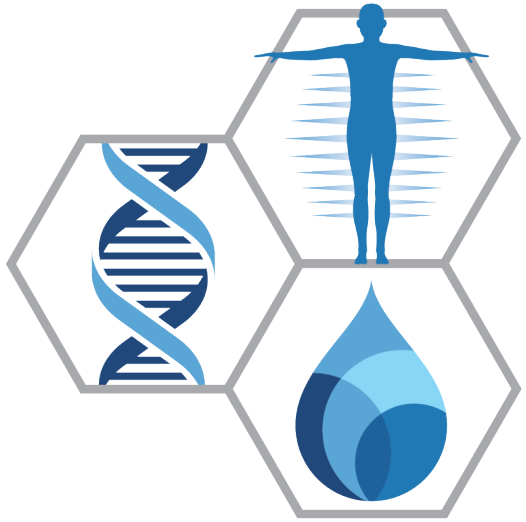


UNC Chapel Hill | SUPERFUND Research Program

Progress in Research

Rebecca Fry, Director

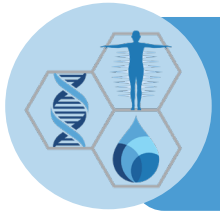
Fernando Pardo Manuel de Villena, Project 2

Julia Rager, DMAC

Kathleen Gray, CEC

Gillings School of Global Public Health

Presentation Overview



Overview

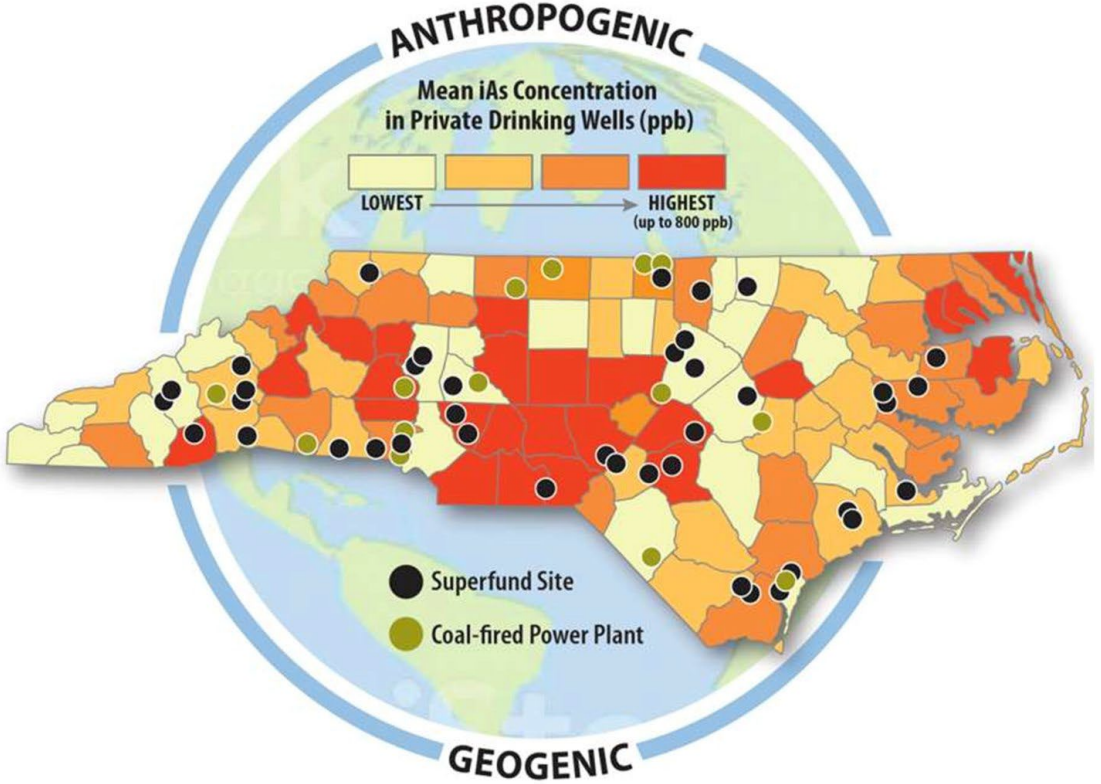
Project 2

DMAC

CEC

Overview of UNC Superfund Research Center

“Protecting vulnerable populations from arsenic-induced metabolic dysfunction with a vision for exposure reduction and disease prevention"



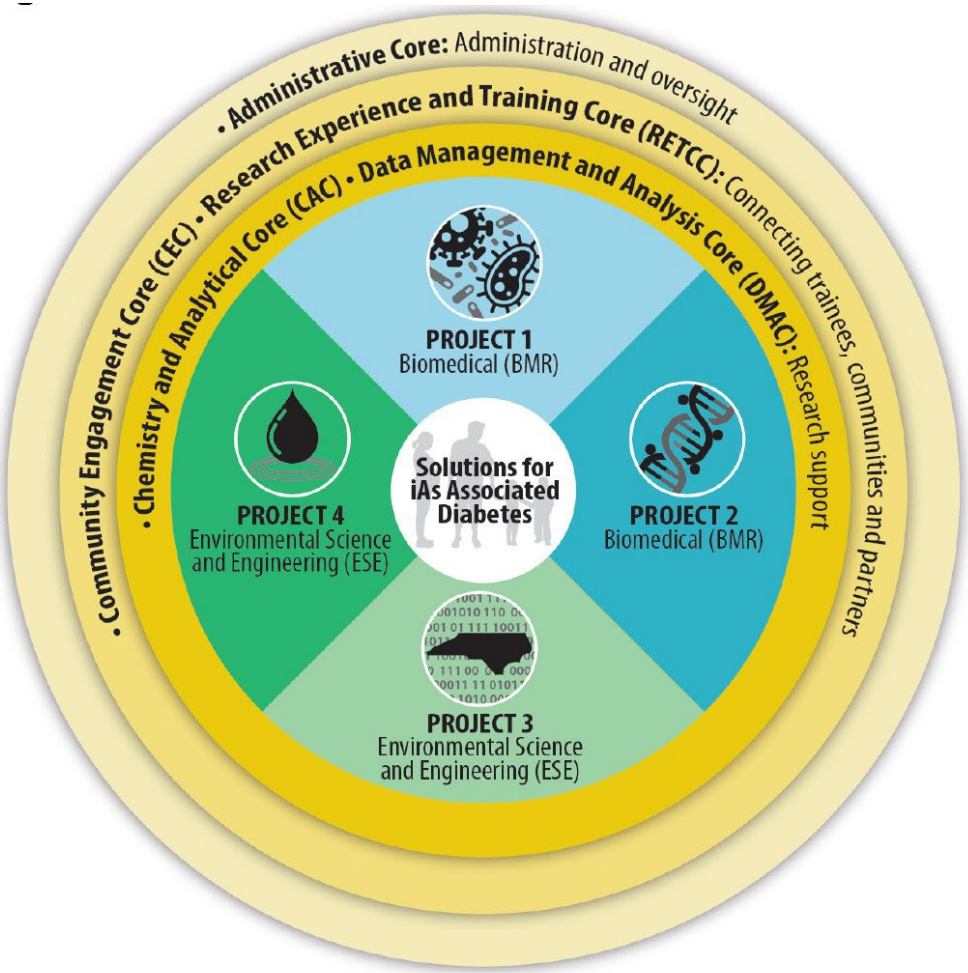
UNC-SRP Overall Aims

1. **Identify** biological mechanisms that contribute to iAs-associated metabolic dysfunction/diabetes and develop effective intervention strategies

2. **Develop** innovative methods and technologies to predict iAs contamination and reduce exposure.

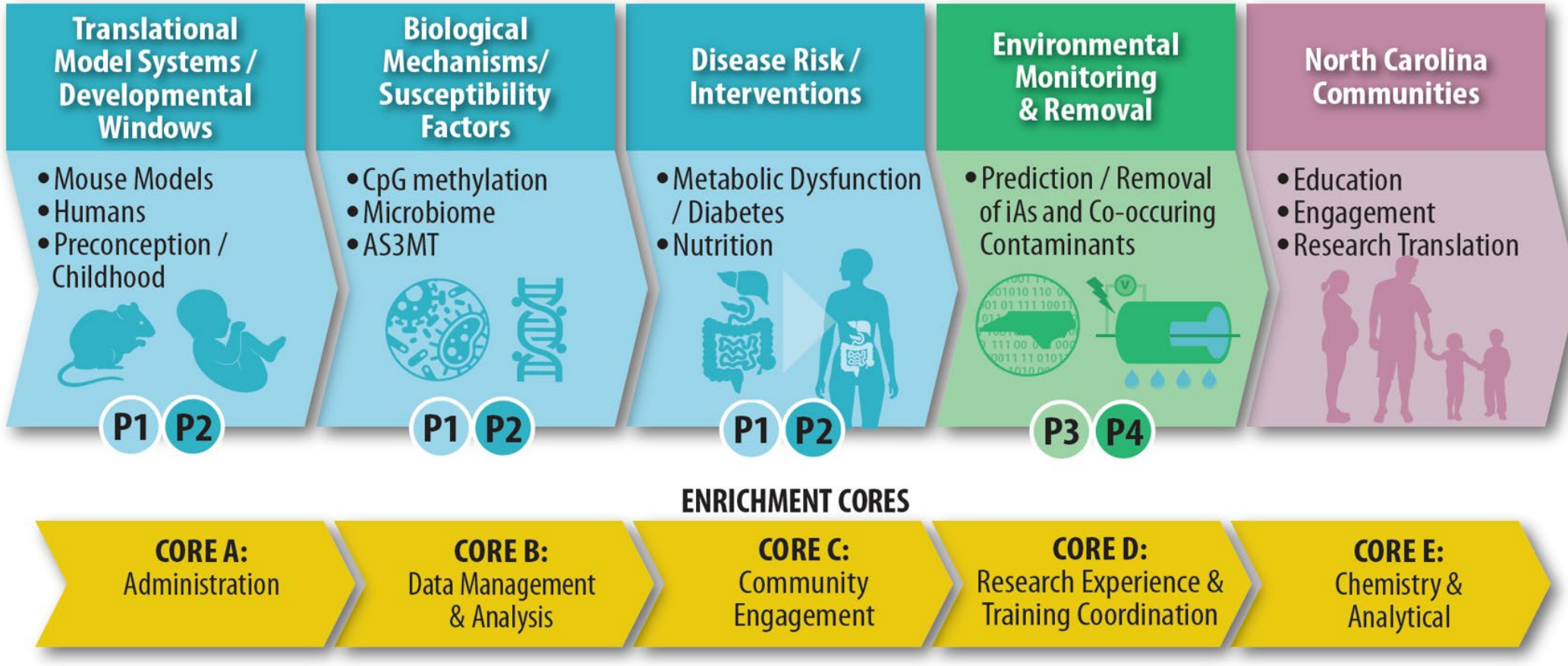
3. **Translate** the science of the UNC-SRP to vulnerable communities, key partners and the broader SRP program through collaboration.

