

# Guidance Document for Consistent Reporting of 'Omics Data From Various Sources

- Transcriptomics Reporting Framework (TRF)
- Metabolomics Reporting Framework (MRF)

Joshua Harrill (US EPA) and Mark Viant (Univ. Birmingham, UK)

WPHA Virtual Meeting

24 June 2020





## **EAGMST Omics Reporting Frameworks**

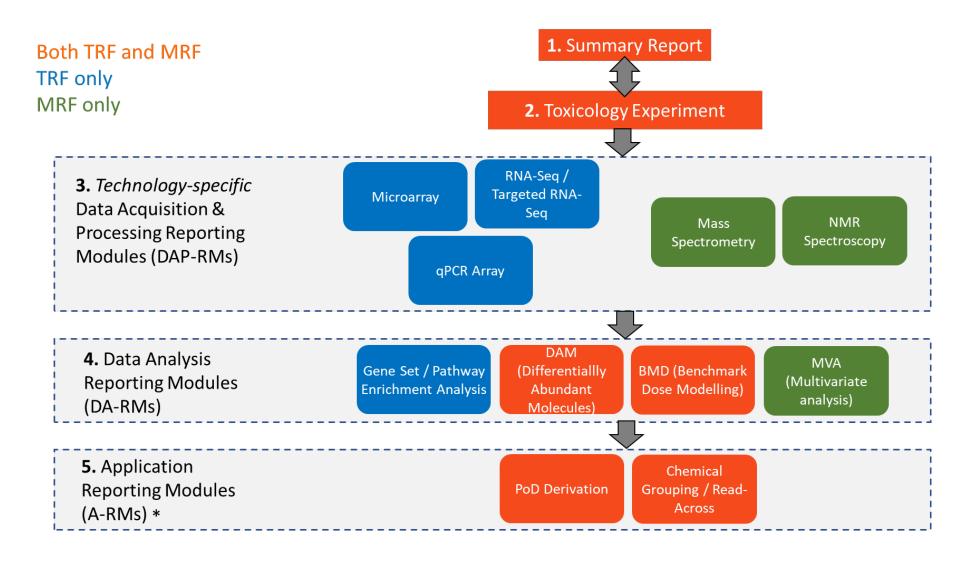
To develop frameworks for the standardisation of reporting of 'omics data generation and analysis, to ensure that all of the information required to understand, interpret and reproduce an 'omics experiment and its results are available.

**Purpose:** to ensure that sufficient information is available to enable an evaluation of the quality of the experimental data and interpretation, and support reproducibility.

**NOT** to stipulate the methods of data analysis or interpretation....**Rather**, provide guidance on reporting of information that fosters transparency and reproducibility.

Project Name	Project Leads
Metabolomics Reporting Framework (MRF)	Mark Viant (U. Birmingham, UK)
Transcriptomics Reporting Framework (TRF)	Joshua Harrill (USEPA) Carole Yauk (Health Canada)
Optimal Data Analysis Framework (ODAF)	Tim Gant (PHE, UK)/Florian Caiment (ECETOC C4 project)

# Modular Structure of Omics Reporting Frameworks Harmonization of TRF and MRF





## TRF Document, Major Topic Areas

#### **TOXICOLOGY EXPERIMENT MODULE:**

- Experiment should be described in sufficient detail to allow another researcher to replicate it.
- Adapted from existing sources
- Information in this section is <u>independent</u> of 'omics platform

#### PROCESSING AND ANALYSIS OF 'OMICS DATA MODULES:

- The transcriptomics technology, sample processing procedures, methods used to collect raw data and methods used to generate processed data.
- Described in Gant et al. (2017).
- Information in this section is <u>dependent</u> on 'omics platform

### **DOWNSTREAM ANALYSIS REPORTING MODULES [DA-RMs]**

Detail the steps and resources necessary to reproduce a computational analysis of the processed data.

### **APPLICATION REPORTING MODULES [A-RMs]**

Details the steps used to further analyze the omics data and metadata specifically in the context
of an application of regulatory interest.



