across different laboratories



Injection Number	Sample Type
1	System Suitability Blank Sample
2	System Suitability Sample 1
3	System Conditioning QC sample 1
4	System Conditioning QC sample 2
5	System Conditioning QC sample 3
6	System Conditioning QC sample 4
7	Blank Extraction Sample 1
8	System Conditioning QC sample 5
9	System Conditioning QC sample 6
10	System Conditioning QC sample 7
11	System Conditioning QC sample 8
12	Pooled QC sample 9
13	Pooled QC sample 10
14	Standard Reference Material injection 1
15	Biological sample 1
16	Biological sample 2
17	Biological sample 3
18	Biological sample 4
19	Biological sample 5
20	Pooled QC Sample 11
21	Biological sample 6
22	Biological sample 7
23	Biological sample 8
24	Biological sample 9
25	Biological sample 10
26	Pooled QC Sample 12
27	Biological sample 11
28	Biological sample 12
29	Biological sample 13
30	Biological sample 14
31	Biological sample 15
32	Pooled QC Sample 13
33	Biological sample 16
34	Biological sample 17
35	Biological sample 18
36	Biological sample 19
37	Biological sample 20
38	Pooled QC Sample 16
39	Standard Reference Material injection 2

Broadhurst et al. 2018 Metabolomics, 14, 72

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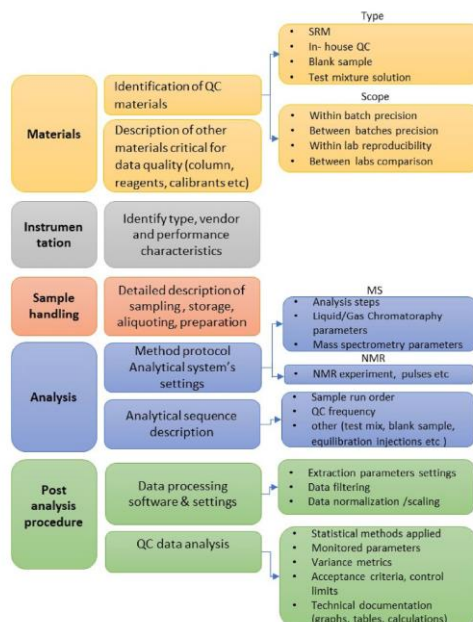


Evans et al. 2021
Metabolomics. ; 16(10)

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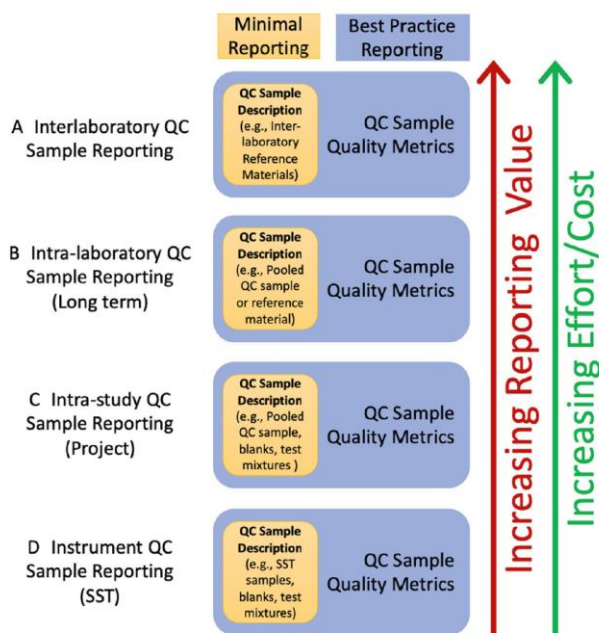


