

The inTelligence And Machine Learning (TAME) Toolkit for Introductory Data Science in Environmental Health

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Assistant Professor | University of North Carolina at Chapel Hill (UNC)

Department of Environmental Sciences and Engineering (ENVR)

Institute for Environmental Health Solutions (IEHS)

Center for Environmental Medicine and Lung Biology (CEMALB)

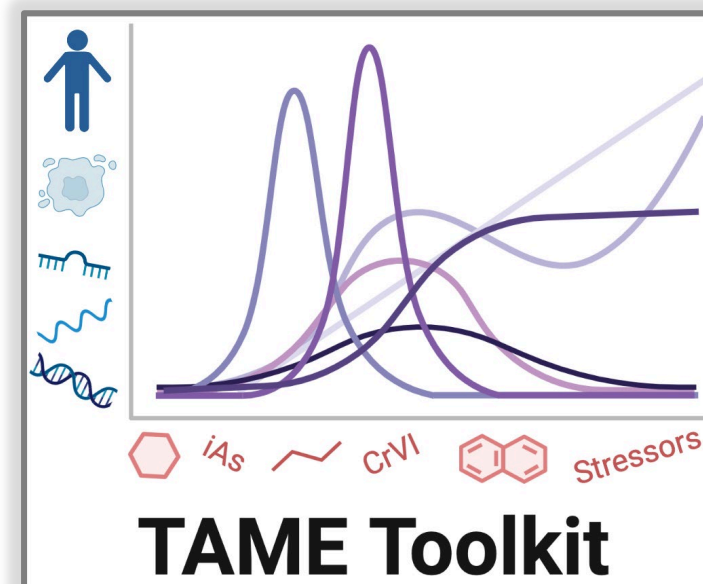
Curriculum in Toxicology and Environmental Medicine (CiTEM)

Kyle Roell, PhD

Data Analyst | University of North Carolina at Chapel Hill (UNC)

Department of Environmental Sciences and Engineering (ENVR)

Institute for Environmental Health Solutions (IEHS)

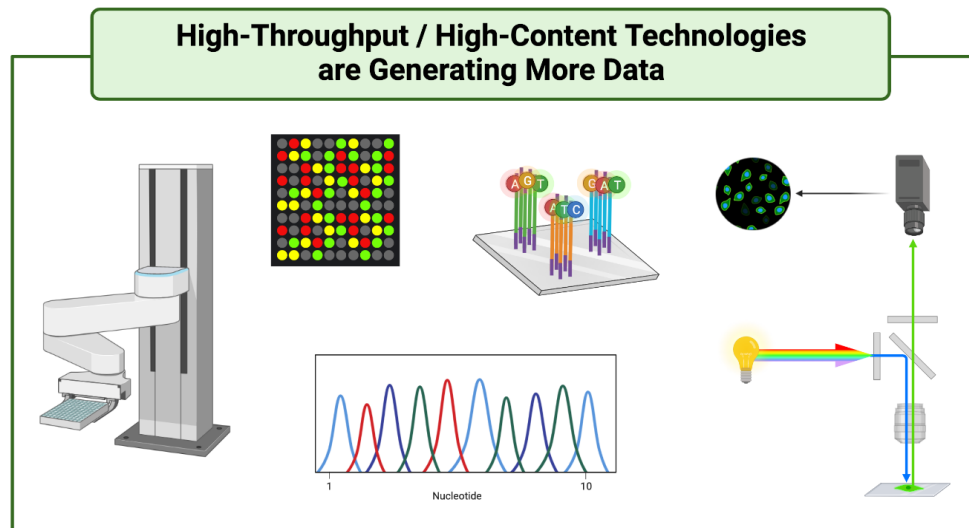


Presentation Schedule



- Introduction to TAME and its development – Dr. Julia Rager
- Real-time demonstration of how to use TAME – Dr. Kyle Roell
- Q&A is encouraged throughout and also at the end

Need for Improved Data Science Training



are Generating More Data

The collage consists of six distinct images arranged in a 2x3 grid. The top row features a robotic arm on the left, a microarray with colored spots in the center, and a DNA microarray with labeled bases (A, G, T, C) on the right. The bottom row shows a chromatogram with multiple peaks on the left, a glowing light bulb with a rainbow spectrum on the center, and a microscope on the right.

Common, Integrating Multiple Variable Types

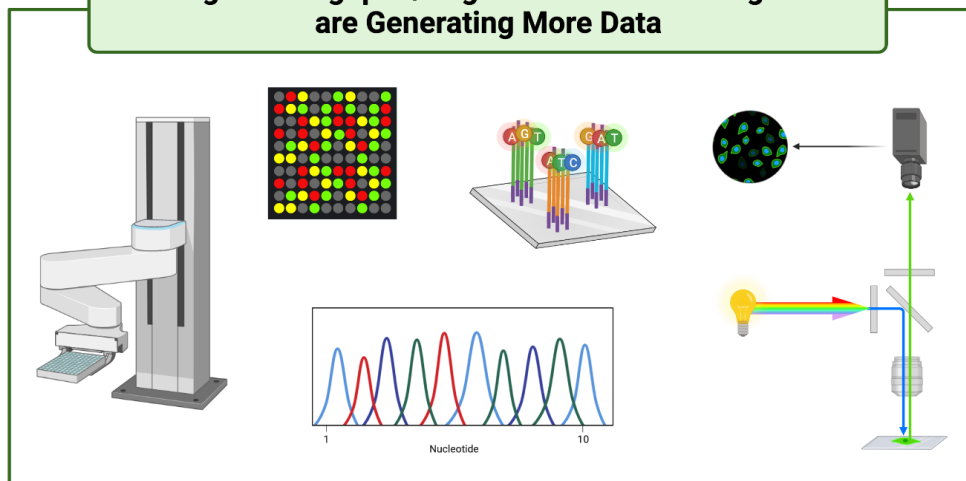
The collage includes the following icons:

- DNA double helix
- Red brick
- Phosphate group (PO₄)
- Earth globe
- Group of stylized people
- Red wavy line
- Red comb
- Pink cell
- Cigarette
- Gray mouse
- Blue liver
- Blue brain
- Person sitting
- Person standing