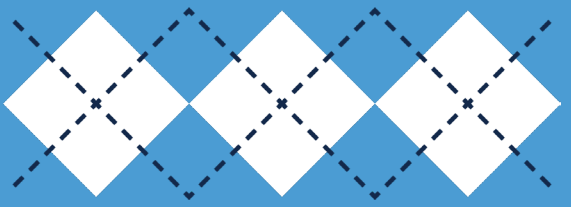
UNC-SRP has eight integrated research goals



1. Identify biomarkers of iAs exposure, metabolism and disease
2. Establish environmentally-relevant concentrations for toxicity testing and risk prediction
3. Employ methods of disease prevention/nutritional intervention
4. Identify at risk areas for remediation efforts
5. Predict, measure and remove iAs and co-occurring contaminants
6. Provide analytical support for chemical exposure and data management
7. Characterize developmental windows of susceptibility
8. Engage NC communities

UNC-SRP uses interdisciplinary approaches to evaluate and address iAs contamination in NC





Project 2: *Preconception iAs exposure: Diabetes and epigenetic inheritance*

P2 PRECONCEPTION iAS EXPOSURE: DIABETES AND EPIGENETIC INHERITANCE

P2 Co-Leads and Key Collaborators

Mirek Styblo

Fernando Pardo Manuel de Villena

Rebecca Fry

Fei Zou

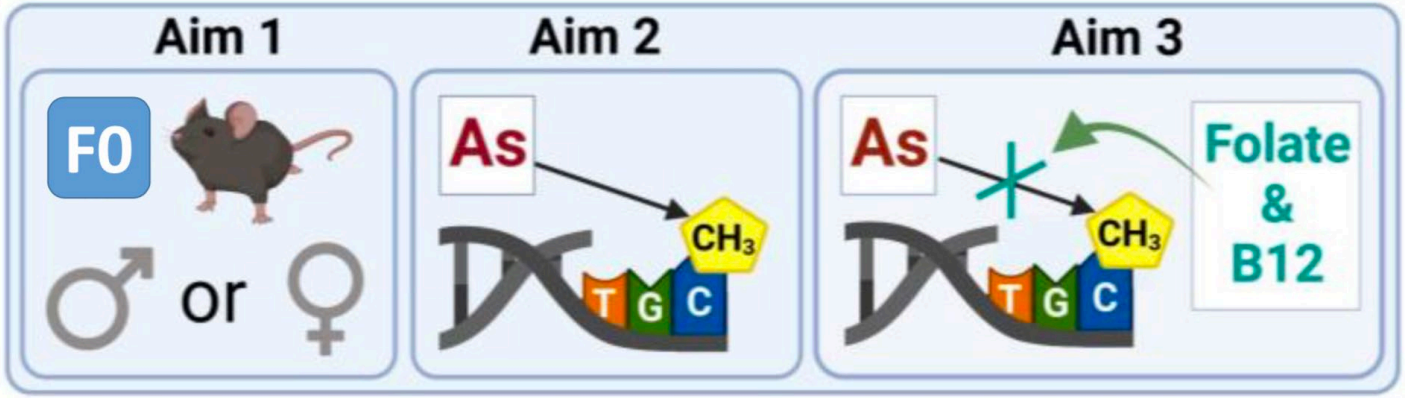
Transgenerational diabetogenic effects of preconception exposure to inorganic arsenic in C57BL/6 mice are associated with dysregulation of DNA methylation and gene expression in G1 and G2 offspring

Inorganic Compounds | Published: 12 June 2025

Volume 99, pages 3979–4001 (2025) Cite this article

Save article

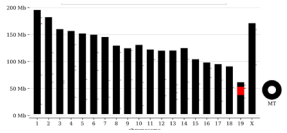
Bingzhen Shang, Tianyi Liu, Hadley Hartwell, Christelle Douillet, Abhishek Venkatratnam, Shi Qing, Madison Miller, Fei Zou, Sergey A. Krupenko, Folami Y. Ideraabdullah, Fernando Pardo-Manuel de Villena, Rebecca C. Fry & Miroslav Stýblo



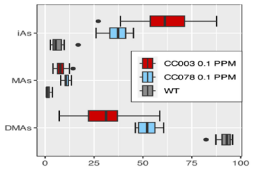
Humanized mouse model

mAs3mt ⇨ *hAS3MT*

Diverse Genetic Backgrounds

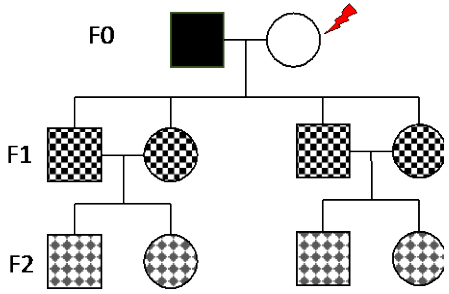


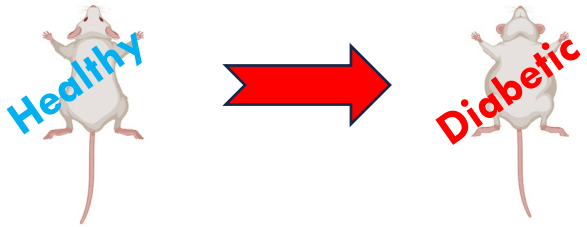
Supportive Preliminary Results



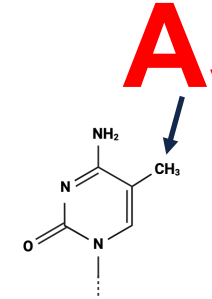
Aim 1: Parent-specific Preconception Effects

Hypothesis: transgenerational effects of arsenic are parent, sex, dose, generation and genetic background dependent

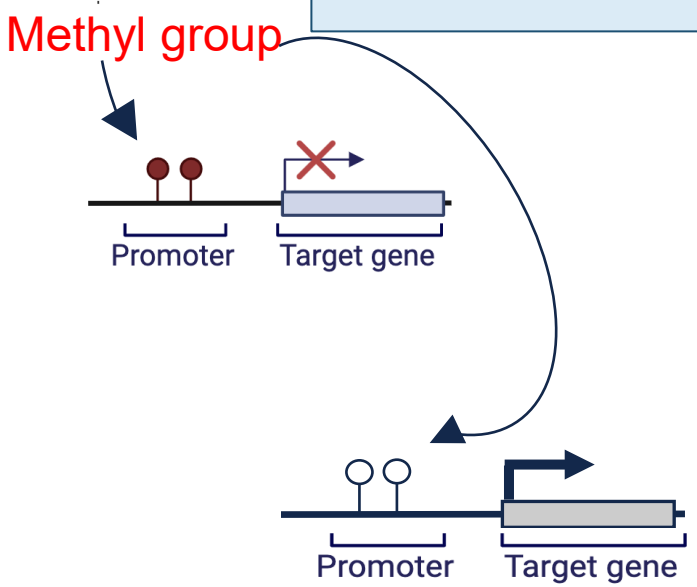




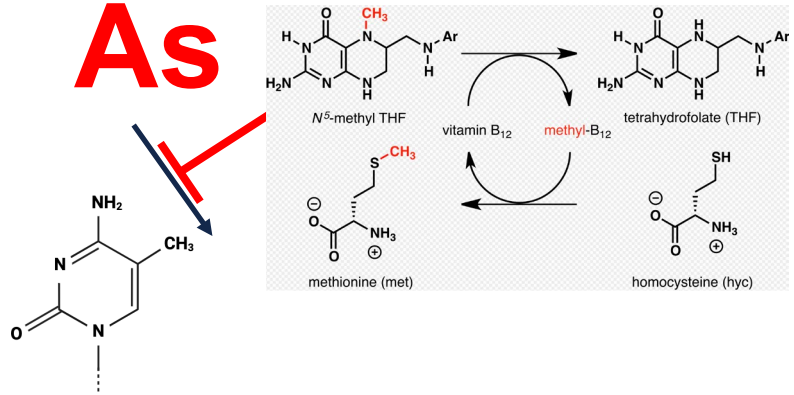
Aim 2: Role of the Epigenome



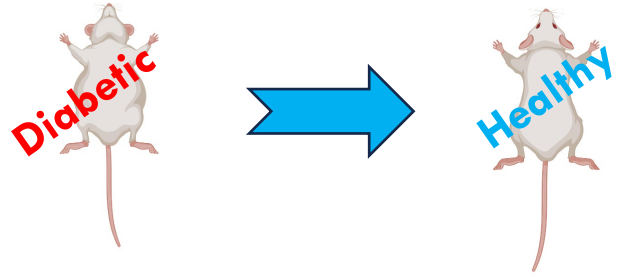
Hypothesis: preconception arsenic exposure alters the epigenome in a transmissible way leading to differential expression at key genes



Aim 3: Rescue by Dietary Supplementation

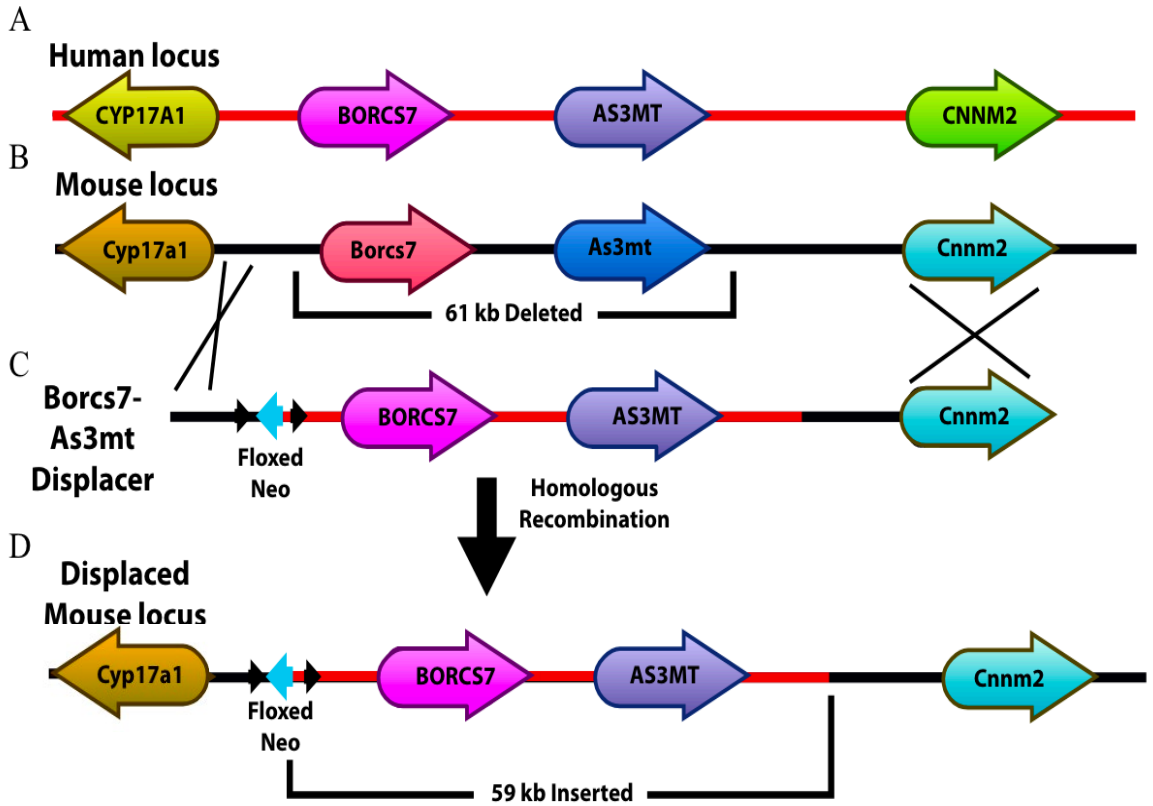


Hypothesis: Folate and B12 supplementation protect against transmissible epigenetic alterations