Information that should be documented in manuscripts



Kirwan et al 2022

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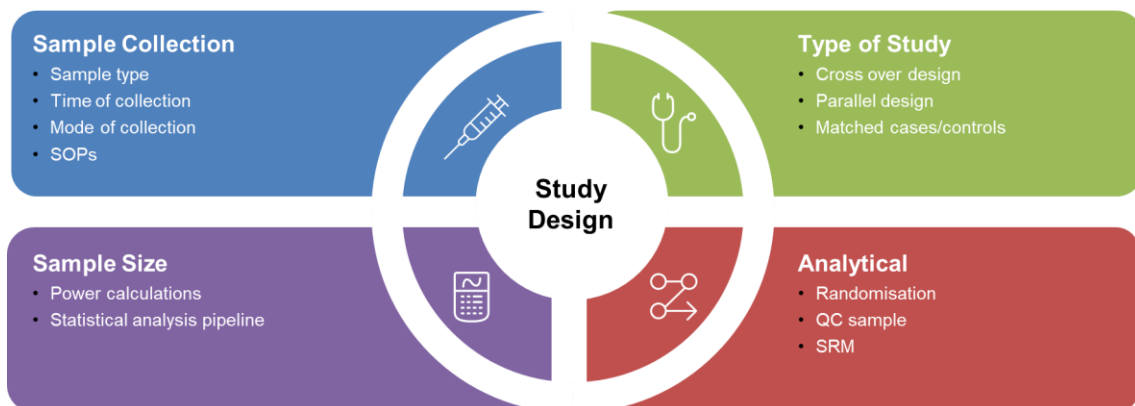


Kirwan et al 2022

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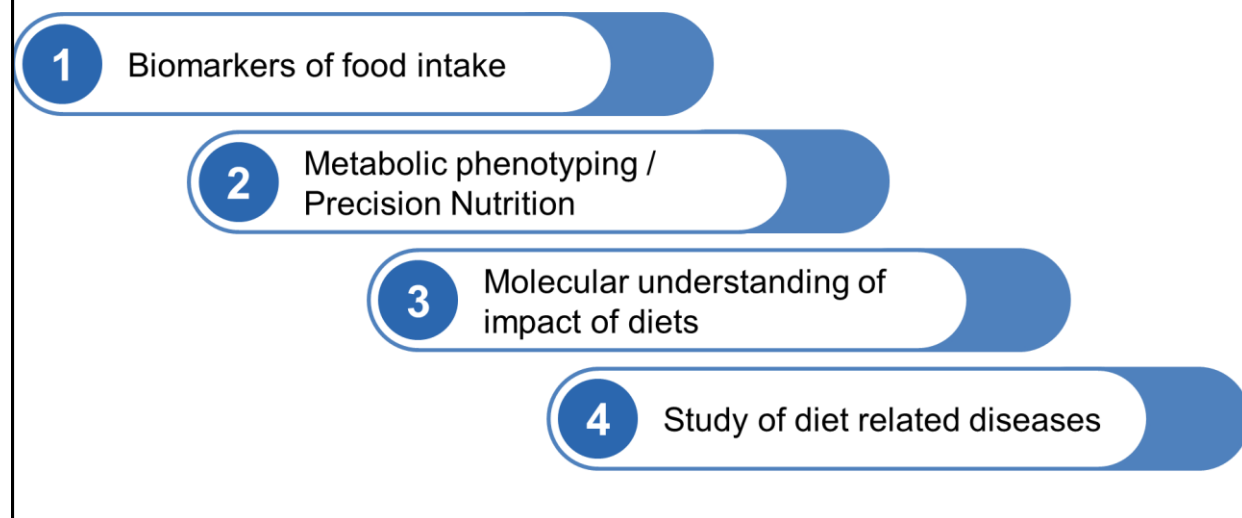
Summary



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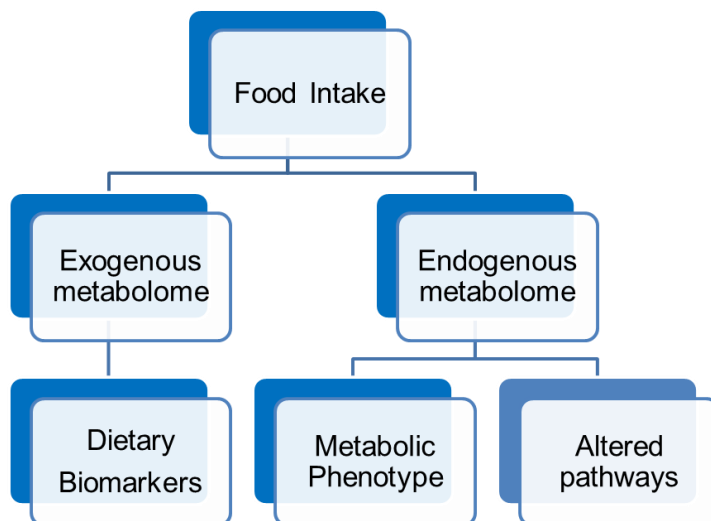