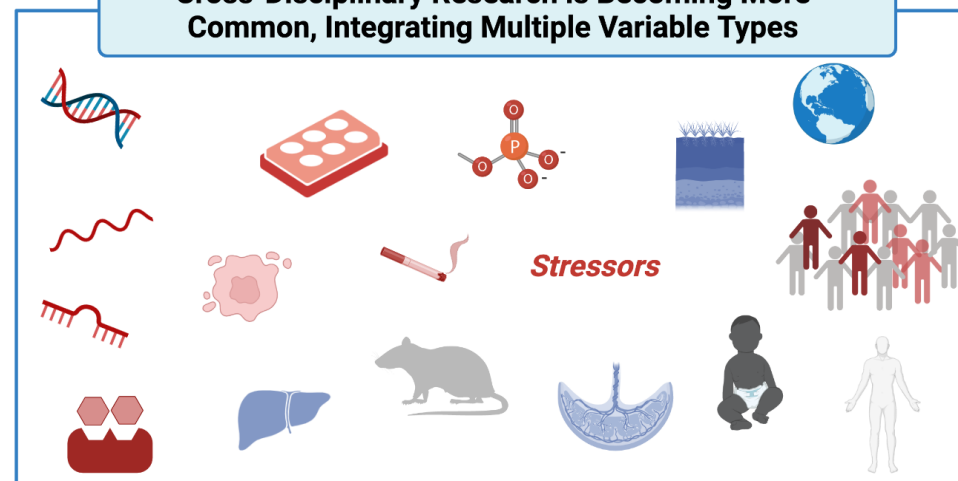
Stressors

Need for Improved Data Science Training

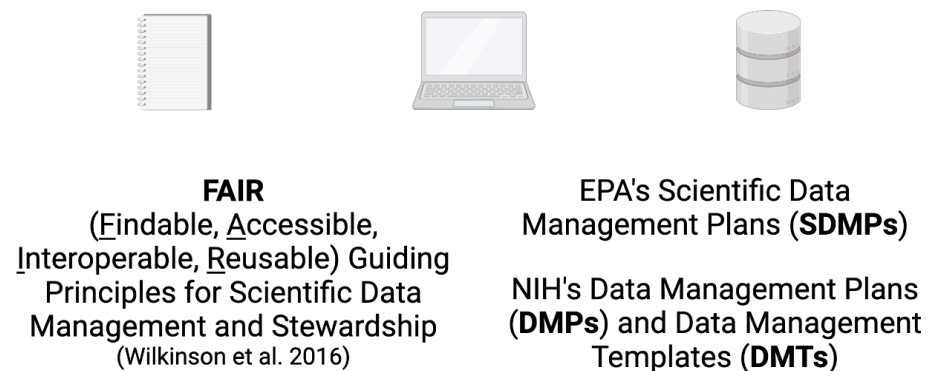
High-Throughput / High-Content Technologies are Generating More Data



Cross-Disciplinary Research is Becoming More Common, Integrating Multiple Variable Types

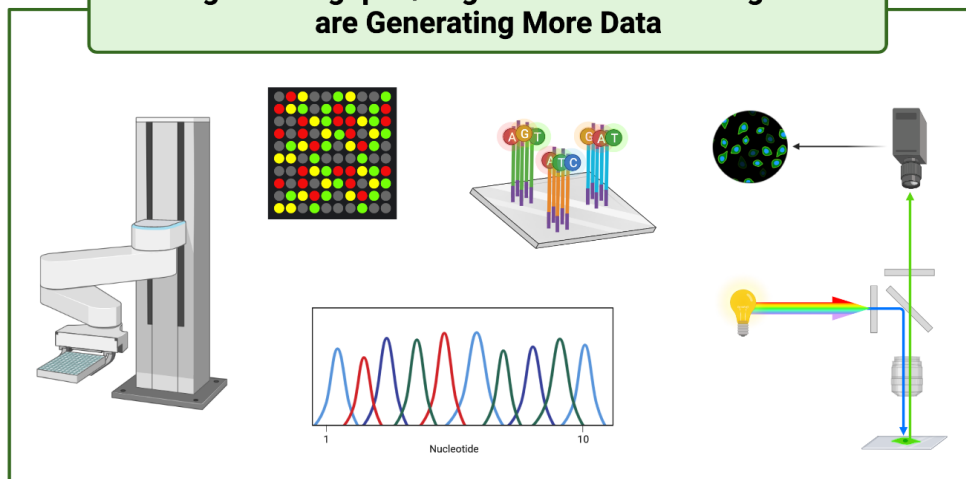


Data Preservation Efforts and Record Keeping are Becoming Pillars to Scientifically Sound Research