Humanized mouse model

mAs3mt ⇨ *hAS3MT*

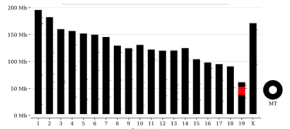


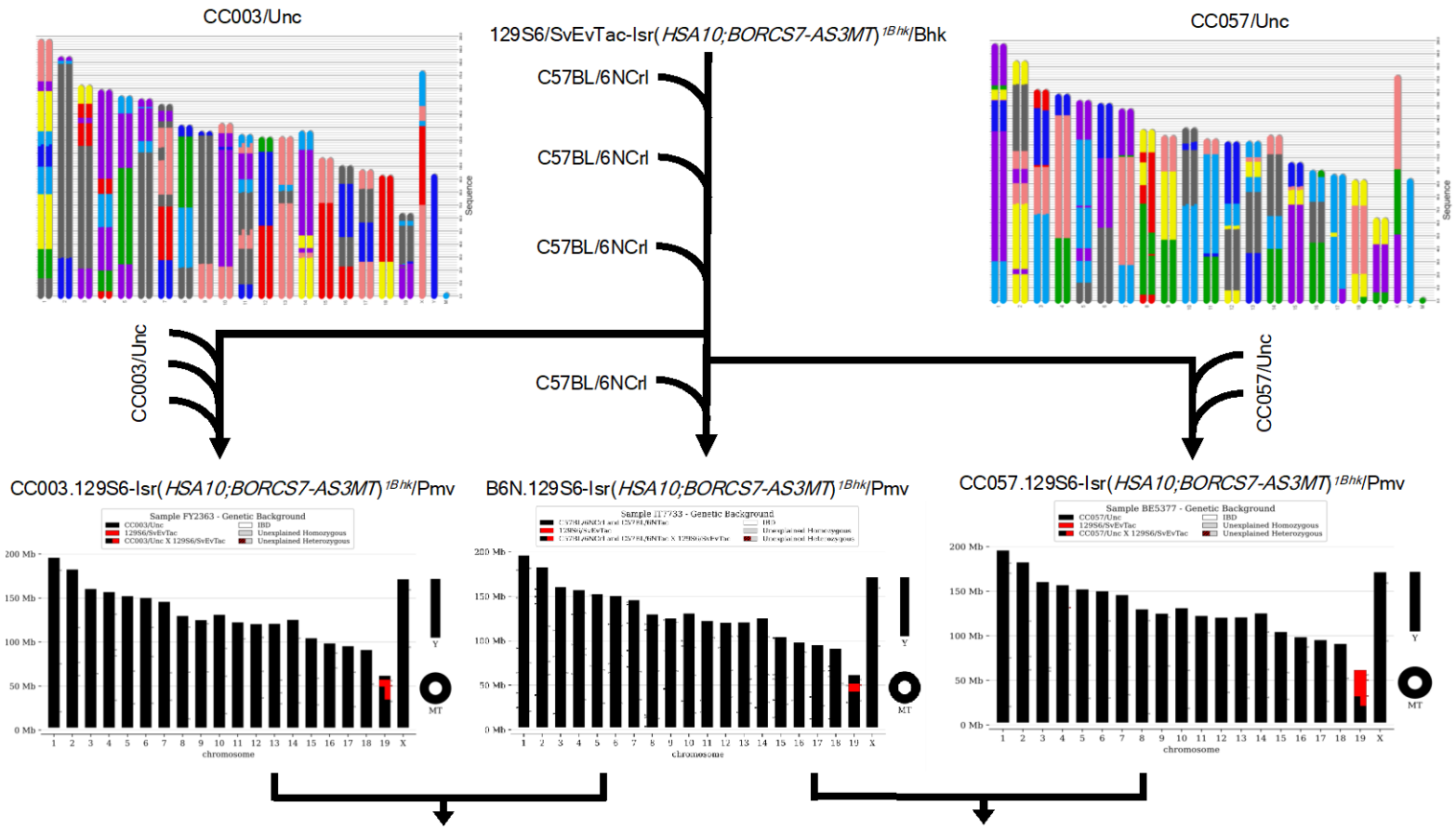
Koller, Beverly H., et al. "Arsenic metabolism in mice carrying a BORCS7/AS3MT locus humanized by syntenic replacement." *Environmental health perspectives* 128.8 (2020): 087003.

Humanized mouse model

mAs3mt ⇨ *hAS3MT*

Diverse Genetic Backgrounds





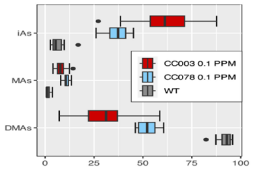
~10 Million SNPs in (B6xCC)F1 and (CCxB6)F1 Offspring

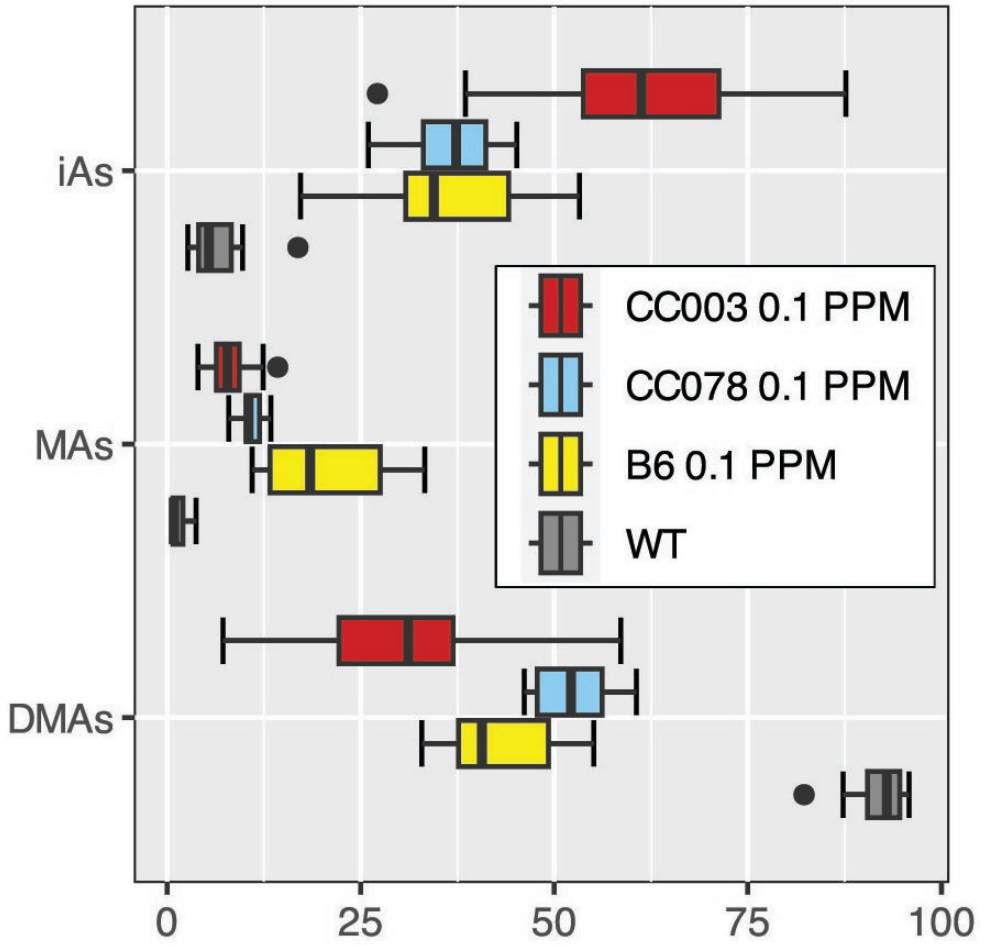
Humanized mouse model

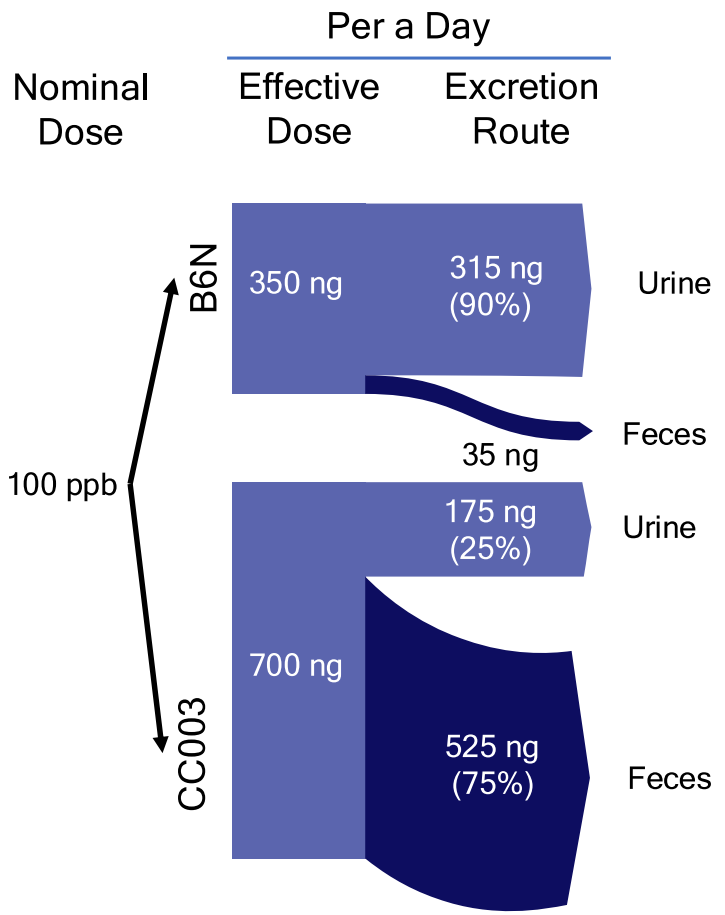
mAs3mt ⇨ *hAS3MT*

Diverse Genetic Backgrounds

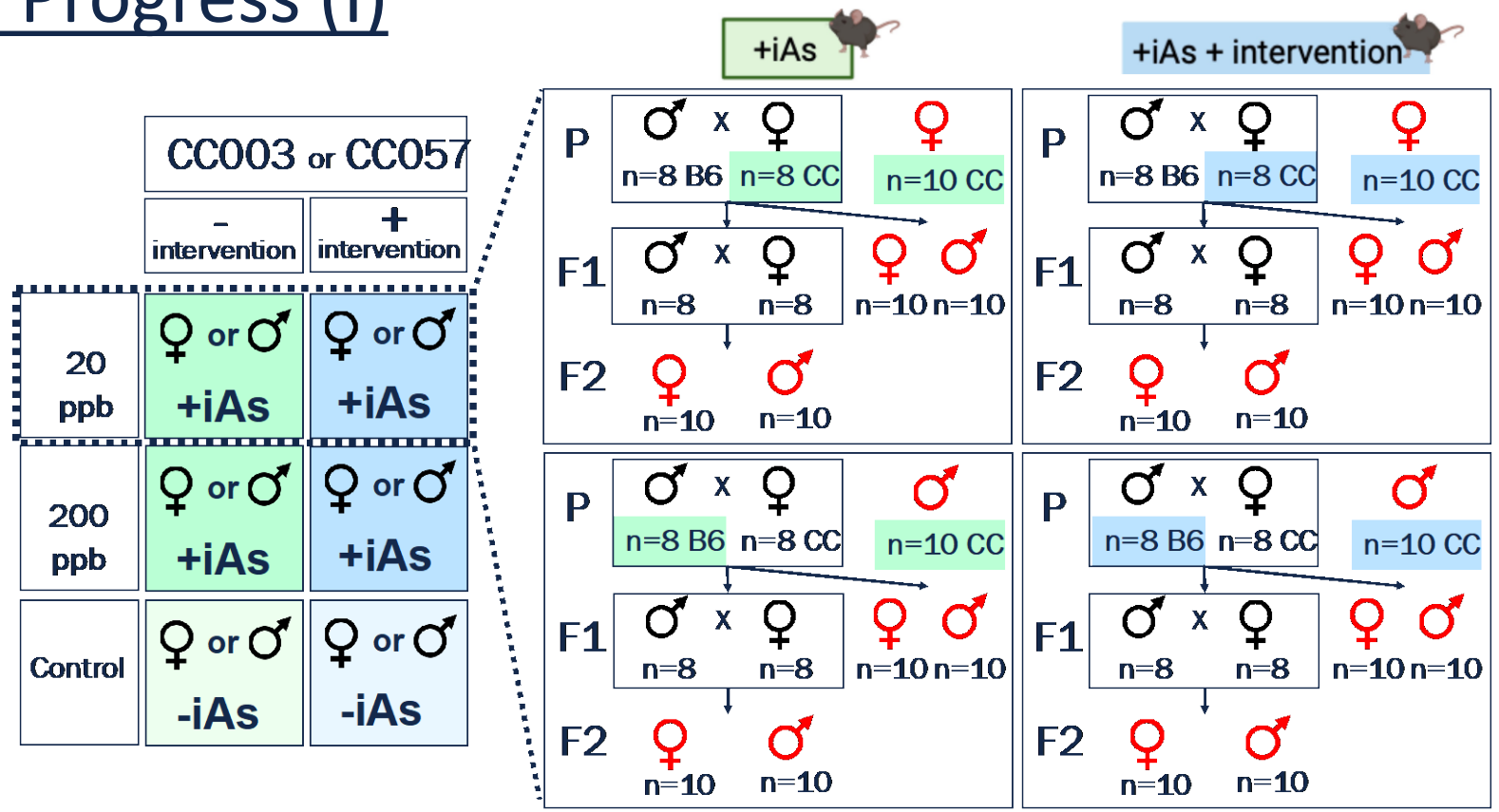
Supportive Preliminary Results







Design and Progress (I)