## TRF



## **Transcriptomics Reporting Framework (TRF)**

#### Table of Contents

1. Introduction	
1.1. Background	
1.2. Scope	
1.3. Related 'Omics Standards Projects	
1.4. References	
2. Experiment	
2.1. Study Rationale	
2.2. Test and Control Items	
2.3. Test System Characteristics	1
2.4. Study Design	
2.5. Treatment Conditions	1
2.6. Study Exit & Sample Collection	
2.7. Sample identification codes	
2.8. Supporting Data Streams	2
2.9. References	2
3. Processing and Analysis of Microarray Data	
3.1. Technology	2
3.2. Transcriptomics Experimental Design	
3.3. Specification of raw data	
3.4. Data Normalisation	
3.5. Data Filtering	
3.6. Identification and removal of low quality or outlying data sets	4
4. Data Analysis Reporting Module for Differentially Expressed Gene Identification	
4.1. Statistical software	
4.2. Contrasts for which DEGs were identified	
4.3. Assay experimental design	
4.4. Statistical analysis to identify DEGs	4
4.5. Outputs	
4.6. References	
7.0, References	

#### • Stylistic alignment:

- Previous OECD guidance in the biological sciences (where applicable)
- MERIT Project / Metabolomics Reporting Framework (MRF) – In Progress

#### Reporting Format

- Narrative text followed by Reporting Fields
- Excel spreadsheet for reporting
- Consistent vocabulary across modules



## Reporting structure

	A		В	C	D
	RELEVANT MODULE	REPORTING	CATEGORY	REPORTING ELEMENT	DESCRIPTION OF ELEMENT
	Summary Report	Study identi	fier	Unique study identifier	Unique code
1					
5		Study ration	ale	Objective of study	Controlled vocabulary: point-of-departure; hazard
6				Background information (supporting the objective)	Free text elaboration of above
7					
8		Links to rela	ted study records	Standardised toxicology dataset (e.g., linked to OEC	
9				Omics complete dataset (e.g., linked to MetaboLight	ts, e.g. MTBLSxx
0					
1	Toxicology Experiment Module	Test item (c	hemical) and vehicle	Test item name	
2				Test item identifier	SMILES or InChiKey
3				Vehicle name	
4					
5		Test system	characteristics		
6		EITHER in	vivo	a. Species	
7				b. Strain	
8				c. Sex	
9				d. Age	
0.0		OR in vitr	О	a. Cell type	
1				b. Species of origin	
2					
13		Exposure co	nditions	Test item concentration(s)	
4				Route of administration	
25				Schedule (single dose or repeated dosing)	
6				Frequency of repeated dosing	
7				Exposure duration(s)	
8					
		Biological sa	imples	Type (e.g., in vitro: cells, media, etc.; in vivo: cells,	
9				tissue, biofluid, whole organism, etc.)	
				Sample preservation method (e.g., fresh, frozen,	
0		-		paraffin-embedded, etc.)	
1				Number of biological replicates per treatment	
2	TDF whatfarm an addis date	Camula r		Cample preparation mathed to a DNA	
	TRF platform-specific data acquistion and processing Reportin	Sample prep	paration	Sample preparation method (e.g., RNA extraction method, cell lysis, etc.)	
3	Module	В		method, cell lysis, etc.)	
4	Module				
		Technology		Type (e.g., data acquisition and processing module	
5				used - DNA microarray, RNA-seq, etc.)	
				Manufacturer(s) and model(s) (e.g., Agilent microarr	ay,
6				etc.)	
	> Study Summar		Experiment	Processing microarray data DARM DEG	<b>(+)</b>

- Executive summary included
- Modular
  - Flexible/expandable
  - Add new modules as new platforms or analytical approaches released
- Mandatory/optional reporting fields
- Database compatibility
- Summary, Experiment and DAM DARM harmonized with MRF



### Objective: review efficacy of TRF reporting modules through case studies

#### **Submitter:**

Andrew Williams (Health Canada)

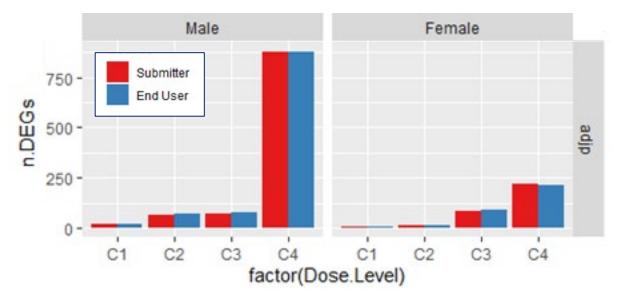
- 1) Identify dataset
- 2) Compute DEGs
- 3) Fill in TRF
  - a) Microarray
  - b) DAM DA-RM
- 4) Ease-of-use commentary

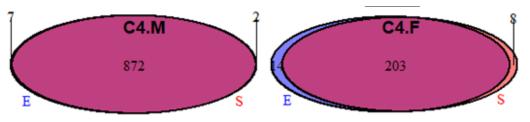


1) Provide completed TRF sans results to End User.