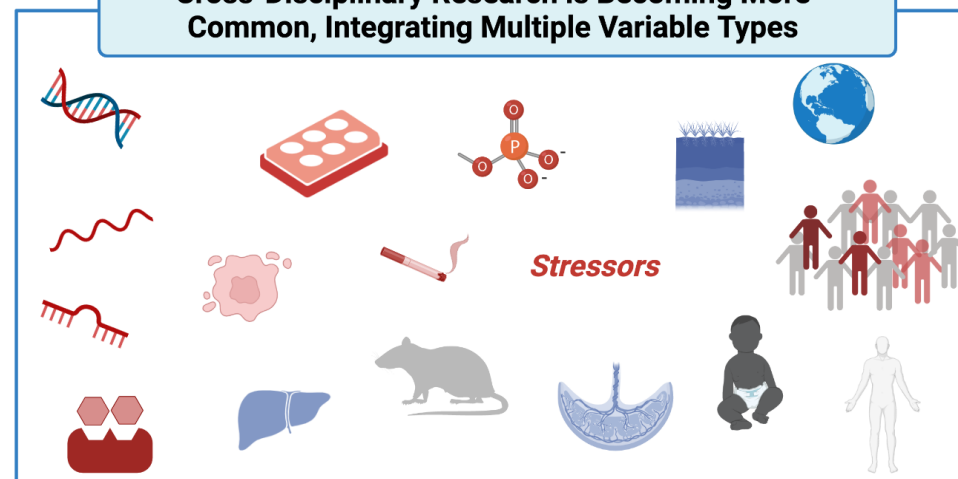


Need for Improved Data Science Training

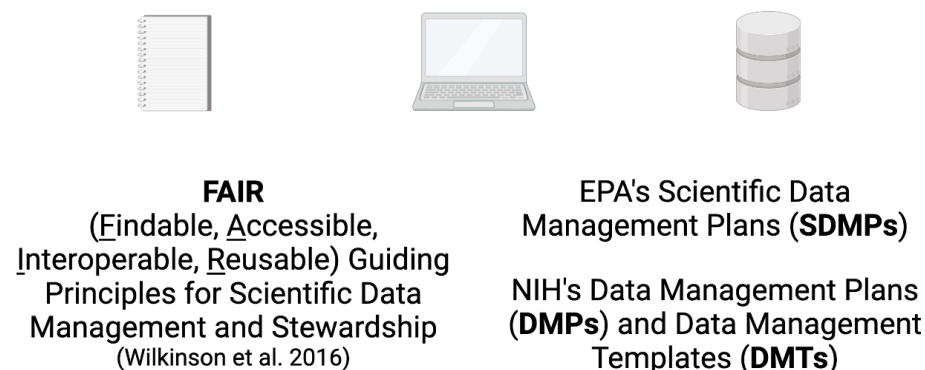
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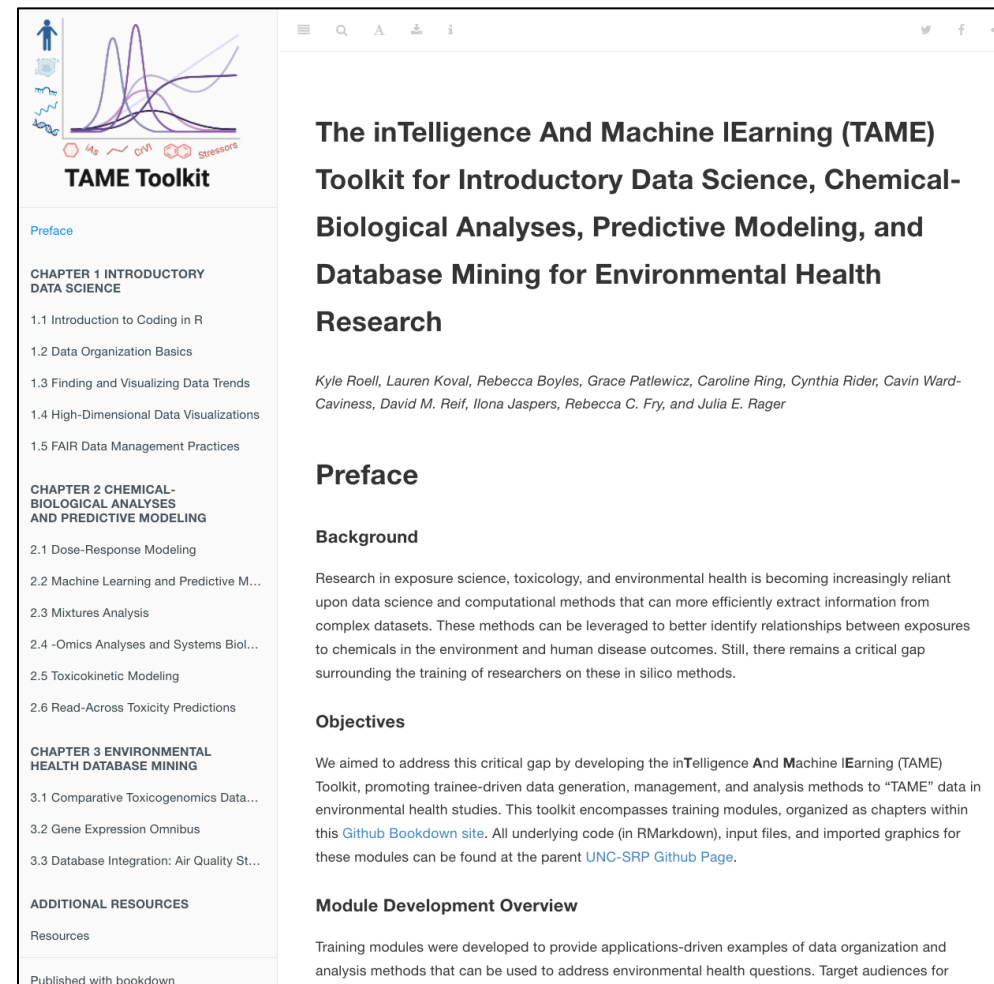


How can we make use of these growing resources to better understand environmental stressors???

DATA SCIENCE TRAINING

Data Science Training through TAME Toolkit

- Multiple authors share knowledge and translate experiences gathered by multiple authors on data management and analysis methods to address real-world issues in environmental health through carefully developed training modules
- This training effort is currently being launched as the **inTelligence And Machine LEarning (TAME) Toolkit**
- Promotes didactic data generation, management, and analysis methods to “**TAME**” data in environmental health studies



The screenshot shows the TAME Toolkit bookdown interface. On the left is a navigation sidebar with a table of contents. The main content area on the right displays the title page and the beginning of the Preface. The title is 'The inTelligence And Machine LEarning (TAME) Toolkit for Introductory Data Science, Chemical-Biological Analyses, Predictive Modeling, and Database Mining for Environmental Health Research'. The authors listed are Kyle Roell, Lauren Koval, Rebecca Boyles, Grace Patlewicz, Caroline Ring, Cynthia Rider, Cavin Ward-Caviness, David M. Reif, Ilona Jaspers, Rebecca C. Fry, and Julia E. Rager. The Preface section begins with the heading 'Background' and a paragraph stating that research in exposure science, toxicology, and environmental health is becoming increasingly reliant on data science and computational methods. It then lists 'Objectives' and 'Module Development Overview'.

TAME Toolkit

Preface

CHAPTER 1 INTRODUCTORY DATA SCIENCE

1.1 Introduction to Coding in R

1.2 Data Organization Basics

1.3 Finding and Visualizing Data Trends

1.4 High-Dimensional Data Visualizations

1.5 FAIR Data Management Practices

CHAPTER 2 CHEMICAL-BIOLOGICAL ANALYSES AND PREDICTIVE MODELING

2.1 Dose-Response Modeling

2.2 Machine Learning and Predictive M...

2.3 Mixtures Analysis

2.4 -Omics Analyses and Systems Biol...

2.5 Toxicokinetic Modeling

2.6 Read-Across Toxicity Predictions

CHAPTER 3 ENVIRONMENTAL HEALTH DATABASE MINING

3.1 Comparative Toxicogenomics Data...

3.2 Gene Expression Omnibus

3.3 Database Integration: Air Quality St...

ADDITIONAL RESOURCES

Resources

Published with bookdown

The inTelligence And Machine LEarning (TAME) Toolkit for Introductory Data Science, Chemical-Biological Analyses, Predictive Modeling, and Database Mining for Environmental Health Research

Kyle Roell, Lauren Koval, Rebecca Boyles, Grace Patlewicz, Caroline Ring, Cynthia Rider, Cavin Ward-Caviness, David M. Reif, Ilona Jaspers, Rebecca C. Fry, and Julia E. Rager

Preface

Background

Research in exposure science, toxicology, and environmental health is becoming increasingly reliant upon data science and computational methods that can more efficiently extract information from complex datasets. These methods can be leveraged to better identify relationships between exposures to chemicals in the environment and human disease outcomes. Still, there remains a critical gap surrounding the training of researchers on these in silico methods.