78 mice per cohort
(1,872 mice)

2 parental sex → Effect of sex in preconception exposure

x

3 exposure doses → Effect of exposure and dose

x

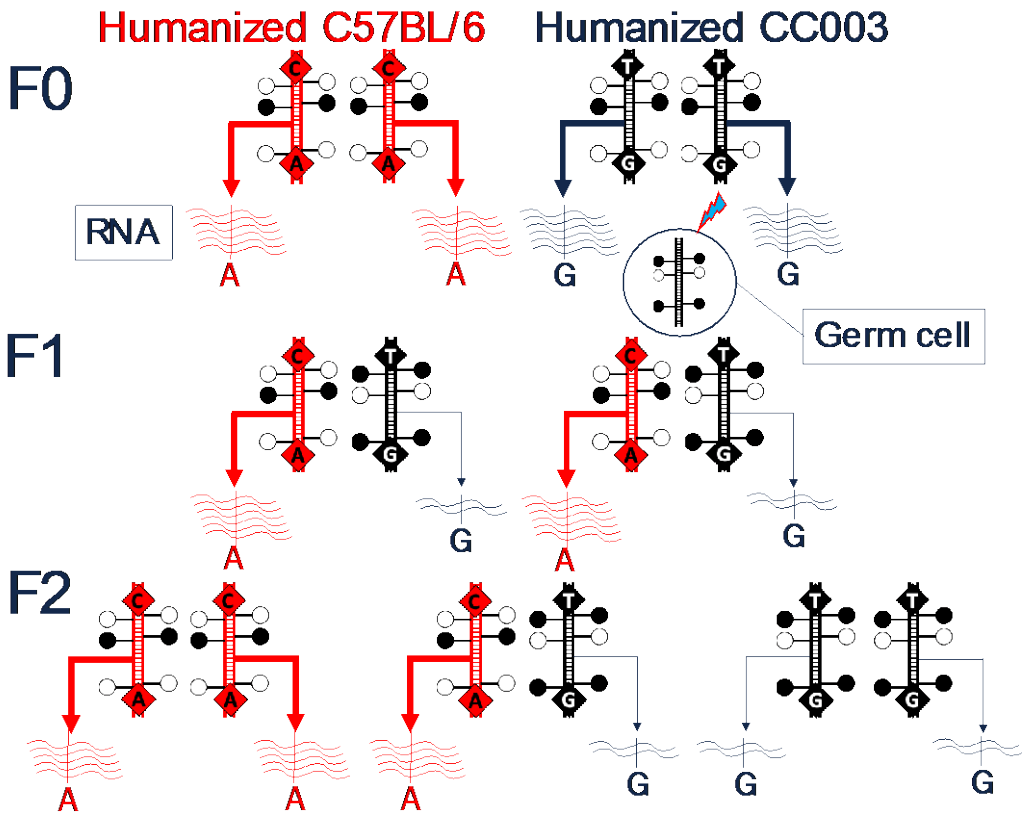
2 interventions → Effect of dietary intervention

x

2 humanized strains → Effect of genetics background

24 experimental cohorts each with 78 mice across 3 generations

Design and Progress (II)



Factorial Design

24 cohorts
78 mice per cohort
(1,872 mice)
59 weeks/cohort

10-12 batches

Factors included in every cohort
Dose
Strain

Factors varying between cohorts
Parental sex
Intervention

Status

1-2 cohorts completed
2-3 cohorts in progress

Focused on completing breeding early

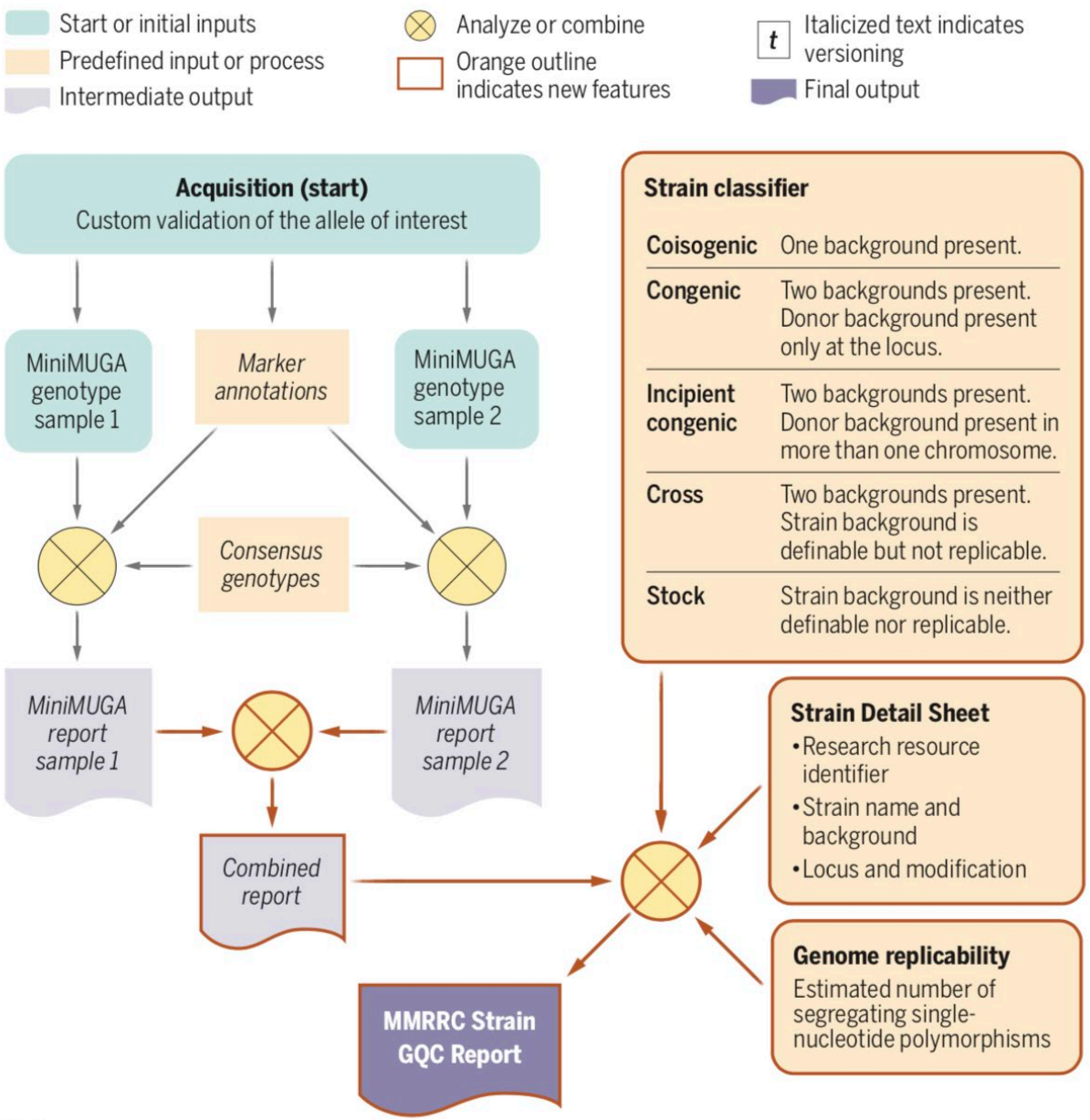
Tissue collection for molecular phenotyping ongoing

Physiological phenotyping ongoing

Products and Deliverables

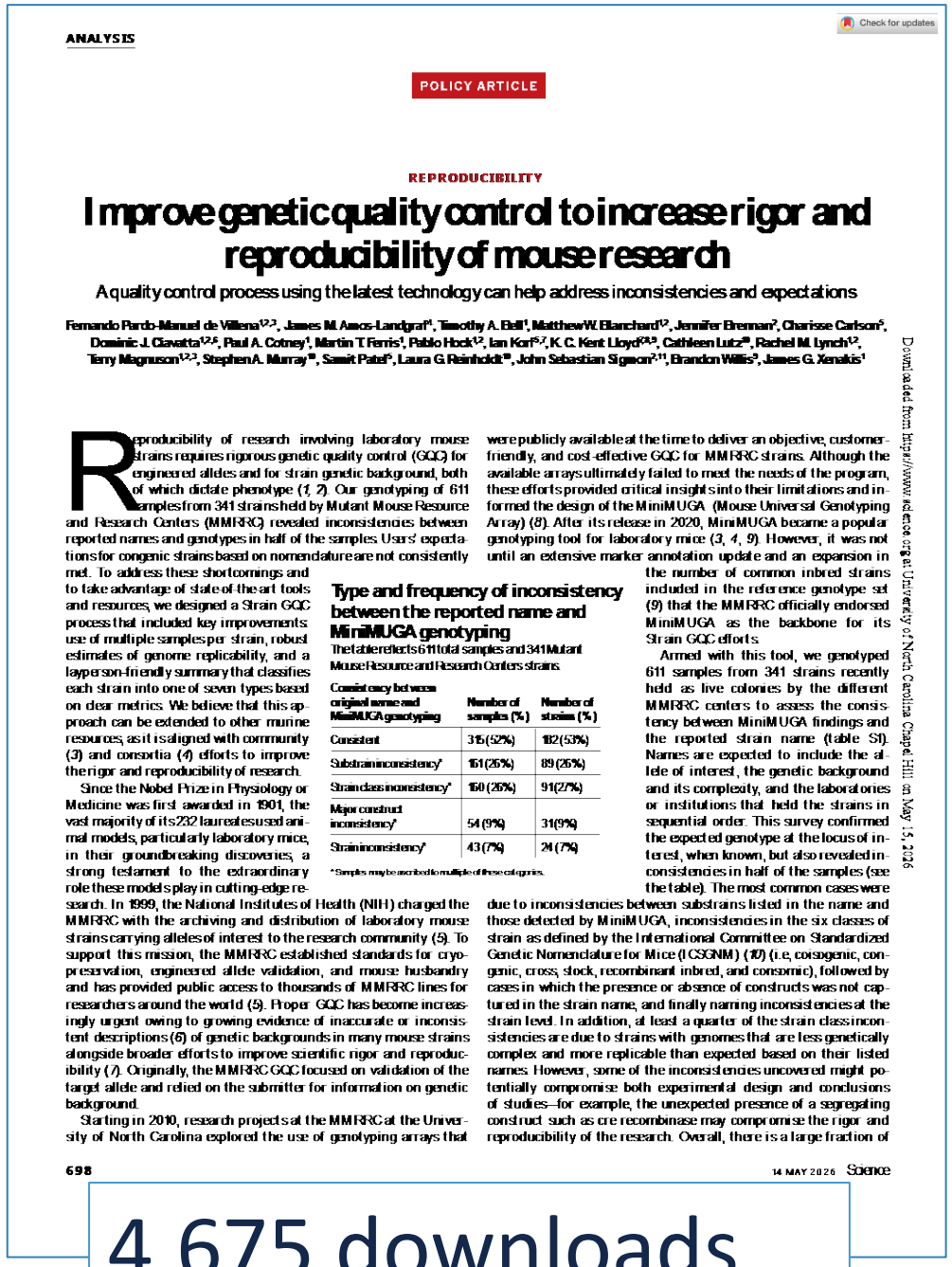
- Manuscript in preparation describing the effects (on metabolic traits) of arsenic exposure in humanized *AS3MT* mice in the CC backgrounds:
  - Strain effects
  - Sex effects
  - Diet effects
  - Interaction
- Six humanized *AS3MT* mouse strains (129, B6 and CC genetic backgrounds) archived by the MMRRC-UNC
- *AS3MT* humanized mice distributed to P1, and investigators outside of UNC
- Biological samples supplied to P1 (microbiome)
- *AS3MT* humanized mice were instrumental in defining a new Strain GQC process to be used by all MMRR Centers and proposed as the new standard for mouse-based research (generation, distribution, reporting and funding)

The strain genetic quality control workflow



Science 14 MAY 2026

The strain classifier relies on a large genotyping dataset across multiple generations for multiple congenic lines carrying the *AS3MT* humanized gene (SRP product)



ANALYSIS

Check for updates

POLICY ARTICLE

REPRODUCIBILITY

Improve genetic quality control to increase rigor and reproducibility of mouse research

A quality control process using the latest technology can help address inconsistencies and expectations

Fernando Pardo-Manuel de Villena[1,2,3], James M. Anaos-Landgraf[4], Timothy A. Bell[1], Matthew W. Blanchard[1,2], Jennifer Brennan[2], Charisse Carlson[5], Dominic J. Ciavatta[1,2,6], Paul A. Cotney[1], Martin T. Ferris[1], Pablo Hock[1,2], Ian Korf[6,7], K. C. Kent Lloyd[8,9,3], Cathleen Lutz[10], Rachel M. Lynch[1,2], Terry Magnuson[1,2,3], Stephen A. Murray[10], Samit Patel[5], Laura G. Reinholdt[10], John Sebastian Sigmon[2,11], Brandon Willis[5], James G. Xenakis[1]

Reproducibility of research involving laboratory mouse strains requires rigorous genetic quality control (GQC) for engineered alleles and for strain genetic background, both of which dictate phenotype (*1*, *2*). Our genotyping of 611 samples from 341 strains held by Mutant Mouse Resource and Research Centers (MMRRC) revealed inconsistencies between reported names and genotypes in half of the samples. Users' expectations for congenic strains based on nomenclature are not consistently met. To address these shortcomings and to take advantage of state-of-the-art tools and resources, we designed a Strain GQC process that included key improvements: use of multiple samples per strain, robust estimates of genome replicability, and a layperson-friendly summary that classifies each strain into one of seven types based on clear metrics. We believe that this approach can be extended to other murine resources, as it is aligned with community (*3*) and consortia (*4*) efforts to improve the rigor and reproducibility of research.