Metabolomics in nutrition



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Metabolomics in nutrition



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Food Intake Biomarkers

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Food Intake Assessment

Food diaries, FFQ, 24 hr recalls



Limitation-1

Measurements over short periods of time may be unrepresentative



Limitation-3

Errors in reporting intakes



Limitation-2

Recall of eating behaviour can be difficult



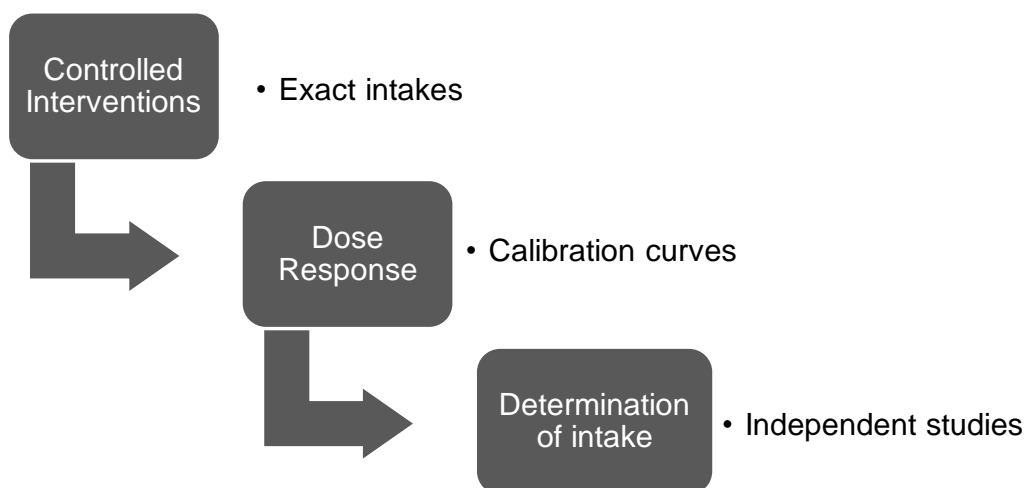
Limitation-4

Recording process alters dietary habits

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Approach



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Food Intake Biomarkers



Identify biomarkers of legume intake

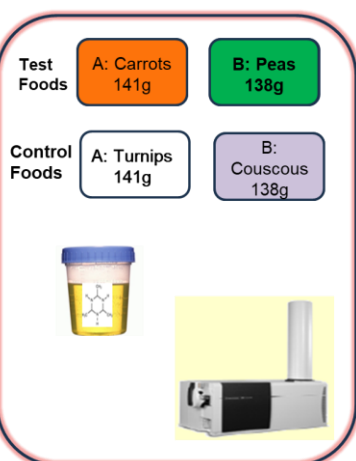
Confirmation of biomarkers

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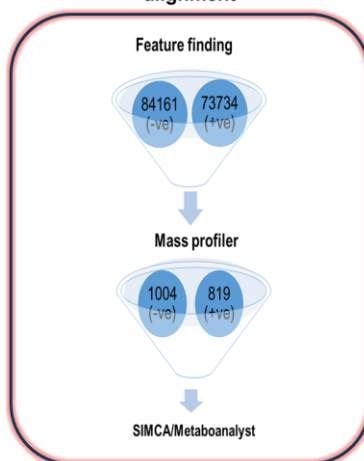
Legume biomarker discovery