- **End User:**
- Leah Wehmas (US EPA)
- 1) Review completed TRF
- 2) Reproduce DEG analysis
- 3) Ease-of-use commentary
- **Referee:**
- 1) Concordance analysis
- 2) Summarize ease-of-use commentaries





Comparison of DEGs identified by Submitter and End User (adjp)



## Case study next steps

#### Additional case studies:

- More developer and user feedback and participation
- Testing on different platforms (Affymetrix, RNA-seq)
- Testing different analytical platforms (open source in computing environment versus web application)
  - Application of RNA-seq data in the Optimal Data Analysis Framework case study





## Section Workgroups

Title	Identity		Roles	
Section Leads	Experiment Microarray RNA-Seq qPCR array DARM.1 [DAM] DARM.2 [BMD]	Raffaella Corvi [ JRC ] Vikrant Vijay [ NCTR ] Florian Caiment [ Maastricht ] Jason O'Brien [ ECCC ] Lyle Burgoon [ ERDC ] Scott Auerbach [ NIEHS ] and Mark Viant [ Birmingham ]	Coordinate workgroup activities  Maintain draft of section  Manage timelines for deliverables	
Workgroup Members	Variable		Contribute text and content for sections	
"Floating" Facilitators	Joshua Harrill [ US EPA ] Carole Yauk [ Health Canada ]		Ensure consistency and cross-talk with other workgroups.  Monitor progress in accordance with project timeline Foster discussion.	
OECD Secretariat	Magda Sachana		Project administration / OECD liaison	

All members of the TRF workgroup have the opportunity to comment on each section.

Project group leads (Harrill & Yauk) integrate sections into the final documents.



## Project Timeline and Milestones Completed

Date	Milestones
April, 2018	Kickoff teleconference / recruiting for workgroups
June, 2018	Work initiated (P), Experiment (P), Microarray (P) and DARM.1 (P) modules
June, 2018	OECD WPHA & EAGMST Meeting – Project update (presentation), feedback incorporated
Dec, 2018	First drafts of Introduction (P), Experiment (P), Microarray (P) and DARM.1 (P)
March, 2019	Circulation of TRF (microarray) first draft to working group members for feedback/revision
June, 2019	Feedback from EAGMST (Summary module developed)
Dec, 2019	First complete TRF Introduction (P), Experiment (P), Microarray (P) and DARM.1 (P) Excel spreadsheet for data entry (P)
Dec, 2019	Launch reproducibility case study to test microarray processing and DARM.1
March 2020	First TRF application (Agilent microarray data set) complete at Health Canada – sent to EPA to test reproducibility (part 1 round-robin)
March 2020	First draft of RNA-seq data processing module completed (sent to team for review)
June 2020	First draft of the qPCR module complete
June, 2020	Harmonization of Summary, Toxicology Experiment, and DAM DARM with MRF

# **>>**

## **Upcoming** Key Project Milestones

Date	Milestone
June 2020	Evaluate TRF reproducibility case study; revise; repeat for Affymetrix arrays
July, 2020	Working group revisions of qPCR processing module
Sept, 2020	Launch of RNA-seq module reproducibility case study
Sept, 2020	First draft of BMD modeling DARM.2
Dec, 2020	Launch qPCR and BMD [DARM.2] reproducibility case study
Dec, 2020	Reproducibility case study to test microarray processing and DARM.1 module complete
Dec, 2020	Complete RNA-seq and BMD [DARM.2] reproducibility case study
Jan, 2021	Complete TRF1 (microarray and DEG) case study; TRF ready for EAGMST review
March, 2021	Complete TRF2 (RNA-seq and DEG) case study; molecules ready for EAGMST review
May, 2021	Launch qPCR and BMD [DARM.2] reproducibility case study



## MRF



Title	Identity	Roles
Expert group members	Tripartite Industry Government / Regulator Academic  ca. 15 very active members, ca. 10 'observers'	-Contribute expert knowledge and text wherever possible across the whole MRF guidance document -Ensure consistency of whole document
Facilitator	Mark Viant [ Univ Birmingham ]	-Foster discussion -Monitor progress in accordance with project timeline -Ensure consistency with TRF
Administrator	David Epps [ Univ Birmingham ]	-Meeting organisation
OECD Secretariat	Magda Sachana	-Project administration / OECD liaison