Since the Nobel Prize in Physiology or Medicine was first awarded in 1901, the vast majority of its 232 laureates used animal models, particularly laboratory mice, in their groundbreaking discoveries, a strong testament to the extraordinary role these models play in cutting-edge research. In 1999, the National Institutes of Health (NIH) charged the MMRRC with the archiving and distribution of laboratory mouse strains carrying alleles of interest to the research community (*5*). To support this mission, the MMRRC established standards for cryopreservation, engineered allele validation, and mouse husbandry and has provided public access to thousands of MMRRC lines for researchers around the world (*5*). Proper GQC has become increasingly urgent owing to growing evidence of inaccurate or inconsistent descriptions (*6*) of genetic backgrounds in many mouse strains alongside broader efforts to improve scientific rigor and reproducibility (*7*). Originally, the MMRRC GQC focused on validation of the target allele and relied on the submitter for information on genetic background.

Starting in 2010, research projects at the MMRRC at the University of North Carolina explored the use of genotyping arrays that were publicly available at the time to deliver an objective, customer-friendly, and cost-effective GQC for MMRRC strains. Although the available arrays ultimately failed to meet the needs of the program, these efforts provided critical insight into their limitations and informed the design of the MiniMUGA (Mouse Universal Genotyping Array) (*8*). After its release in 2020, MiniMUGA became a popular genotyping tool for laboratory mice (*3*, *4*, *9*). However, it was not until an extensive marker annotation update and an expansion in the number of common inbred strains included in the reference genotype set (*9*) that the MMRRC officially endorsed MiniMUGA as the backbone for its Strain GQC efforts.

Armed with this tool, we genotyped 611 samples from 341 strains recently held as live colonies by the different MMRRC centers to assess the consistency between MiniMUGA findings and the reported strain name (table S1). Names are expected to include the allele of interest, the genetic background and its complexity, and the laboratories or institutions that held the strains in sequential order. This survey confirmed the expected genotype at the locus of interest, when known, but also revealed inconsistencies in half of the samples (see the table). The most common cases were due to inconsistencies between substrains listed in the name and those detected by MiniMUGA, inconsistencies in the six classes of strain as defined by the International Committee on Standardized Genetic Nomenclature for Mice (ICSGNM) (*10*) (i.e, coisogenic, congenic, cross, stock, recombinant inbred, and consomic), followed by cases in which the presence or absence of constructs was not captured in the strain name, and finally naming inconsistencies at the strain level. In addition, at least a quarter of the strain class inconsistencies are due to strains with genomes that are less genetically complex and more replicable than expected based on their listed names. However, some of the inconsistencies uncovered might potentially compromise both experimental design and conclusions of studies—for example, the unexpected presence of a segregating construct such as cre recombinase may compromise the rigor and reproducibility of the research. Overall, there is a large fraction of

Type and frequency of inconsistency between the reported name and MiniMUGA genotyping

The table reflects 611 total samples and 341 Mutant Mouse Resource and Research Centers strains.

Consistency between original name and MiniMUGA genotyping	Number of samples (%)	Number of strains (%)
Consistent	315 (52%)	182 (53%)
Substrain inconsistency*	161 (26%)	89 (26%)
Strain class inconsistency*	160 (26%)	91 (27%)
Major construct inconsistency*	54 (9%)	31 (9%)
Strain inconsistency*	43 (7%)	24 (7%)

*Samples may be ascribed to multiple of these categories.

4,675 downloads

Impact

Altmetrics

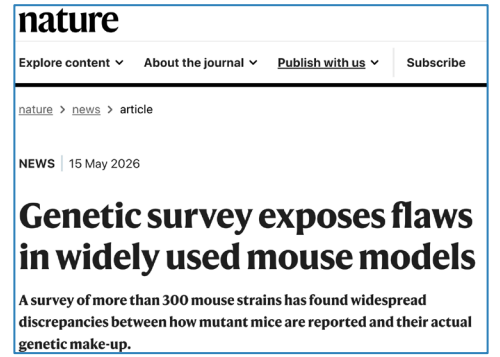
Picked up by **9** news outlets

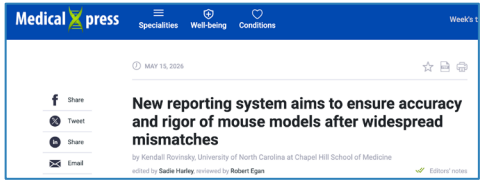
Posted by **60** X users

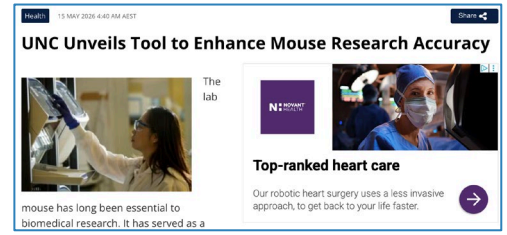
Referenced in **1** Wikipedia pages

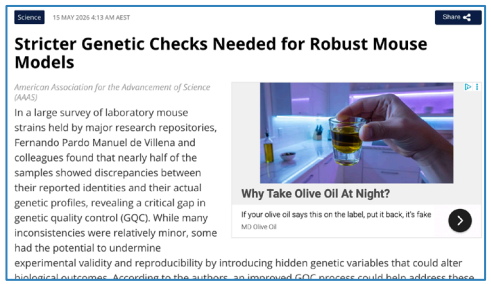
Referenced by **25** Bluesky users

1 readers on Mendeley









Adoption

MMRRC
Mutant Mouse Resource & Research Centers
Supported by NIH

20th Transgenic Technology Meeting
Leiden, The Netherlands
15 - 18 September 2026

UNC SCHOOL OF MEDICINE

Acknowledgements

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Martin Ferris PhD
Rebecca Fry PhD
Pablo Hock
Tianyi Liu
Rachel Lynch PhD
Gustavo Nativio
Franklin Sandridge
Avani Sarawastula
J Sebastian Sigmon, PhD
Ginger D Shaw
Qing Shi
Mirek Styblo PhD
Abhishek Venkatratnam, PhD
Joyce Woo
James Xenakis PhD
Yuanyuan Yan
Fei Zou PhD

The UNC Chapel Hill Superfund Research Program (UNC-SRP) NIEHS. P42ES031007. PD/PI: Fry, R

Data Management and Analysis Core

UNC-SRP DMAC Overview

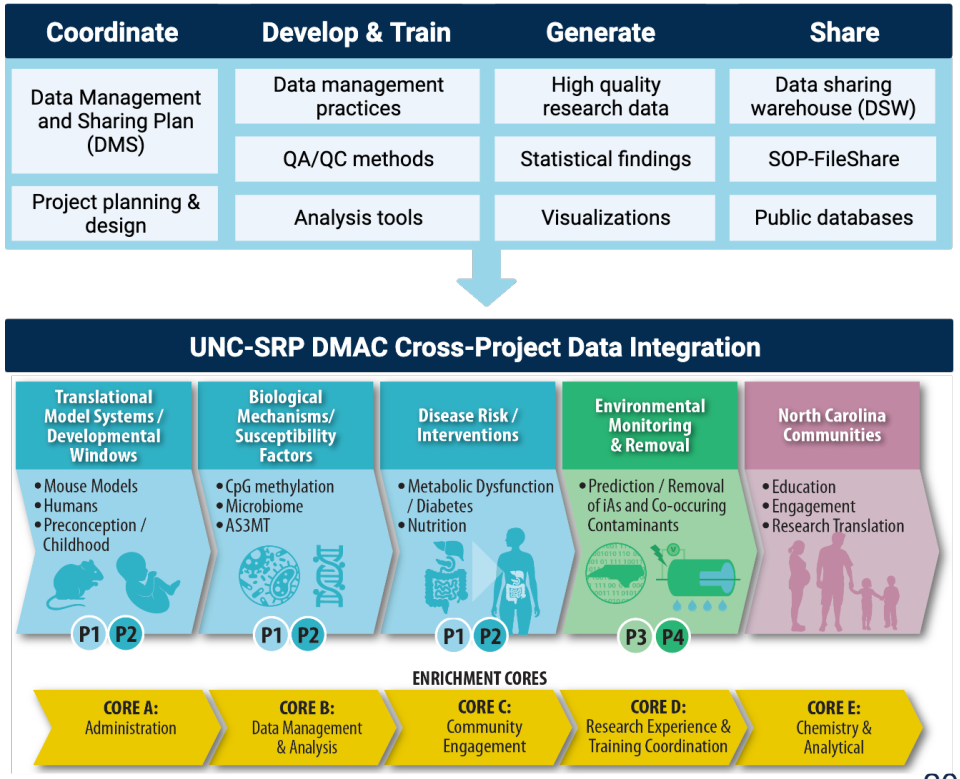
The DMAC is a critical support core with the **goal of facilitating the data management, sharing, integration, and analysis needs of UNC-SRP researchers to elucidate multi-factorial determinants of iAs-induced metabolic dysfunction/diabetes**

Core Leads

Julia Rager (Co-Lead)
Associate Professor in the Department of Environmental Sciences and Engineering