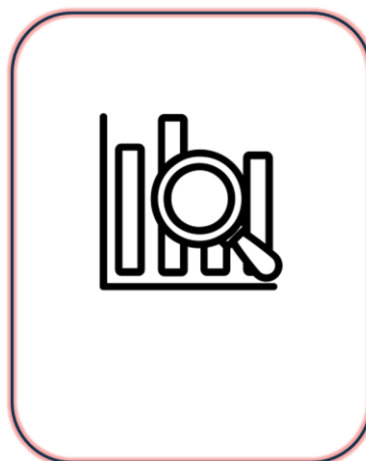
Foods, sample collection and analysis



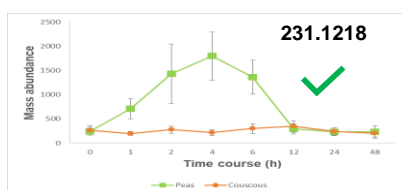
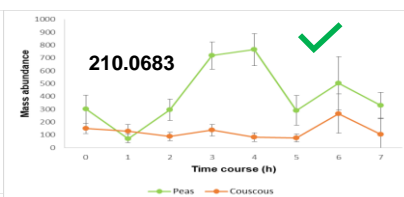
Feature extraction and alignment



Statistical analysis



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Accurate mass (M1 scan)



LC-MS/MS



Markers identified

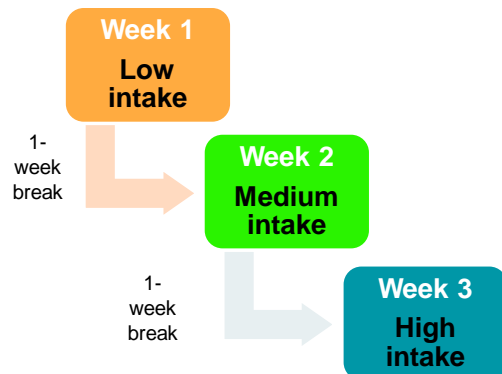
2-Isopropylmalic acid (Level 1)

Asparaginyl valine (Level 2)

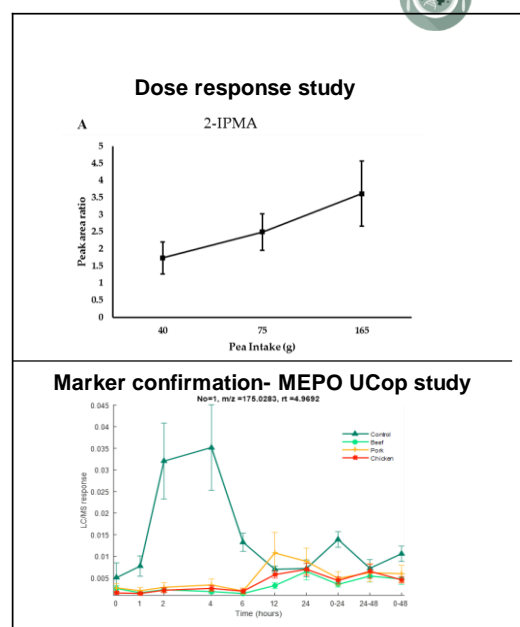
N-Carbamoyl-2-amino-2-(4-hydroxyphenyl)acetic acid (Level 2)

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Biomarker Validation



- *Samples collected



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Biomarker Examples



Discovery and Validation of Banana Intake Biomarkers Using Untargeted Metabolomics in Human Intervention and Cross-sectional Studies

Natalia Vázquez-Manjarrez,^{1,2} Christoph H Weinert,³ Maria M Ulaszewska,⁴ Carina I Mack,³ Pierre Michéau,¹ Mélanie Pétera,¹ Stephanie Durand,³ Estelle Pujos-Guillot,⁴ Björn Egert,³ Fulvio Mattivi,^{4,6} Achim Bub,⁷ Lars Ove Dragsted,² Sabine E Kulling,³ and Claudine Manach¹