Objectives

We aimed to address this critical gap by developing the inTelligence And Machine LEarning (TAME) Toolkit, promoting trainee-driven data generation, management, and analysis methods to “TAME” data in environmental health studies. This toolkit encompasses training modules, organized as chapters within this [Github Bookdown site](#). All underlying code (in RMarkdown), input files, and imported graphics for these modules can be found at the parent [UNC-SRP Github Page](#).

Module Development Overview

Training modules were developed to provide applications-driven examples of data organization and analysis methods that can be used to address environmental health questions. Target audiences for

<https://uncsrp.github.io/Data-Analysis-Training-Modules/>

<https://github.com/UNCSRP>

Wonderful Team of TAME Contributors



Kyle Roell
Data Analyst,
UNC-SRP, UNC



Lauren Koval
PhD Candidate,
Ragerlab, UNC



Rebecca Boyles
Data Management Director
and Scientist, RTI

Headshot not
preferred

Grace Patlewicz
Chemistry and
Cheminformatics Scientist,
US EPA



Caroline Ring
Computational Exposure
Scientist, US EPA



Cynthia Rider
Mixtures Toxicologist,
NIEHS / NTP



Gavin Ward-Caviness
Computational Biologist,
US EPA



David Reif
Professor and NCSU-SRP
Data Management and Analysis
Lead, NCSU



Ilona Jaspers
Professor and Curriculum in
Environmental Medicine and
Toxicology Director, UNC

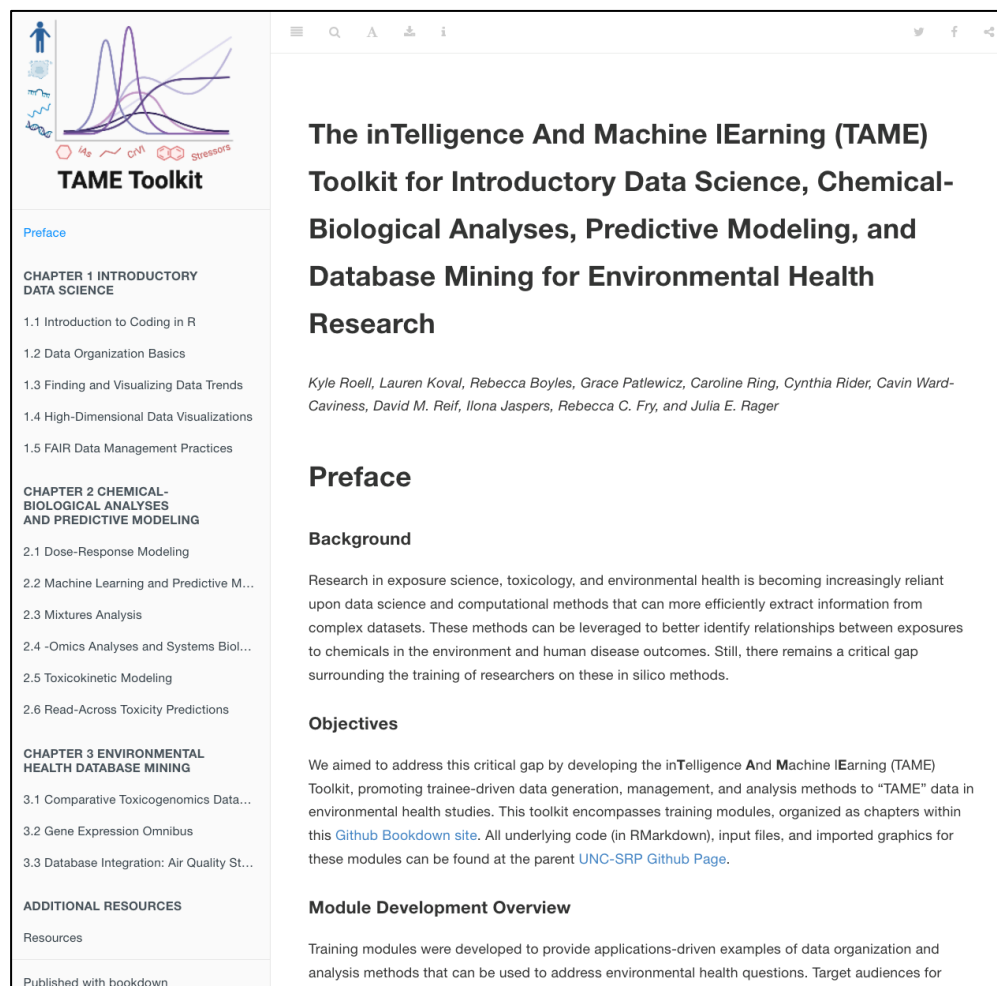


Rebecca Fry
Professor and Superfund
Research Program (UNC-SRP)
Director, UNC



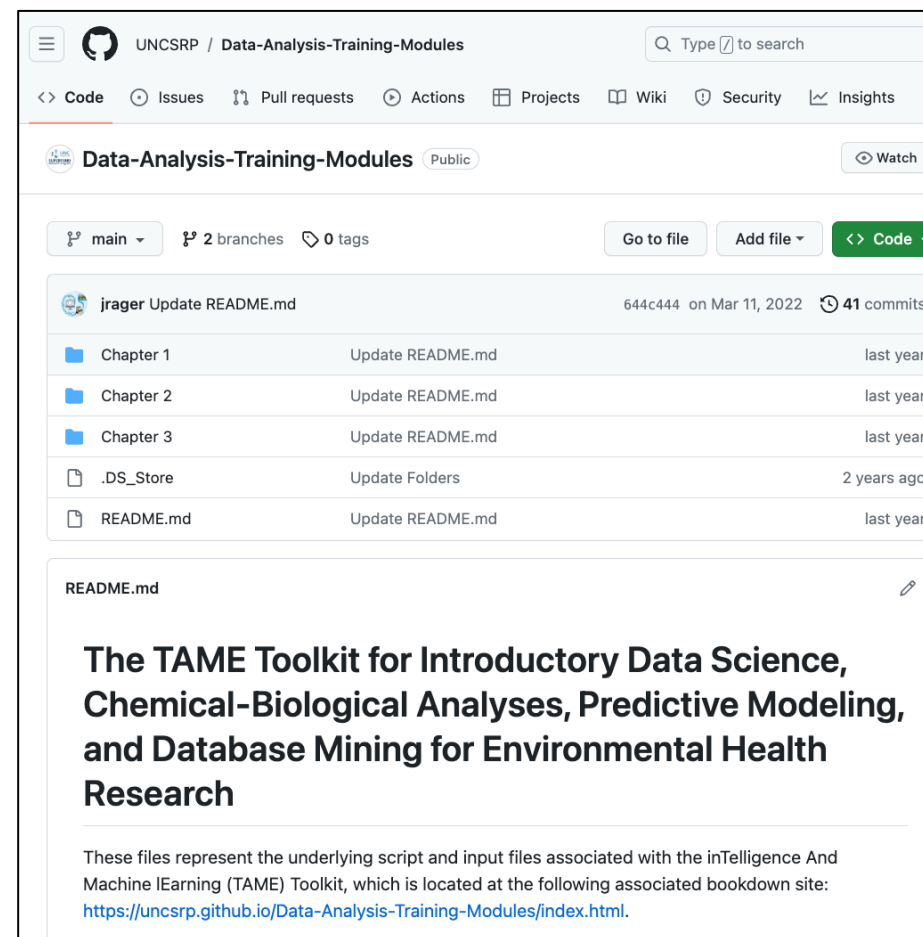
Julia Rager
Assistant Professor and UNC-
SRP Data Management and
Analysis Co-Lead, UNC