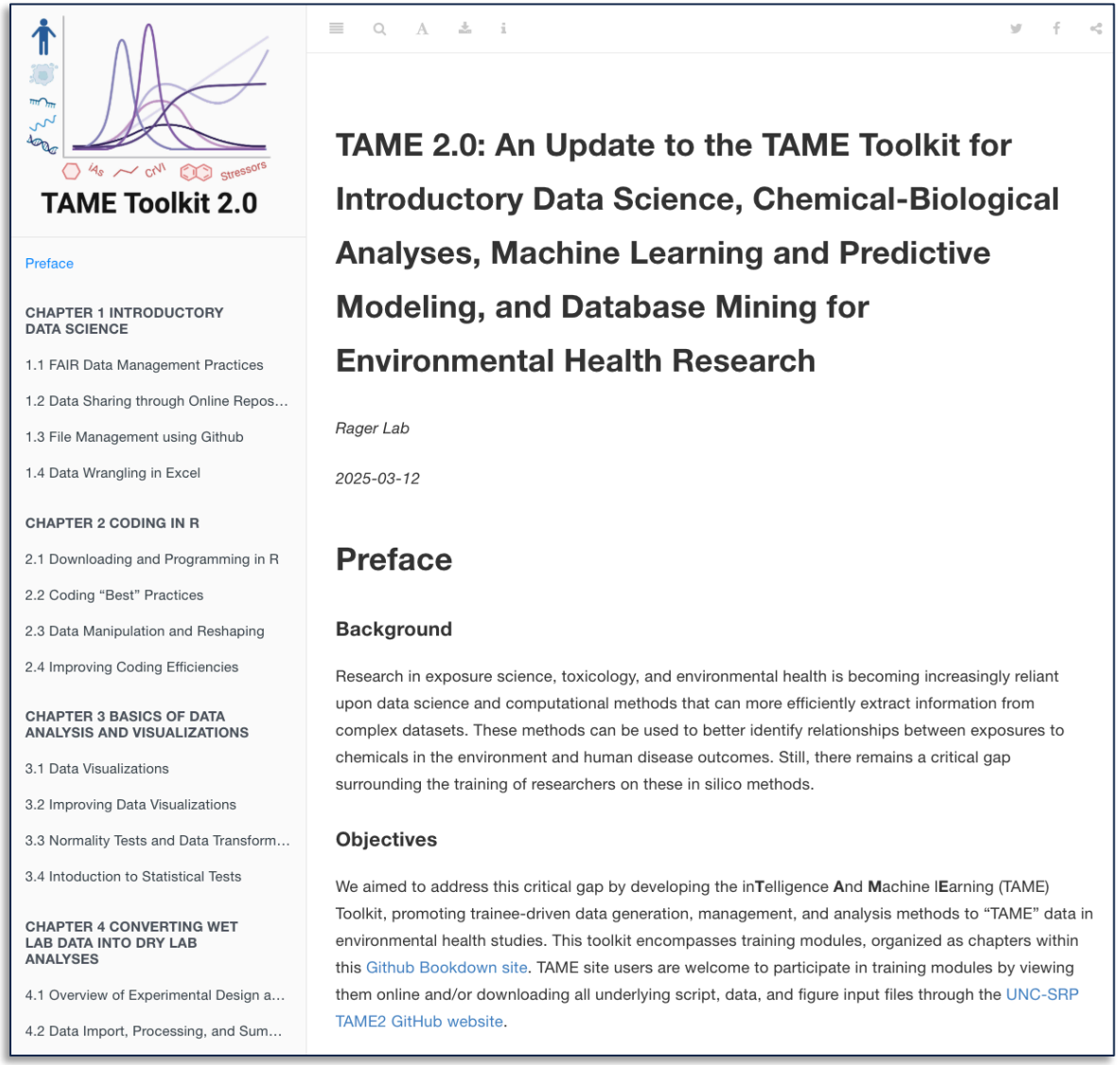
Fei Zou (Co-Lead)
Professor in the UNC Department of Biostatistics and Department of Genetics

Didong Li (Co-I)
Assistant Professor in the Department of Biostatistics



Example Data Science Training

- The inTelligence And Machine lEarning (TAME) Toolkit
- Online website that provide guided script-based examples on how to **“TAME” your data** in environmental health
- Originally launched in 2022, and continues to be updated



Example Training Module Walk-Through

4.5 Multi-Group and Multi-Variable Comparisons and Visualizations

This training module was developed by Elise Hickman, Alexis Payton, and Julia E. Rager.

All input files (script, data, and figures) can be downloaded from the UNC-SRP TAME2 GitHub website.

Introduction to Training Module

In the previous module, we covered how to apply two-group statistical testing, one of the most basic types of statistical tests. In this module, we will build on the concepts introduced previously to apply statistical testing to datasets with more than two groups, which are also very common in environmental health research. We will review common multi-group overall effects tests and post-hoc tests, and we will demonstrate how to apply these tests and how to graph the results using the same example dataset as in previous modules in this chapter, which represents concentrations of inflammatory biomarkers secreted by airway epithelial cells after exposure to different concentrations of acrolein.

Training Module's Environmental Health Questions

This training module was specifically developed to answer the following environmental health questions:

1. Are there significant differences in inflammatory biomarker concentrations between different doses of acrolein?
2. Do TNF-α concentrations significantly increase with increasing dose of acrolein?

Workspace Preparation and Data Import

Here, we will import the processed data that we generated at the end of TAME 2.0 Module 4.2, introduced in **TAME 2.0 Module 4.1 Overview of Experimental Design and Example Data** and the associated demographic data. These data represent $\log_2$ concentrations of inflammatory biomarkers secreted by airway epithelial cells after exposure to four different concentrations of acrolein (plus filtered air as a control). We will also load packages that will be needed for the analysis, including previously introduced packages such as *openxlsx*, *tidyverse*, *DT*, *ggpubr*, and *rstatix*.

Cleaning the global environment

```
rm(list=ls())
```

Loading R packages required for this session

```
library(openxlsx)
library(tidyverse)
library(DT)
library(rstatix)
library(ggpubr)
```

Set your working directory

```
setwd("/filepath to where your input files are")
```

Importing example dataset

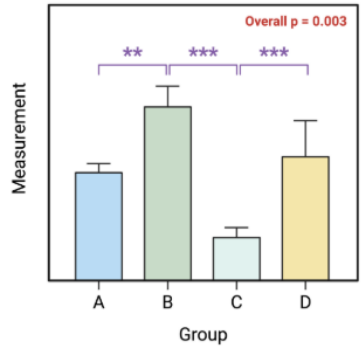
```
biomarker_data <- read.xlsx("Chapter_4/Module4_5_Input/Module4_5_InputData1.xlsx")
demographic_data <- read.xlsx("Chapter_4/Module4_5_Input/Module4_5_InputData2.xlsx")

# View data
```

Example Training Module Walk-Through

Overview of Multi-Group Statistical Tests

Before applying statistical tests to our data, let's first review the mechanics of multi-group statistical tests, including overall effects tests and post-hoc tests.



The **overall p-value** comes from the main statistical test (e.g., t-test, Wilcoxon test, ANOVA, Kruskal-Wallis, Friedman Test).

Pairwise p-values are derived from post-hoc tests such as pairwise t-tests, pairwise Wilcox tests, Tukey's HSD, and Dunn's test.

Overall Effects Tests

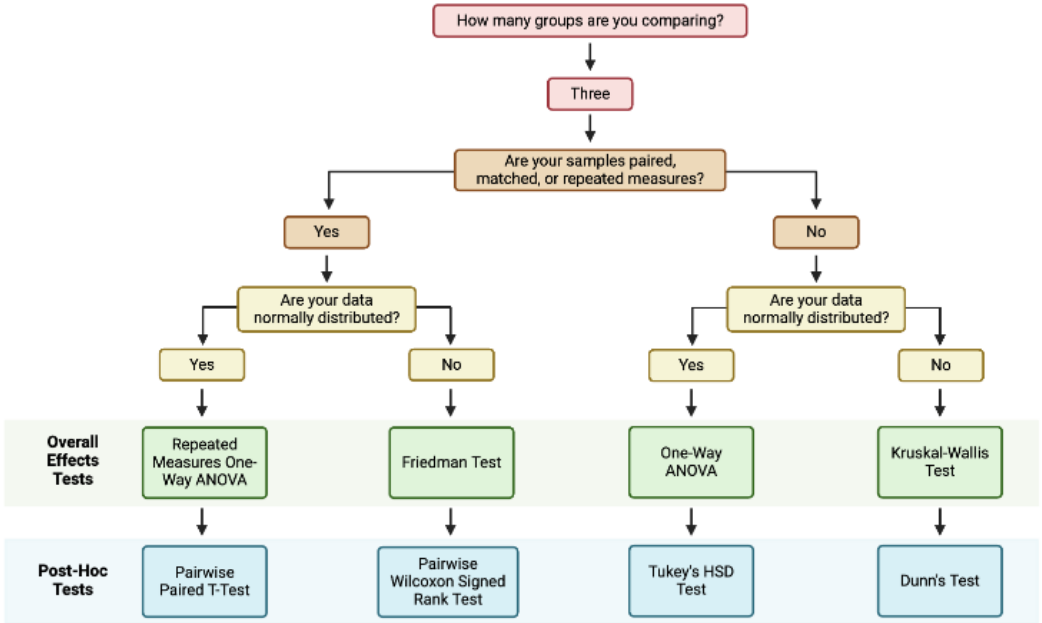
The first step for multi-group statistical testing is to run an overall effects test. The null hypothesis for the overall effects test is that there are no differences among group means. A significant p-value rejects the null hypothesis that the groups are drawn from populations with the same mean and indicates that at least one group differs significantly from the overall mean. Similar to two-group statistical testing, choice of the specific overall statistical test to run depends on whether the data are normally or non-normally distributed and whether the experimental design is paired:

MULTI-GROUP OVERALL TEST		Data Distribution	
		Parametric (Normal)	Non-Parametric (Non-Normal)
Matched/ paired design?	Yes	Repeated Measures One-Way Analysis of Variance (ANOVA)	Friedman Test
	No	One-Way ANOVA	Kruskal-Wallis Test

Importantly, overall effects tests return **one** p-value regardless of the number of groups being compared. To determine which pairwise comparisons are significant, post-hoc testing is needed.

Which test should I choose?

Use the following flowchart to help guide your choice of statistical test to compare multiple groups:



Example Training Module Walk-Through

Multi-Group Analysis Example

To determine whether there are significant differences across all of our doses, the Friedman test is the most appropriate due to our matched experimental design and non-normally distributed data. The `friedman_test()` function is part of the rstatix package. This package also has many other helpful functions for statistical tests that are pipe/tidyverse friendly. To demonstrate how this test works, we will first perform the test on one variable:

```
biomarker_data %>% friedman_test(IL1B ~ Dose | Donor)
```

```
## # A tibble: 1 × 6
##   .y.       n statistic    df      p method
## * <chr> <int>     <dbl> <dbl>  <dbl> <chr>
## 1 IL1B     16      12.5     4 0.0140 Friedman test
```

A p-value of 0.01 indicates that we can reject the null hypothesis that all of our data are drawn from groups that have equivalent means.

Now, we can run a `for` loop similar to our two-group comparisons in **TAME 2.0 Module 4.4 Two Group Comparisons and Visualizations** to determine the overall p-value for each endpoint:

```
# Create a vector with the names of the variables you want to run the test on
endpoints <- colnames(biomarker_data %>% select(IL1B:VEGF))

# Create data frame to store results
dose_friedmanres <- data.frame()

# Run for loop
for (i in 1:length(endpoints)) {

  # Assign a name to the endpoint variable.
  endpoint <- endpoints[i]
```

	Variable	Overall	0 vs. 0.6	0 vs. 1	0 vs. 2	0 vs. 4	0.6 vs. 1	0.6 vs. 2	0.6 vs. 4	1 vs. 2	1 vs. 4	2 vs. 4
1	IL1B	1.40e-02	*	*	*	*	ns	ns	*	ns	ns	ns
2	IL6	1.56e-02	ns	ns	ns	*	ns	ns	*	ns	*	*
3	IL8	4.07e-10	*	ns	****	****	ns	***	****	****	****	***
4	IL10	2.84e-03	**	ns	ns	ns	**	ns	**	ns	ns	ns
5	TNFa	8.90e-07	ns	ns	**	**	*	***	***	*	**	ns
6	VEGF	2.34e-07	ns	*	***	ns	*	***	ns	***	ns	ns

Showing 1 to 6 of 6 entries Previous 1 Next

Answer to Environmental Health Question 1

*With this, we can answer **Environmental Health Question #1*** : Are there significant differences in inflammatory biomarker concentrations between different doses of acrolein?

Answer: Yes, there are significant differences in inflammatory biomarker concentrations between different doses of acrolein. The overall p-values for all biomarkers are significant. Within each biomarker, at least one pairwise comparison was significant between doses, with a majority of these significant comparisons being with the highest dose (4 ppm).

Example Training Module Walk-Through

Visualization of Multi-Group Statistical Results

The statistical results we generated are a lot to digest in table format, so it can be helpful to graph the results. As our statistical testing becomes more complicated, so does the code used to generate results. The *ggpubr* package can perform statistical testing and overlay the results onto graphs for a specific set of tests, such as overall effects tests and unpaired t-tests or Wilcoxon tests. However, for tests that aren't available by default, the package also contains the helpful `stat_pvalue_manual()` function that can be added to plots. This is what we will need to use to add the results of our pairwise, paired Wilcoxon test with BH correction, as there is no option for BH correction within the default function we might otherwise use (`stat_compare_means()`). We will first work through an example of this using one of our endpoints, and then we will demonstrate how to apply it to facet plotting.