A metabolomic study of biomarkers of meat and fish intake^{1,2}

William Cheung,⁵ Pekka Keski-Rahkonen,³ Nada Assi,³ Pietro Ferrari,³ Heinz Freisting,³ Sabina Rinaldi,³ Nadia Slimani,² Raül Zamora-Ros,⁶ Milena Rundle,⁶ Gary Frost,⁶ Helena Gibbons,⁶ Eibhlín Cars,⁶ Lorraine Brennan,⁶ Amanda J Cross,⁷ Valeria Pula,⁸ Salvatore Panico,⁸ Carlotta Sacerdote,⁸ Domenico Palli,⁹ Rosario Tumino,¹⁰ Tilman Kühn,¹¹ Rudolf Kaack,¹² Heiner Boeing,¹³ Anna Floegel,¹⁴ Francesca Mancini,^{14,15} Marie-Christine Boutron-Ruault,¹⁴⁻¹⁶ Laura Baglio,^{17,18} Antonia Trichopoulos,^{19,20} Andromiki Naska,^{19,20} Philippos Orfanos,^{19,20} and Augustin Scalbert^{1,6}

REVIEW

Open Access

Biomarkers of cereal food intake

Rikard Landberg¹, Kati Hämäläinen², Kieran Tsuchi³, Mar García-Alay^{4,5}, Izabela Biskup³, Rafael Llorach^{4,5}, Xiaofei Yin⁶, Lorraine Brennan⁶ and Marijka Kolehmainen⁷



Ulaszewska et al. *Genes & Nutrition* (2018) 13:29
https://doi.org/10.1186/s12263-018-0620-8

Genes & Nutrition

REVIEW

Open Access

Food intake biomarkers for apple, pear, and stone fruit

Marynka Ulaszewska¹, Natalia Vázquez-Manjarrez^{2,3}, Mar García-Alay^{4,5}, Rafael Llorach^{4,5}, Fulvio Mattivi^{4,6}, Lars O. Dragsted⁷, Giulia Pratico⁸ and Claudine Manach⁷



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Biomarker Validation



VALIDATION OF FOOD INTAKE BIOMARKERS

PLAUSIBILITY

Is there a chemical or biological reason for increase in biomarker concentration?

TIME-RESPONSE

Is there a kinetic response?
Do repeated measures show same response?

DOSE-RESPONSE

As the food portion increases does biomarker concentration also increase?

ROBUSTNESS

Are there other confounding foods?
Is biomarker identified after a complex meal?



STABILITY

Is there any degradation of the biomarker in the biofluid?

PERFORMANCE

Has lab analysis examined biomarker accuracy, precision, sensitivity & specificity?

RELIABILITY

How does biomarker intake estimation compare to other dietary assessment methods?

REPRODUCIBILITY

Are the results reproducible in other labs and within other populations?



Dragsted et al 2018

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How do we use the biomarkers?

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Measure of
adherence to the
dietary intervention