TAME Modules Presented through Bookdown



<https://uncsrp.github.io/Data-Analysis-Training-Modules/>

With underlying script and datasets posted on Github:



<https://github.com/UNCSR/>

> [Front Toxicol.](#) 2022 Jun 22;4:893924. doi: 10.3389/ftox.2022.893924. eCollection 2022.

Development of the InTelligence And Machine LEarning (TAME) Toolkit for Introductory Data Science, Chemical-Biological Analyses, Predictive Modeling, and Database Mining for Environmental Health Research

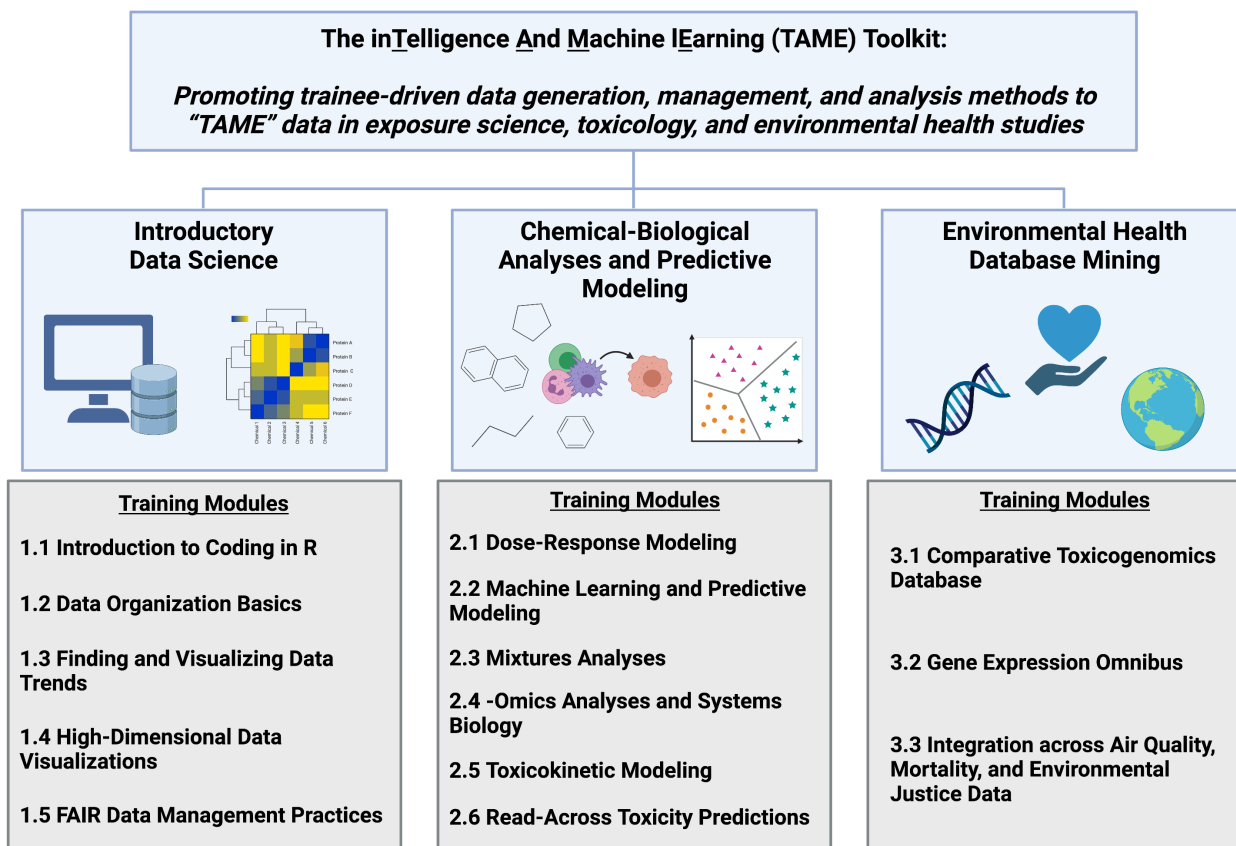
Kyle Roell ¹, Lauren E Koval ^{1 2}, Rebecca Boyles ³, Grace Patlewicz ⁴, Caroline Ring ⁴,
Cynthia V Rider ⁵, Cavin Ward-Caviness ⁶, David M Reif ⁷, Ilona Jaspers ^{1 2 8 9 10},
Rebecca C Fry ^{1 2 8}, Julia E Rager ^{1 2 8 9}

Affiliations + expand

PMID: 35812168 PMCID: [PMC9257219](#) DOI: [10.3389/ftox.2022.893924](#)

[Free PMC article](#)

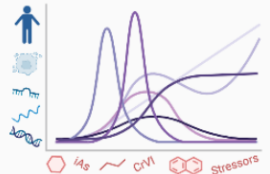
Chapter—Based Content Organization



Content within Each Specific Module

- Introduction to the Topic
- Introduction to the Training Module
- List of Training Module's ***Environmental Health Questions***
- Script Preparations
- Scripted Analysis with Applications-based Environmental Health Questions Sprinkled throughout to Keep Participants Engaged
- Concluding Remarks and Additional Resources

Screenshots in the Mixtures Sufficient Similarity Module



2.3 Mixtures Analysis

This training module was developed by Dr. Cynthia Rider, with Dr. Julia E. Rager.

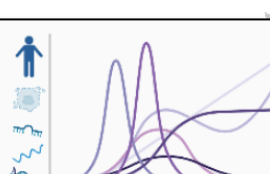
Fall 2021

Introduction to Mixtures Toxicology and *In Silico* Mixtures

Humans are rarely, if ever, exposed to single chemicals at a time. Multiple stressors in their everyday environments in the form of environmental chemicals and pharmaceuticals, and they can also be exposed to socioeconomic factors and other attributes that can place them at risk for disease. Because it is not possible to test every possible combination of stressors that might be experienced in their lifetime, approaches that take into account mixtures modeling are needed.

