

Nutrimetabolomics: Biomarker Discover, Data Quality Control, Bioinformatics Tools and Computing Hardware

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Contents

Preface	5
Introduction	6
0.1 Biomarker Discovery	6
1 A Mini-review on Biomarkers of Whole Grain Barley and Whole Grain Wheat Intake	7
2 Discovering Barley Intake Biomarkers in Urine by UPLC-MS Based Untargeted Metabolomics	8
3 Barley Intake Biomarker: Compound Identification and Structure Elucidation	9
3.1 Abstract	9
3.2 Introduction	9
3.2.1 Phytosterol and Fragmentation Behaviour	9
3.3 Materials and methods	9
3.3.1 Chemicals	9
3.3.2 Apparatus	9
3.3.3 UPLC-MS/MS analysis of Sitostanol	9
4 Discovering Novel Intake Biomarkers of Whole Grain Wheat Intake by LC-MS Based Untargeted Metabolomics	10
5 Data Quality Control (QC) and Quality Assurance (QA) in LC-MS Based Untargeted Metabolomics	11
5.1 Introduction	13
6 Several R Functions Facilitating LC-MS Based Metabolomics Data Analysis Workflow	14
6.1 abstract	14
6.2 "Tidy" High-throughout Analysis Data, Exemplified by RNA sequencing data	14
6.3 m2r	14
6.4 plot_excretion	14
6.5 plot_intervention	14
7 Implementing A Streamlined Metabolomics Data Analysis Workflow (EZMS) Based on R Programming Language	15

8	Using a Budgeted Device to Compute High-throughout Metabolomics Data	16
8.1	Abstract	16
8.2	Introduction	16
	Closing Remarks	17

Acronyms

GC-MS Gas Chromatography-Mass Spectrometry. 4

LC-MS Liquid Chromatography-Mass Spectrometry. 4

Preface

Introduction

0.1 Biomarker Discovery

Definition of Biomarker

Biomarker Classification

Biomarker Systematic review

Credibility of BFIs: Putative biomarker, Candidate biomarker, partially validated biomarker and fully-validated biomarker

Biomarker Validation

1 A Mini-review on Biomarkers of Whole Grain Barley and Whole Grain Wheat Intake

2 Discovering Barley Intake Biomarkers in Urine by UPLC-MS Based Untargeted Metabolomics

3 Barley Intake Biomarker: Compound Identification and Structure Elucidation

3.1 Abstract

3.2 Introduction

3.2.1 Phytosterol and Fragmentation Behaviour

Phytosterols ubiquitously occur in plant-based food[sterolmsms]. They were claimed to have health beneficial effects, such as lowering cholesterol. They occur in food as free sterols (FS), steryl esters (SE), and glycosylated conjugates comprised of steryl glucosides (SG) and acylated steryl glucosides (ASG).

Specific sterol profiles characteristic to certain plant families have been identified showing that a broad range of minor sterols occurs as free sterols or glycosylated conjugates

3.3 Materials and methods

3.3.1 Chemicals

Sitostanol standard (CAS Number 83-45-4, Avanti Polar Lipids Inc., USA) was transported and stored in -20 °C. Ethanol

3.3.2 Apparatus

UPLC-MS system (column: C18,) QTOF (VION, Waters, Milford, USA)

3.3.3 UPLC-MS/MS analysis of Sitostanol

[doi:10.1021/jf501509m] Mobile phase A: H₂O Mobile phase B: Methanol

Binary methods developed and optimized

Analysis methods referred[sterolmsms]. Sitostanol stock solution (1 mg/mL) was prepared in 100% ethanol. Further, stock solution was diluted by methanol, with the concentration of 0.02 mg/mL.

ESI positive mode was used to ionize.

4 Discovering Novel Intake Biomarkers of Whole Grain Wheat Intake by LC-MS Based Untargeted Metabolomics

5 Data Quality Control (QC) and Quality Assurance (QA) in LC-MS Based Untargeted Metabolomics

This is an abstract

Keywords:

5.1 Introduction

6 Several R Functions Facilitating LC-MS Based Metabolomics Data Analysis Workflow

6.1 abstract

I would like to test whether it's possible to input an abstract here.,

6.2 "Tidy" High-throughout Analysis Data, Exemplified by RNA sequencing data

6.3 m2r

6.4 plot_excretion

6.5 plot_intervention

7 Implementing A Streamlined Metabolomics Data Analysis Workflow (EZMS) Based on R Programming Language

8 Using a Budgeted Device to Compute High-throughout Metabolomics Data

8.1 Abstract

High-throughout metabolomics data is characterized as high computing and storage resource demanding.

How to compute the data locally (without sending it to a high-performance server) with a budgeted device could be an interesting topic to explore. Because this would provide possibilities to protect privacies in home-appliance or fulfil the real-time analysis tasks in some extreme conditions (such as in polar region or some areas with poor Internet connectivity)

why do i do this? because in the future, metabolomics analysis could become smart-home appliance, such as smart toilet or smart mirror. people can get their metabolome examined daily in their home. such a good vision raised several problems. data privacy problem and cost. because metabolome is considered as personal privacy. therefore, leak these privacy could result in bad results. however, if computed locally, whether it's possible to control the cost.

In this study, we simulated a computing task.

Not only limited to human metabolome for risk analysis. it could also be applied in the fridge for example, to detect microorganisms' characteristic metabolome.

in less developed countries, or in portable devices, transmitting the data could be very expensive (via satellite for example, in polar areas), therefore, computing such a dataset whether it's possible.

8.2 Introduction

Potential Use environment

hello

Closing Remarks