Objective
measures of
dietary intake

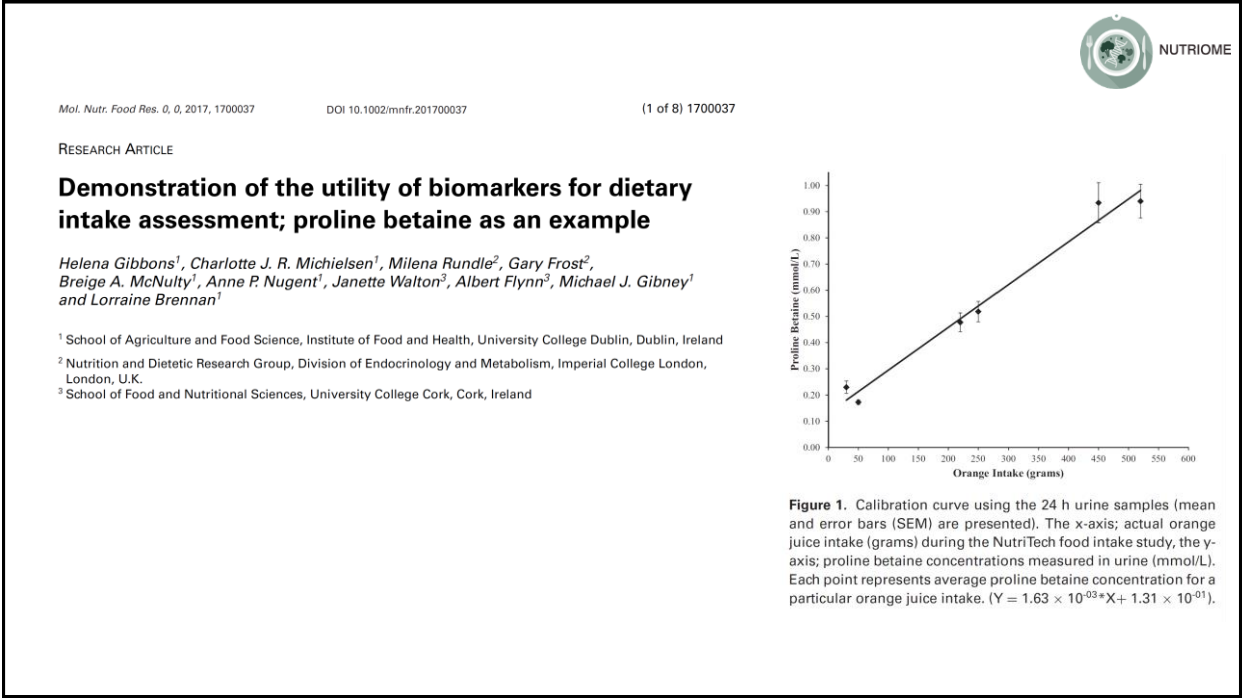


Correct self-
reported data



Relationships with
health/disease
parameters

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Calibration method

Citrus intake data

- $i = 1, \dots, n$: subject in the study (with $n = 565$);
- W_i : mean daily self-reported citrus intake (g/day);
- M_i : biomarker-derived estimates of citrus intake (g/day).

The aim is to estimate :

- \hat{X}_i : calibrated mean daily citrus intake (g/day).

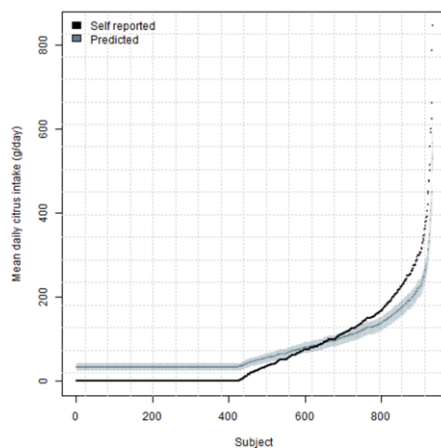
CALIBRATION EQUATIONS:

$$M_i = \beta_0 + \beta_1 W_i + \epsilon_i,$$

$$\hat{X}_i = \hat{\beta}_0 + \hat{\beta}_1 W_i$$

With $\epsilon_i \sim N(0, \sigma^2)$.

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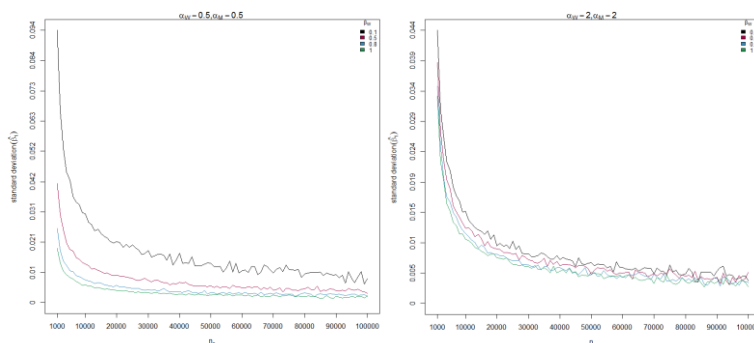
- Developed an on-line App
- <https://adiet.shinyapps.io/Bio-Intake/>

D'Angelo et al. 2019 AJCN

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How much biomarker data do you need ?



The figures above present the variability of the estimated slope coefficient $\hat{\beta}_1$ in the “best” and “worst” case scenarios.