Some helpful resources that provide further background on the modeling include the following:

- Carlin DJ, Rider CV, Woychik R, Birnbaum LS. Unraveling the complexity of mixtures: an NIEHS priority. *Environ Health Perspect.* 2013;121(11):1585-1592. PMID: [31704565](#).
- Drakvik E, Altenburger R, Aoki Y, Backhaus T, Bahadori T, Demeneix B, Hougaard Bennekou S, van Klaveren J, Knebelson R, Posthuma L, Reiber L, Rider C, Rüegg J, Testa G, van der Water B, Yamazaki K, Öberg M, Bergman Å. Statement on the need for mixtures research: mixtures and their risks for human health and the environment. *Environ Health Perspect.* 2015;123(11):1115-1121. PMID: [26111111](#).



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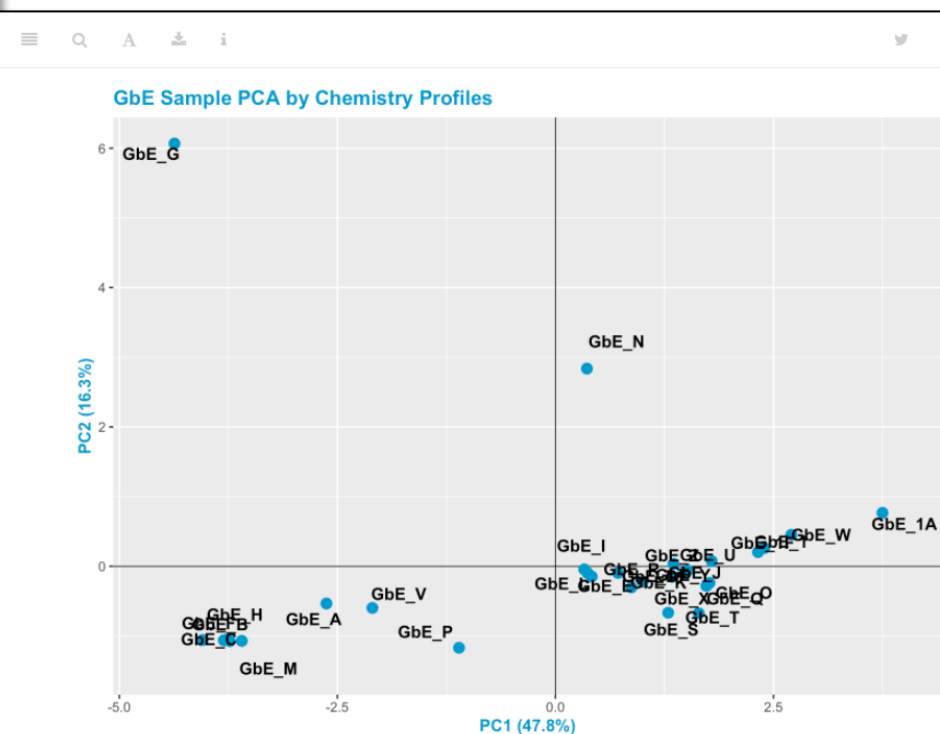
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This plot tells us a lot about sample groupings based on chemical profiles!

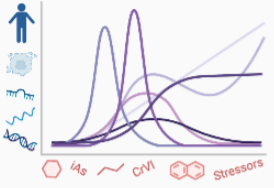


With this, we can answer **Environmental Health Question 1**: Based on the chemical analysis, which *Ginkgo biloba* extract looks the most different?



Answer: GbE_G

Screenshots in a Machine Learning Module



TAME Toolkit

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2.1 Dose-Response Modeling

2.2 Machine Learning and Predictive M...

Introduction to Training Module

K-means Analysis

Principal Component Analysis

Combining K-Means with PCA

Concluding Remarks

2.3 Mixtures Analyses

2.4 -Omics Analyses and Systems Biol...

2.5 Toxicokinetic Modeling

2.6 Read-Across Toxicity Predictions

2.2 Machine Learning and Predictive

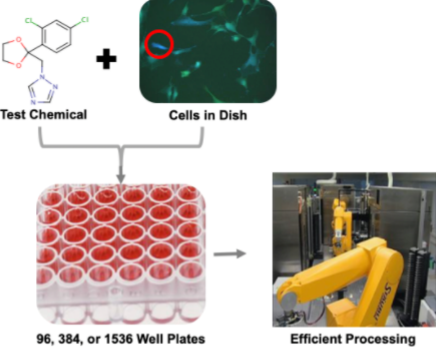
The development of this training module was led by [Dr. David M. Reif](#)

Fall 2021

Introduction to Machine Learning (ML) and Predictive Mo

The need for predictive modeling

- We can screen for biological responses to a variety of chemical exposures efficiently, leveraging technologies like cell-based high-throughput screening



Test Chemical + Cells in Dish

96, 384, or 1536 Well Plates

Efficient Processing

Response (Efficacy)

Chem

- These screening efforts result in increasing amounts of data, which can be stored in big databases



Assay A₁



TAME Toolkit

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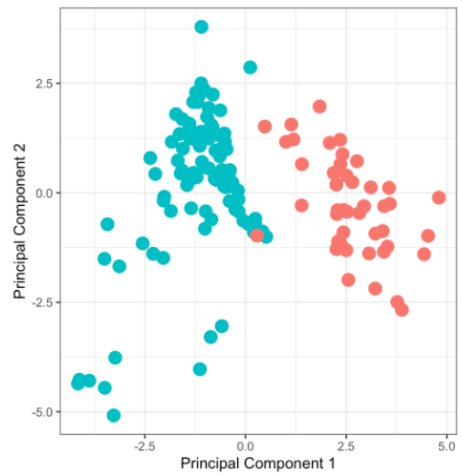
CHAPTER 3 ENVIRONMENTAL HEALTH DATABASE MINING

3.1 Comparative Toxicogenomics Data...

Let's now view, again, the results of the main PCA, focusing on the first two principal components; though this time let's color each chemical according to k-means cluster.

```
ggplot(as.data.frame(my.pca$scores), aes(x=Comp.1, y=Comp.2, color=as.factor(clusters_PCA$cluster))) +
  geom_point(size=4) + theme_bw() +
  ggtitle('Version D: PCA Plot of the First 2 PCs, colored by k-means Clustering') +
  xlab("Principal Component 1") + ylab("Principal Component 2")
```

Version D: PCA Plot of the First 2 PCs, colored by k-means Clustering



as.factor(clusters_PCA\$cluster)

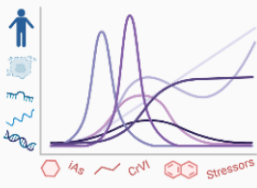
1

2

With this, we can answer **Environmental Health Question 5**: If we did not have information telling us which chemical belonged to which class, could we use PCA and k-means to accurately predict whether a chemical is a PFAS vs statin?