## MRF builds on the Ecetoc





**PERSPECTIVE** 

https://doi.org/10.1038/s41467-019-10900-y

**OPEN** 

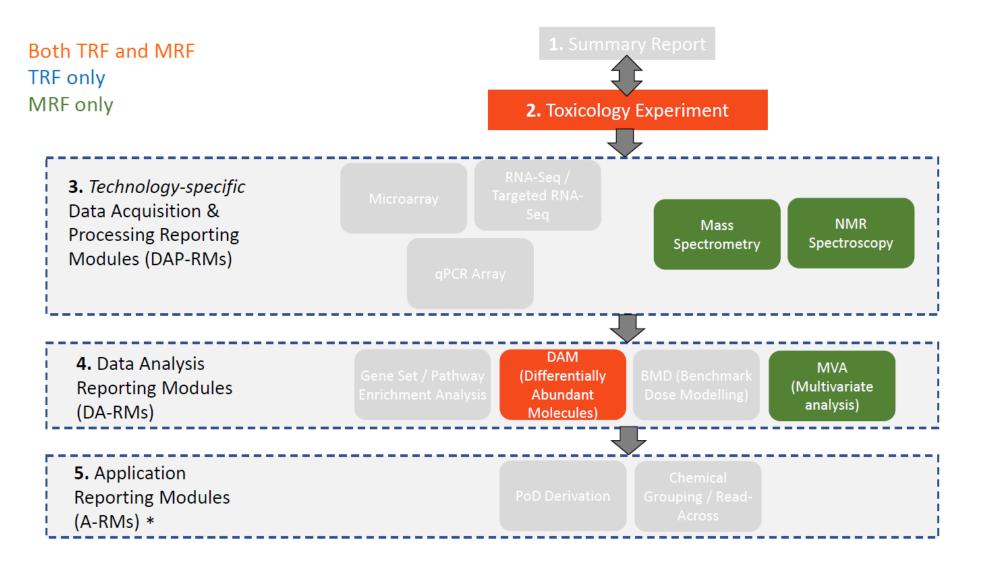
# Use cases, best practice and reporting standards for metabolomics in regulatory toxicology

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Mark R. Viant <sup>1,12</sup>, Timothy M.D. Ebbels <sup>2,12</sup>, Richard D. Beger <sup>3</sup>, Drew R. Ekman <sup>4</sup>, David J.T. Epps <sup>1</sup>, Hennicke Kamp <sup>5</sup>, Pim E.G. Leonards <sup>6</sup>, George D. Loizou <sup>7</sup>, James I. MacRae <sup>8</sup>, Bennard van Ravenzwaay <sup>5</sup>, Philippe Rocca-Serra <sup>9</sup>, Reza M. Salek <sup>10</sup>, Tilmann Walk <sup>11</sup> & Ralf J.M. Weber <sup>1</sup>
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Published July 2019



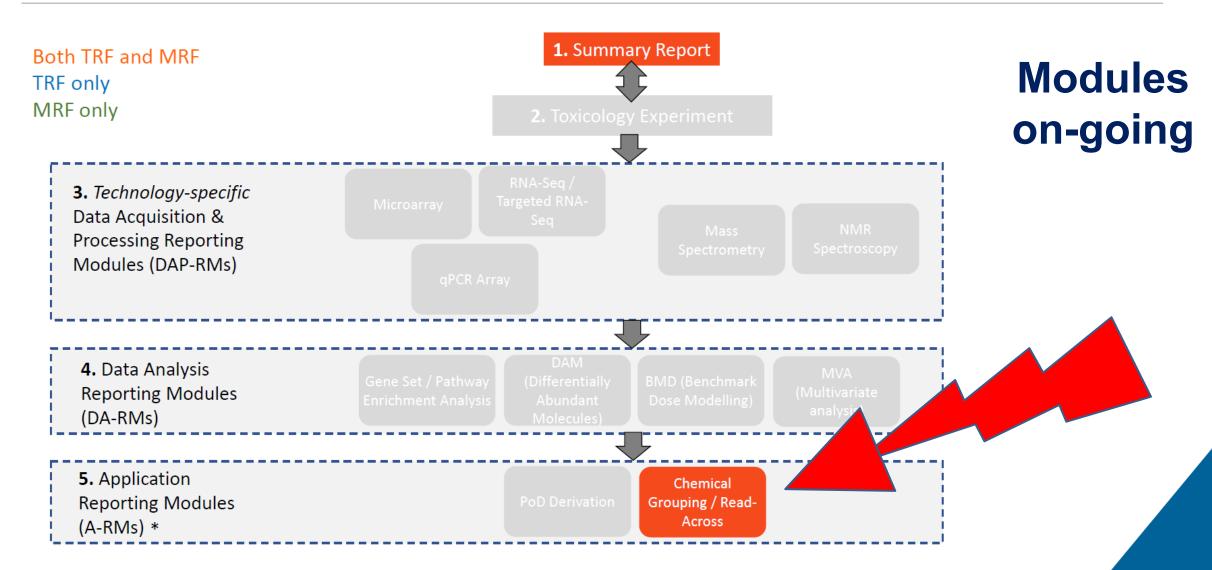
## Modular Structure of Omics Reporting Frameworks