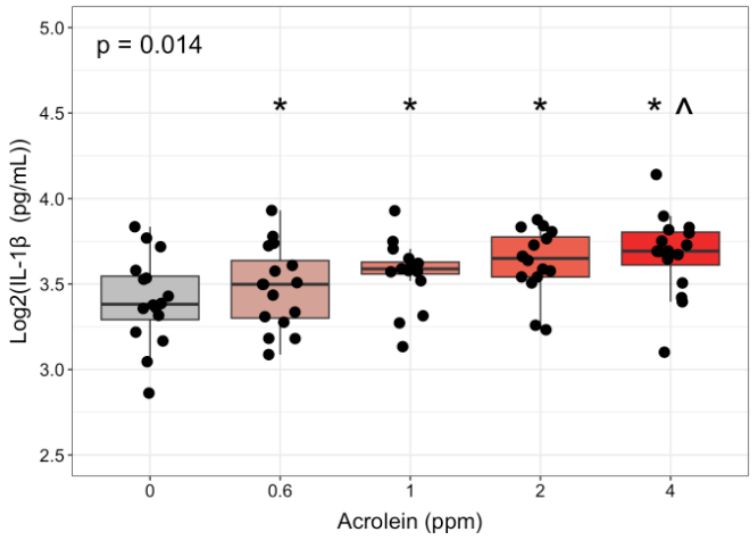
Single Plot

We first need to format our existing statistical results so that they match the format that the function needs as input. Specifically, the dataframe needs to contain the following columns:

- `group1` and `group2` : the groups being compared
- A column containing the results you want displayed (`p` , `p.adj` , or `p.adj.signif` typically)
- `y.position` , which tells the function where to plot the significance markers

Our results dataframe for IL-1β already contains our groups and p-values:

```
datatable(dose_wilcox_posthoc_IL1B)
```



An appropriate title for this figure could be:

"**Figure X. Exposure to 0.6-4 ppm acrolein increases IL-1β secretion in primary human bronchial epithelial cells.** Groups were compared using the Friedman test to obtain overall p-value and Wilcoxon signed rank test for post-hoc testing. * $p < 0.05$ in comparison with 0 ppm, ^ $p < 0.05$ in comparison with 0.6 ppm, n = 16 per group (paired)."

Example Training Module Walk-Through

Concluding Remarks

In this module, we introduced common multi-group statistical tests, including both overall effects tests and post-hoc testing. We applied these tests to our example dataset and demonstrated how to produce publication-quality tables and figures of our results. Implementing a workflow such as this enables efficient analysis of wet-bench generated data and customization of output figures and tables suited to your personal preferences.

Additional Resources

- STHDA: How to Add P-Values and Significance Levels to ggplots using *ggpubr*
- Adding p-values with *ggprism*
- Overview of *ggsignif*

Test Your Knowledge

Functional endpoints from these cultures were also measured. These endpoints were: 1) Membrane Permeability (MemPerm), 2) Trans-Epithelial Electrical Resistance (TEER), 3) Ciliary Beat Frequency (CBF), and 4) Expression of Mucin (MUC5AC). These data were already processed and tested for normality (see Test Your Knowledge for **TAME 2.0 Module 4.2 Data Import, Processing, and Summary Statistics**), with results indicating that two of the endpoints are normally distributed and two non-normally distributed.

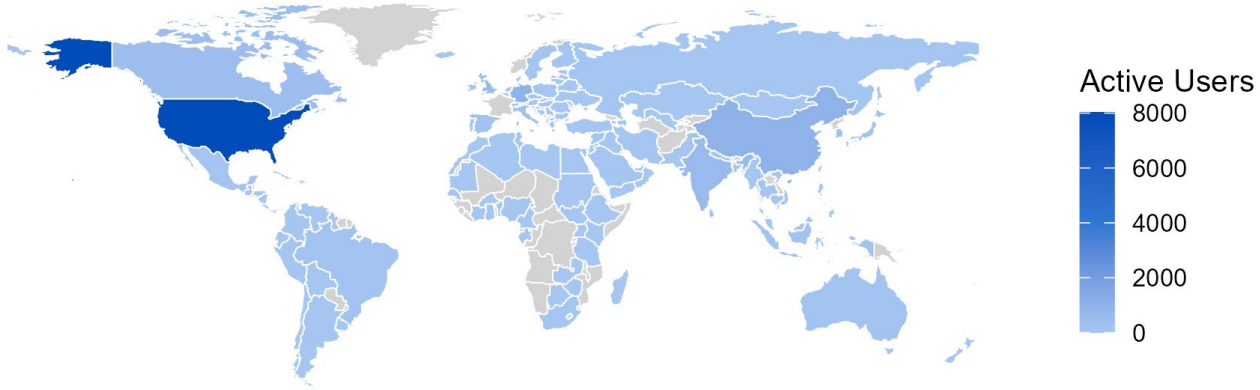
Use the same processes demonstrated in this module and the provided data ("Module4_5_TYKInput.xlsx" (functional data)) to run analyses and make a publication-quality figure panel and table to answer the following question: Are there significant differences in functional endpoints between cells treated with different concentrations of acrolein?

For an extra challenge, try also making your faceted plot in the style of option #1 above, with different symbols, letters, or group names above columns to indicate which group that column in significant in comparison with.

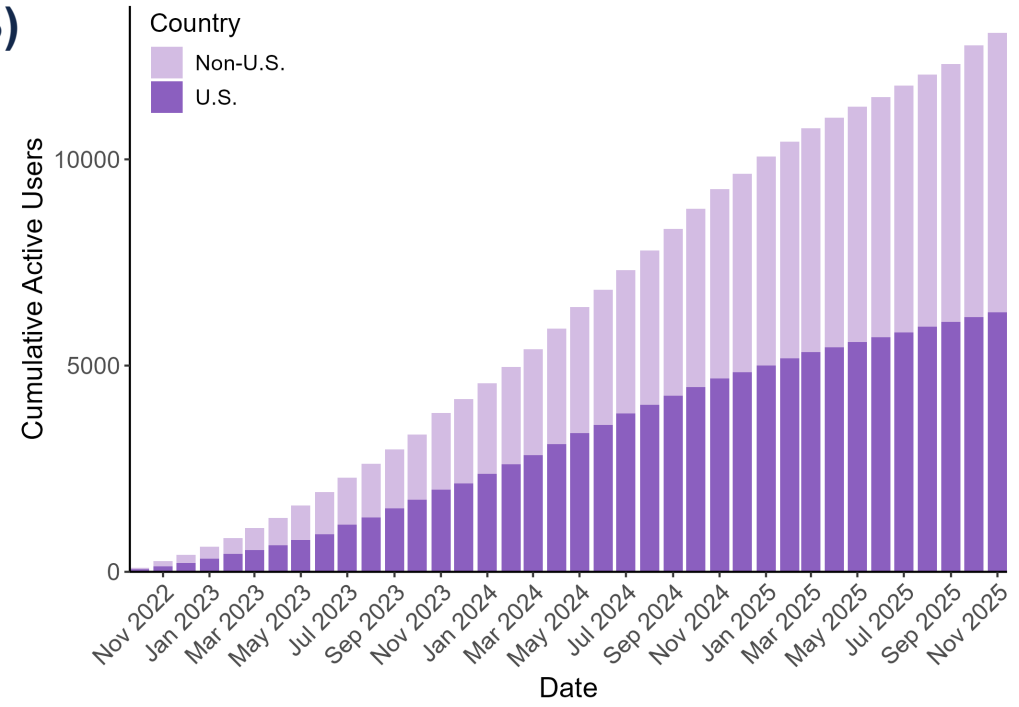
Global Dissemination

Users across over 131 countries have accessed the TAME Toolkit!

A)

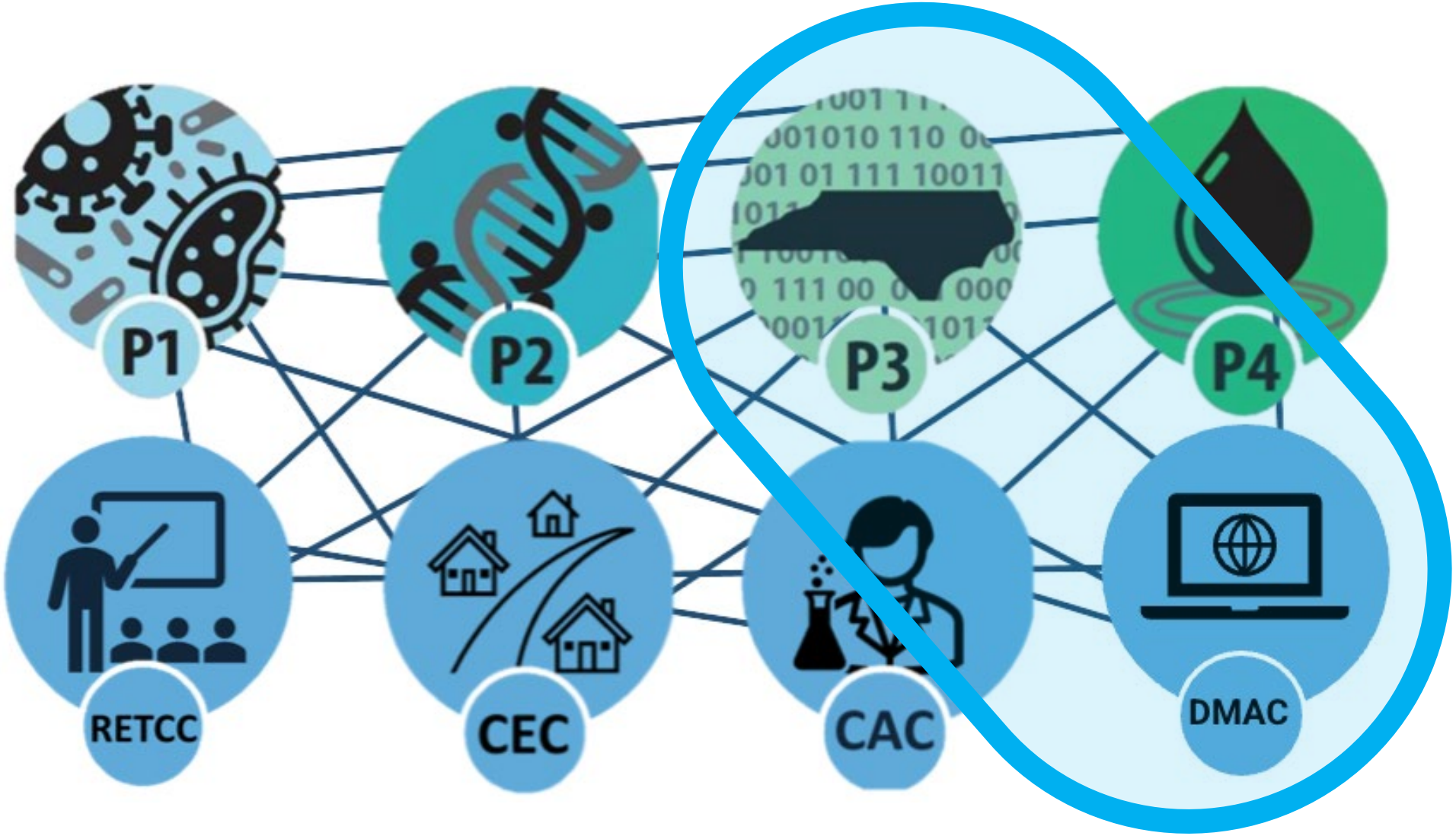


B)