Answer: Yes!! Groupings derived from k-means, displayed in this PCA plot, line up almost exactly with the grouping of chemical classes (see Version C of this plot as the direct comparison).

Screenshots in the -Omics Analyses Module



TAME Toolkit

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- 2.4 -Omics Analyses and Systems Biol...

The Field of "-Omics"

Transcriptomics

Introduction to Training Module

Transcriptomics Data QA/QC

Statistical Analysis of Gene Expressi...

MA Plots

Volcano Plots

Pathway Enrichment Analysis

Concluding Remarks

2.4 -Omics Analyses and System

This training module was developed by Lauren Koval, Dr. Kyle Roell,
Fall 2021

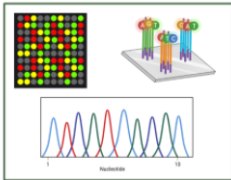
The Field of "-Omics"

The field of "-omics" has rapidly evolved since its inception in the mi... obtained through sequencing of the human genome (see the [Human](#)... advent of high-content technologies. High-content technologies have... assessment of genome-wide, or 'omics'-based, endpoints.

Traditional molecular biology techniques typically evaluate the functi... products. Omics-based methods, on the other hand, utilize non-targ... genes or gene products in a given environmental/biological sample. ... allow for the unbiased investigation of potentially unknown or unders... involved in regulating cell health and disease. These molecular profile... altered in response to toxicant exposures and/or during disease initia...

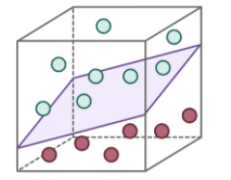
To further understand the molecular consequences of -omics-based... overlaid onto molecular networks to uncover biological pathways and... perturbed at the systems biology level. An overview of these general... content technologies and ending of systems biology, is provided in t... BioRender.com).

High-content technologies measure responses across the genome/epigenome

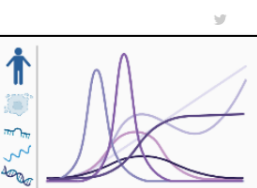


Technologies can include: high-throughput PCR, microarrays, sequencing technologies, and others

Data science & computational approaches to identify patterns within -omics datasets



Example group comparison:
● Unexposed samples
● Exposed samples



TAME Toolkit

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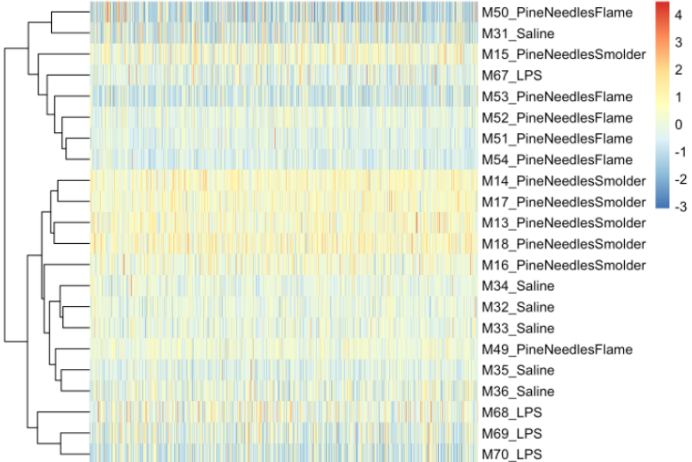
Concluding Remarks

- 2.5 Toxicokinetic Modeling

```

heatmap(scale(countdata_for_clustering), main="Hierarchical Clustering",
        cluster_rows=TRUE, cluster_cols = FALSE,
        fontsize_col = 7, treeheight_row = 60, show_colnames = FALSE)
    
```

Hierarchical Clustering



Like the PCA findings, heirarchical clustering demonstrated an overall lack of potential sample outliers because there were no obvious sample(s) that grouped separately from the rest along the clustering dendrograms.

Therefore, *neither approach points to outliers that should be removed in this analysis.*

With this, we can answer **Environmental Health Question 2**: When preparing transcriptomics data for statistical analyses, what are three common data filtering steps that are completed during the data QA/QC process?

Answer: (1) Background filter to remove genes that are universally lowly expressed; (2) Sample filter to remove samples that may be not have any detectable mRNA; (3) Sample outlier filter to remove samples with underlying data distributions outside of the overall, collective dataset.

TAME Toolkit Dissemination

Course Materials

- Much of this training content was tested through a new course at UNC, ***ENVR 730: Computational Toxicology and Exposure Science***
- Included 17 graduate students from:
 - Department of Environmental Sciences and Engineering (ENVR)
 - Curriculum of Toxicology and Environmental Medicine (CiTEM)
- Received the **Teaching Innovation Award** from the UNC Gillings School of Global Public Health, which is student-nominated!
- We are teaching this course again this Fall

Other Dissemination Efforts

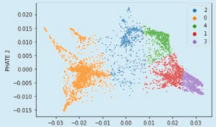
High dimensional data visualization training workshop (virtual, Spring 2022)

UNC SCHOOL of MEDICINE

Curriculum in Toxicology & Environmental Medicine

Do you want to learn more about how to leverage computer script to analyze and visualize high dimensional data?

This two-hour online training workshop represents an applications-focused, tutorial on coding in R/Python, including hands-on activities to analyze chemical and biological data.



Topics will include:

- Introduction to intermediate-level coding concepts, including tidyverse, ggplot2, and helpful packages to implement style guides
- High dimensional data reduction techniques, including PCA and PHATE
- Data clustering techniques
- High dimensional data visualizations, spanning simple scatter plots to more advanced PHATE visualizations
- Real-world applications of these tools using a wildfire smoke chemical exposure dataset and a single-cell sequencing dataset to evaluate human exposures and underlying biology

This class will be open for upper-level undergraduates and graduate students, where some experience with coding is recommended. In preparation for this workshop, participants will be provided instructions on how to quickly set up an RStudio Cloud working environment to allow for easy, hands-on participation in a coding environment.

This workshop is designed to reach target audiences outside of the UNC-Chapel Hill main campus to foster engagement across research institutions.

Workshop to be held via zoom on March 22nd, 2-4 pm eastern time. Student enrollment will be limited to 15, to allow for effective hands-on training, so register today!