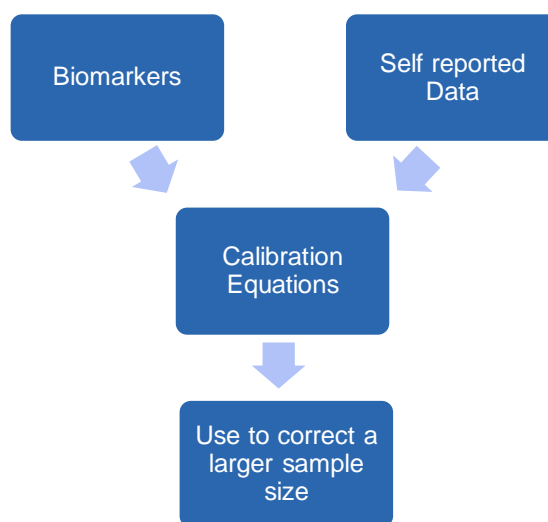
Biomarker data needed for approx. 20-30% of the population

D'Angelo et al. 2019 AJCN

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Calibration method




D'Angelo et al. 2019 AJCN

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Calibration method

NUTRIOME

The Journal of Nutrition
Nutritional Epidemiology

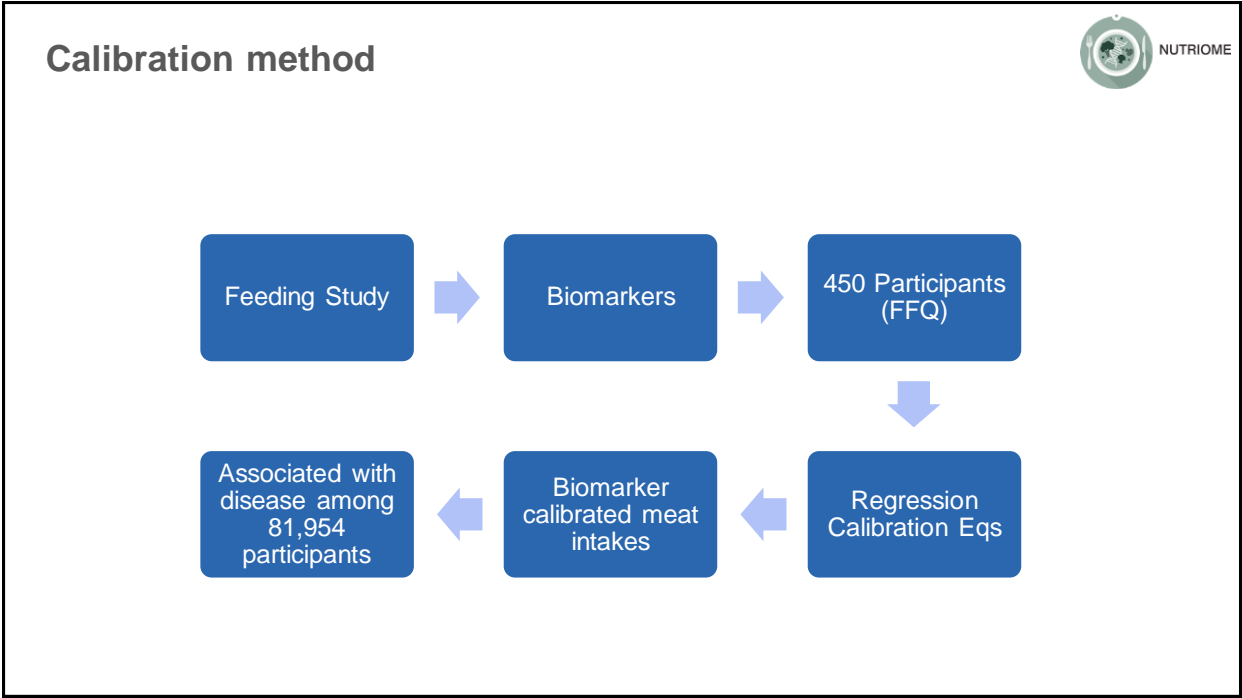


Biomarker-Calibrated Red and Combined Red and Processed Meat Intakes with Chronic Disease Risk in a Cohort of Postmenopausal Women

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Calibration method





TABLE 5 T2D incidence HRs, and 95% CIs for a 40% increment above the median intake for red meat and for red plus processed meat in a Women’s Health Initiative cohorts of 81,954 postmenopausal US women enrolled during 1993–1998 at 40 US clinical centers and followed through February 2020¹