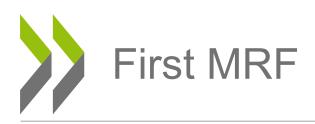


# 5 modules finished



## Modular Structure of Omics Reporting Frameworks





#### **Table of Contents**

#### 1. Introduction

- 1.1 Background, Objective and Scope
- 1.2 Modular Structure of MRF
  - 1. Summary Report (SR)
  - 2. Toxicology Experiment Module (TEM)
  - 3. Data Acquisition & Processing Reporting Modules (DAPRMs)
  - 4. Data Analysis Reporting Modules (DARMs)
  - 5. Application Reporting Modules (ARMs)
- 1.3 Example Use Cases using Modular Reporting
- 2. Summary Report
- 3. Toxicology Experiment Module
- 4. MRF Technology-specific Data Acquisition & Processing Reporting Modules
  - 4.1 Mass Spectrometry Metabolomics Module
  - 4.2 NMR Spectroscopy Metabolomics Module
- 5. Data Analysis Reporting Modules
  - 5.1 Discovery of Differentially Abundant Molecules (using univariate analysis) Module
  - 5.2 Multivariate Statistical Analysis Module
- 6. Application Reporting Modules
  - 6.1 Chemical Grouping for Read-Across Module
- 7. References

- Reporting Format
  - Narrative text followed by Reporting Fields
  - Excel spreadsheet for reporting
- Consistent vocabulary across modules
- Database compatibility
- ca. 80 page document



### Objective: review efficacy of MRF reporting modules through case studies

### Steps

- a) Identify investigators with completed 'toxico-metabolomics' datasets
- b) Request these investigators complete and return the populated MRF reporting modules
- c) MRF expert group review all feedback and update the MRF reporting modules

### **Progress to date**

Mass Spectrometry Module – currently under review by David Crizer, NIEHS (NTP)

We request more user testing and feedback!



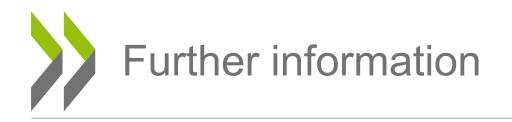
## MRF Project Timeline and Milestones Completed

Date	Milestones
Dec, 2018	Start of MRF project, kickoff teleconference
Feb, 2019	Expand MRF Expert Group to cover all topics
Feb, 2019	Review MERIT document (metabolomics reporting) for completeness
March, 2019	Work initiated on Mass Spectrometry, NMR Spectroscopy, Univariate statistical analysis and Multivariate statistical analysis modules
June, 2019	OECD WPHA & EAGMST meetings – Project update (presentation), feedback incorporated
Sept, 2019	First drafts of Univariate statistical analysis and Multivariate statistical analysis modules
March, 2020	First drafts of Mass Spectrometry, NMR Spectroscopy modules
March, 2020	Work initiated on Grouping / Read-Across module
May, 2020	First complete draft of Mass Spectrometry, NMR Spectroscopy, Differentially Abundant Molecules and Multivariate statistical analysis modules
June, 2020	Checked harmonisation of several modules with TRF
June, 2020	Begin first trial of Mass Spectrometry module
June, 2020	Draft MRF sent to OECD EAGMST for comment



## MRF Upcoming Milestones

Date	Milestone
June, 2020	Receive feedback from OECD WPHA & EAGMST meetings, and integrate into MRF
July, 2020	Complete first draft of Grouping / Read-Across module
July, 2020	Begin first trials of NMR Spectroscopy, Differentially Abundant Molecules and Multivariate statistical analysis modules
Sept, 2020	Begin first trial of Grouping / Read-Across module
Sept, 2020	First draft of BMD modeling DARM.2 with TRF
Oct, 2020	Incorporate feedback from MS, NMR and DARM case study trials
Nov, 2020	Submit MRF Guidance Document to EAGMST for formal review (excluding BMD DARM and Application Reporting Modules)
Dec, 2020	EAGMST review



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