Registration link for March 22, 2-4 pm EST:
<https://www.med.unc.edu/toxicology/workshop-registration/>

Workshop organized through the UNC Computational Biosciences Club (CBC) and Curriculum in Toxicology & Environmental Medicine (CITEM)

CITEM
med.unc.edu/toxicology

Computational Biosciences Club

PRogramming for Environmental HEalth And Toxicology (PREHEAT) Retreat



International Engagement

Viewers have accessed the TAME toolkit world-wide

Google analytics (Sept 2022-current):

Global views across 91 countries:



5,300 total site views

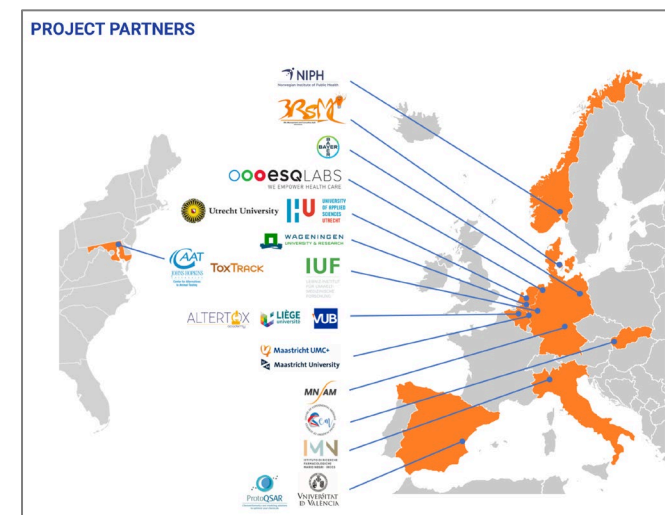
1,441 full site users

Number of users per country
with highest usage:

COUNTRY	USERS
United States	600
Germany	62
Canada	60
India	59
Japan	44
China	39
France	38

International collaborators

For example, the **European Union's ONTOX** project leaders are incorporating TAME materials into their training courses on data analysis and machine learning in toxicology

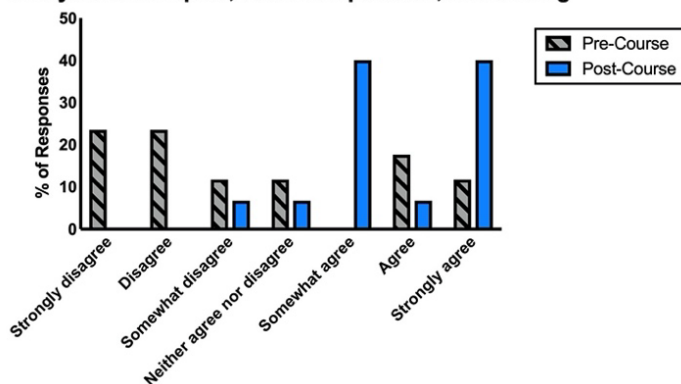


<https://ontox-project.eu/consortium/>

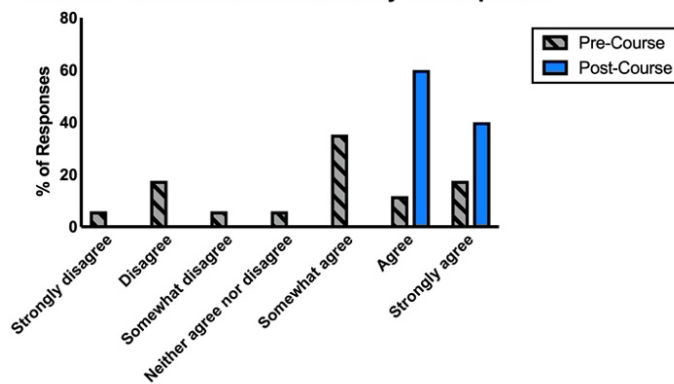
TAME Effectiveness and Feedback

Course Evaluation:

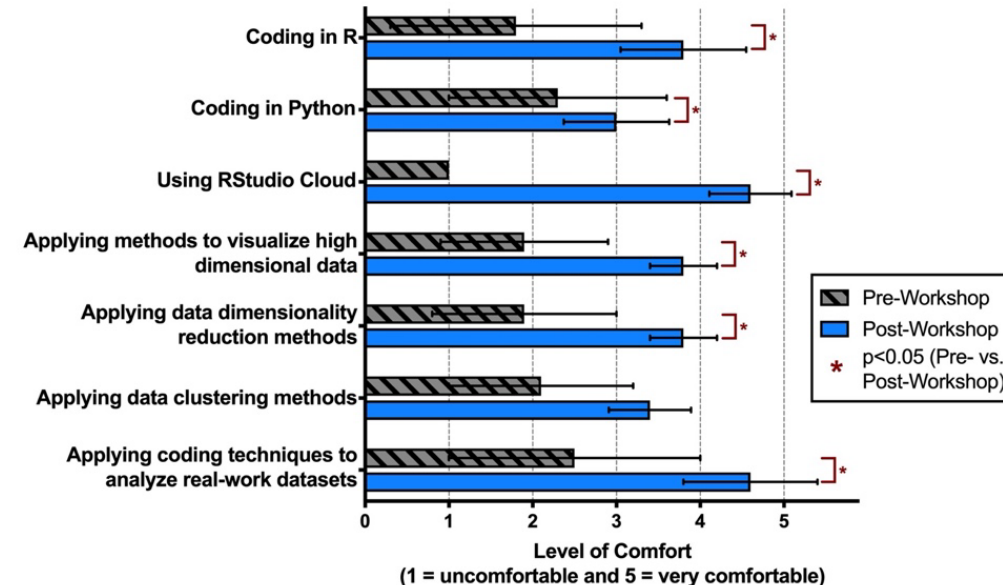
I feel comfortable with high dimensional data analysis techniques, data manipulation, and coding



I am familiar with common methods used to evaluate chemical-induced toxicity and exposure



Virtual Workshop Evaluation:



Consistent Feedback across All Dissemination Efforts

- **Participants want more!** More training time, more modules
- Training at the intro-level, mid-level, and advanced-level
- More basics, including best practices for wet lab data organization and sharing
- We are currently in the process of expanding these training materials...

TAME 2.0 Is Underway!

Expanding and reorganizing content into 6 chapters:

1. Introduction to Data Science
2. Introduction to Coding in R
3. Basics of Data Analysis and Visualizations
4. Machine Learning and Artificial Intelligence
5. Applications in Toxicology and Exposure Science
6. Environmental Health Database Mining

Hoping to launch ~December 2023

Collaborations and Funding



Rager lab

Celeste Carberry (PhD cand)

Elise Hickman (post-doc)

Lauren Koval (PhD cand)

Elena McDermott (MSPH)

Alexis Payton (data analyst)

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