Outcome (n = participants with outcome)	No adjustment for BMI or dietary correlates				With adjustment for BMI and dietary correlates			
	Red meat intake, g/d	P value	Red + processed meat intake, g/d	P value	Red meat intake, g/d	P value	Red + processed meat intake, g/d	P value
T2D (12,145)	1.37 (1.34, 1.39)	<0.001	1.35 (1.33, 1.37)	<0.001	1.08 (1.04, 1.12)	<0.001	1.09 (1.05, 1.13)	<0.001

¹Values are HRs (95% CIs). Red meat median intakes were 24.7 g/d with biomarker calibration and 31.8 g/d without biomarker calibration, and red plus processed meat median intakes were 34.8 g/d with biomarker calibration and 42.2 g/d without biomarker calibration. DM-C, dietary modification comparison group; OS, observational study; T2D, type 2 diabetes.

²HR estimates and 95% CIs are based on Cox models with baseline hazard rates stratified on study component (DM-C or OS), hormone therapy trial status (estrogen plus progestin, estrogen plus progestin placebo, estrogen-alone, estrogen-alone placebo, not randomized), age at enrollment (50–54, 55–59, 60–64, 65–69, 70–74, or ≥75 y), and with adjustment for a disease-specific set of potential confounding factors.

Calibration method





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Associations of Biomarker-Calibrated Healthy Eating Index-2010 Scores with Chronic Disease Risk and Their Dependency on Energy Intake and Body Mass Index in Postmenopausal Women

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Calibration method



TABLE 4 Associations between a 20% increment in HEI-2010 score with and without biomarker calibrations with additional for calibrated energy and adjustment BMI and type 2 diabetes in the WHI¹

	No. of cases (rate per 1000 person-years)	HR (95% CI) ²				
		Uncalibrated	Calibrated ³	Calibrated, adjusted for calibrated total energy ⁴	Calibrated, adjusted BMI	Calibrated, adjusted for calibrated total energy and BMI
Type 2 diabetes ⁵	14,201 (10.14)	0.91 (0.90, 0.93)	0.45 (0.36, 0.55)	0.84 (0.70, 1.02)	0.85 (0.74, 0.97)	0.87 (0.75, 0.99)

¹CT, Clinical Trial; CVD, cardiovascular disease; FFQ, food-frequency questionnaire; E, estrogen; HEI, Healthy Eating Index; OS, Observational Study; P, progesterone; WHI, Women's Health Initiative.

²Cox proportional regression models stratified by 5-y age categories, study component (CT/OS), and HT(hormone therapy) trial arm, and adjusted for linear age, race/ethnicity (White, Black, Hispanic, other race/ethnicity), season of FFQ completion, education (\leq high school, some post-high school, college degree or higher), income ($<$ \$20K, \$20K to $<$ \$35K, \$35K to $<$ \$50K, \$50K to $<$ \$75K, \geq \$75 K), current smoking, alcohol intake (nondrinker, $<$ 1 drink/wk, 1 to $<$ 7 drinks/wk, \geq 7 drinks/wk), total recreational physical activity, dietary supplement use, postmenopausal hormone therapy (never, past, current E-alone, current E+P), history of CVD, and family history of diabetes.

³HEI-2010 scores are biomarker calibrated.

⁴Adjustment for calibrated total energy using doubly labeled water.

⁵Incidence.

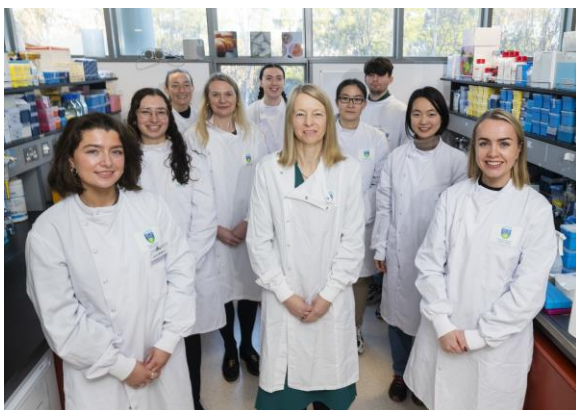
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Conclusions



- Metabolomics – wide range of applications in nutrition research
- Precision Nutrition – metabotypes
- Food Intake Biomarkers

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Funding Agencies



European
Commission