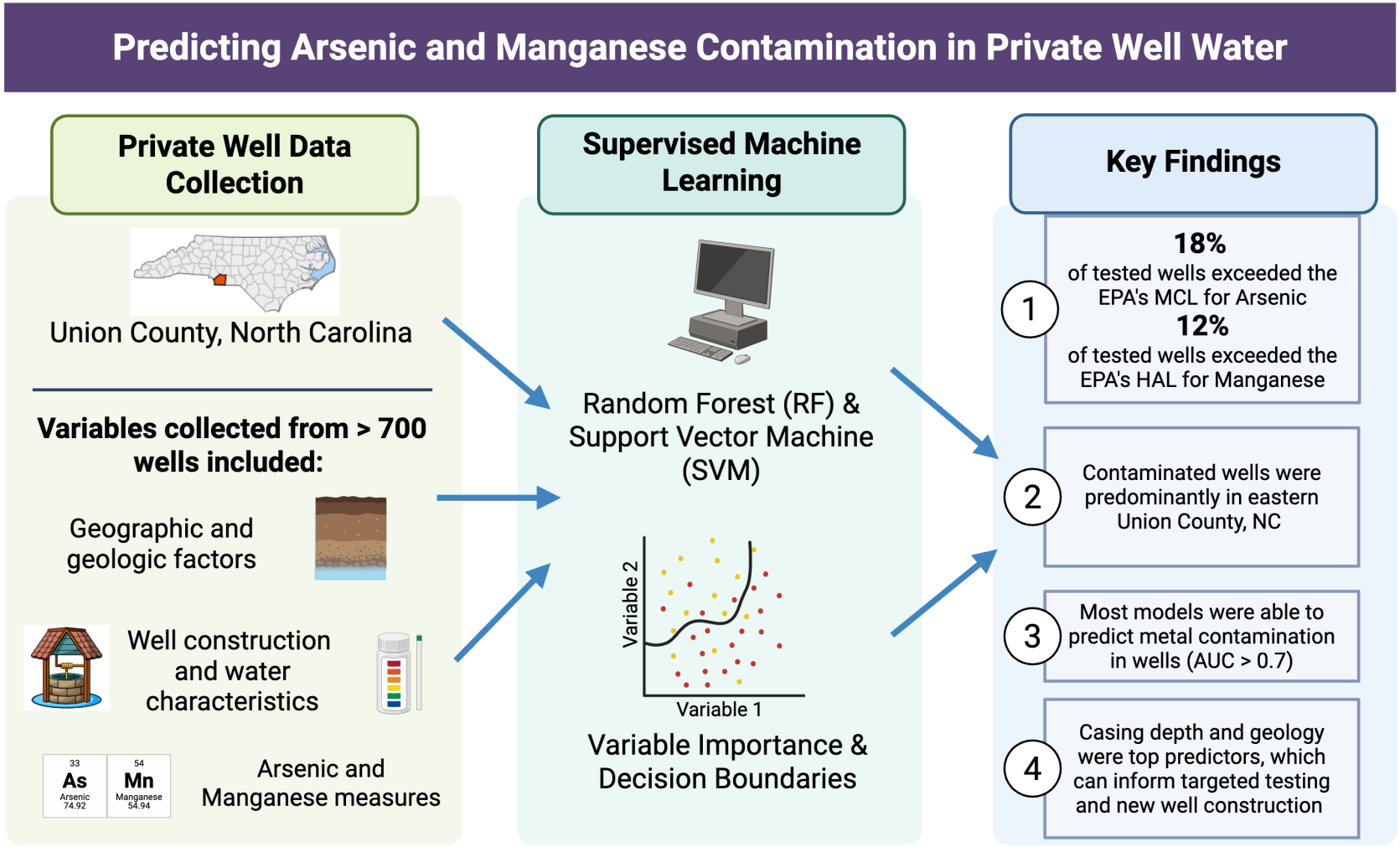


Global usage of the TAME 1.0 and 2.0 website since its launch in 2022. Data are illustrated as **(A)** a worldwide map of users, defined as the number of unique people who have engaged in the website between its 2022 launch up until November 2025. Usage is further displayed in **(B)** as the cumulative site views from September 2022 – November 2025 using data aggregated from Google Analytics.

Data Analysis Support across Projects



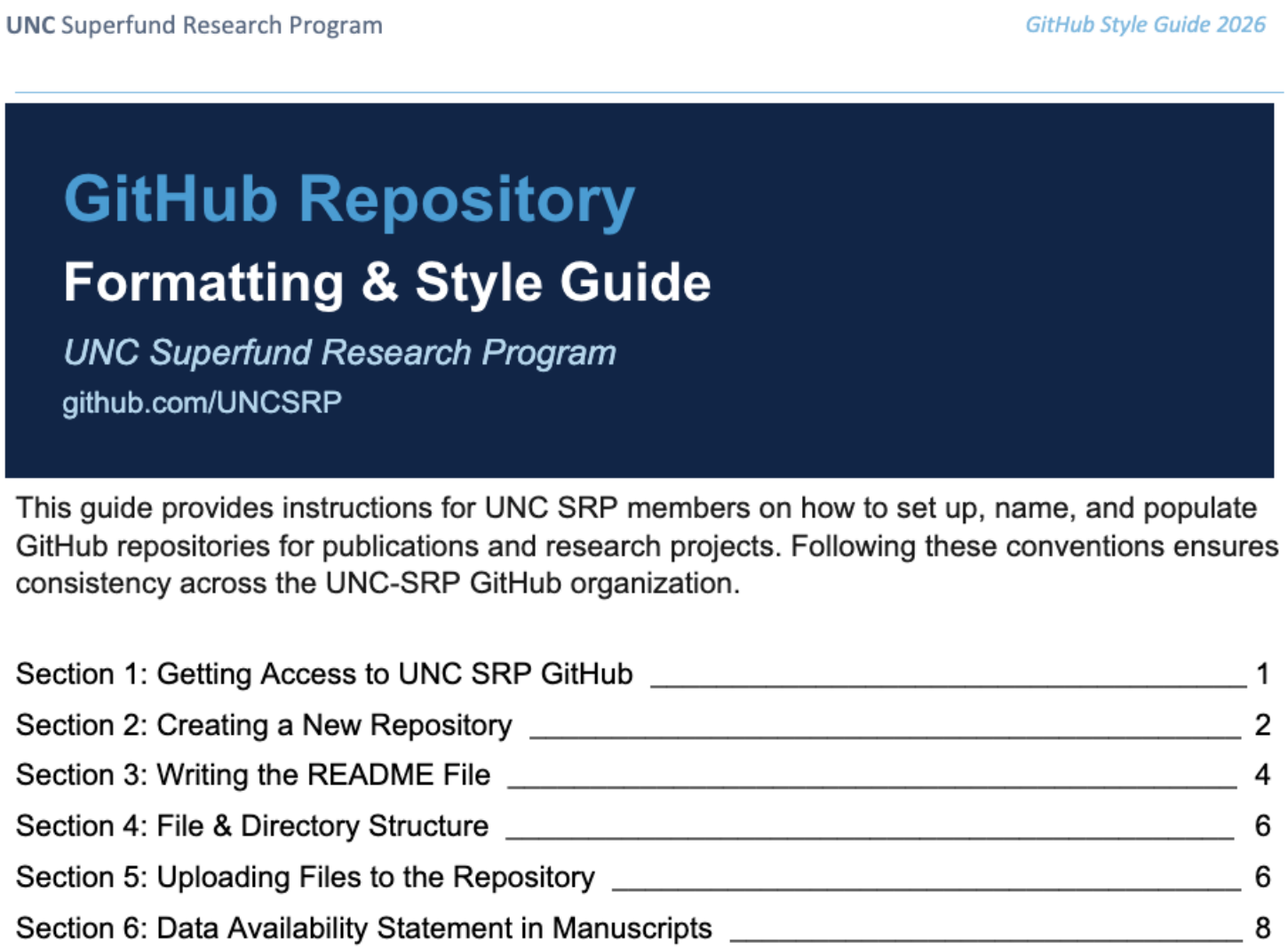
Data Analysis Support across Projects



Payton A, Harrington CE, Miller SL, Colley T, Serre ML, Fry RC, Austin RE, Duckworth OW, Eaves LA, Rager JE. Predicting arsenic and manganese contamination in private well water with Machine Learning: An integrated analysis of geologic, well construction, and permitting data. Sci Total Environ. 2025 Dec 1;1006:180907. PMID: 41240893.

Script Management & Sharing

Training disseminated to UNC-SRP trainees and PIs through a dedicated style guide + hands-on workshops



GitHub Repository

Formatting & Style Guide

UNC Superfund Research Program

github.com/UNCSRP

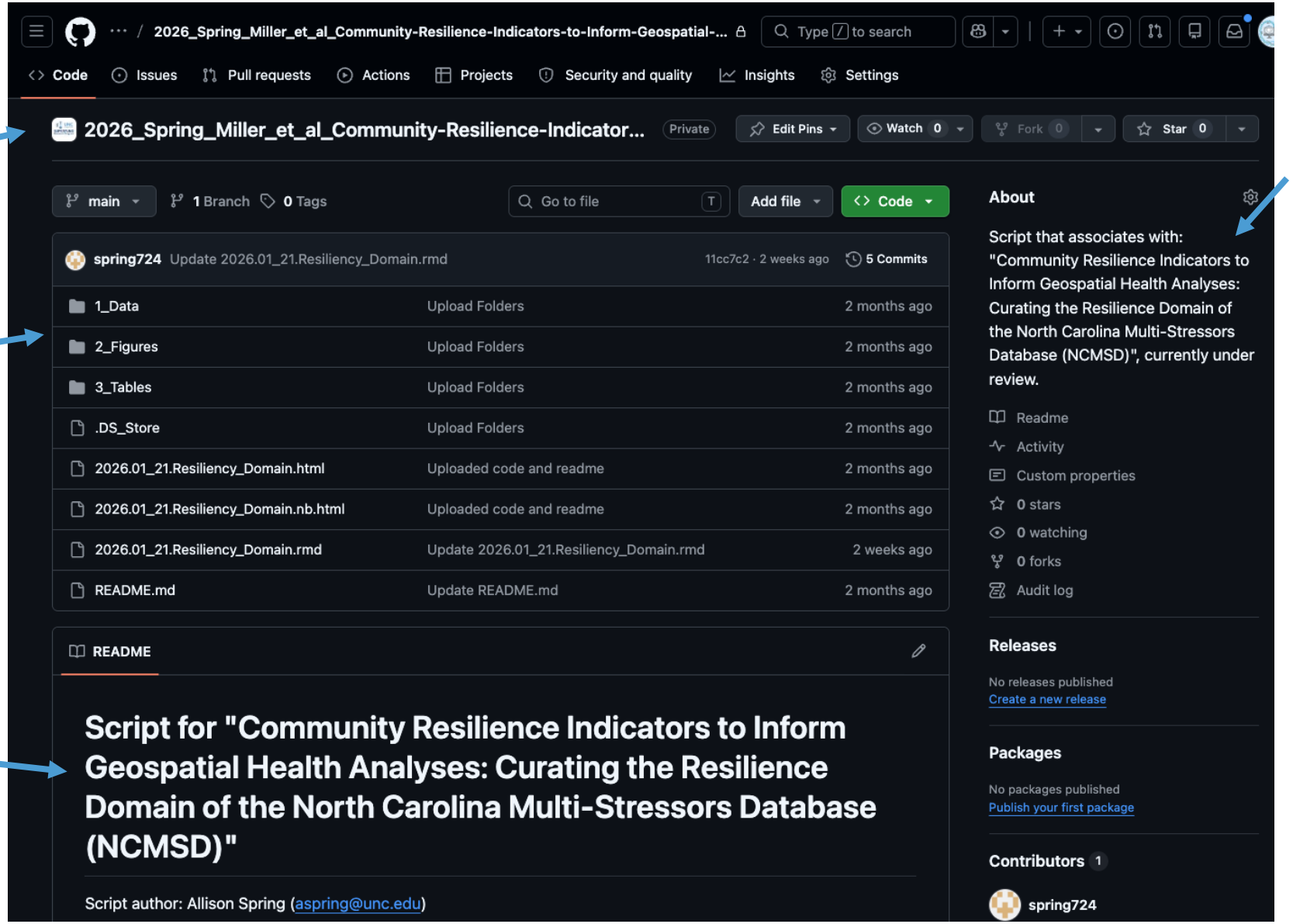
This guide provides instructions for UNC SRP members on how to set up, name, and populate GitHub repositories for publications and research projects. Following these conventions ensures consistency across the UNC-SRP GitHub organization.

Script Management & Sharing

Consist title structures

Consist folder structures

Consist README materials

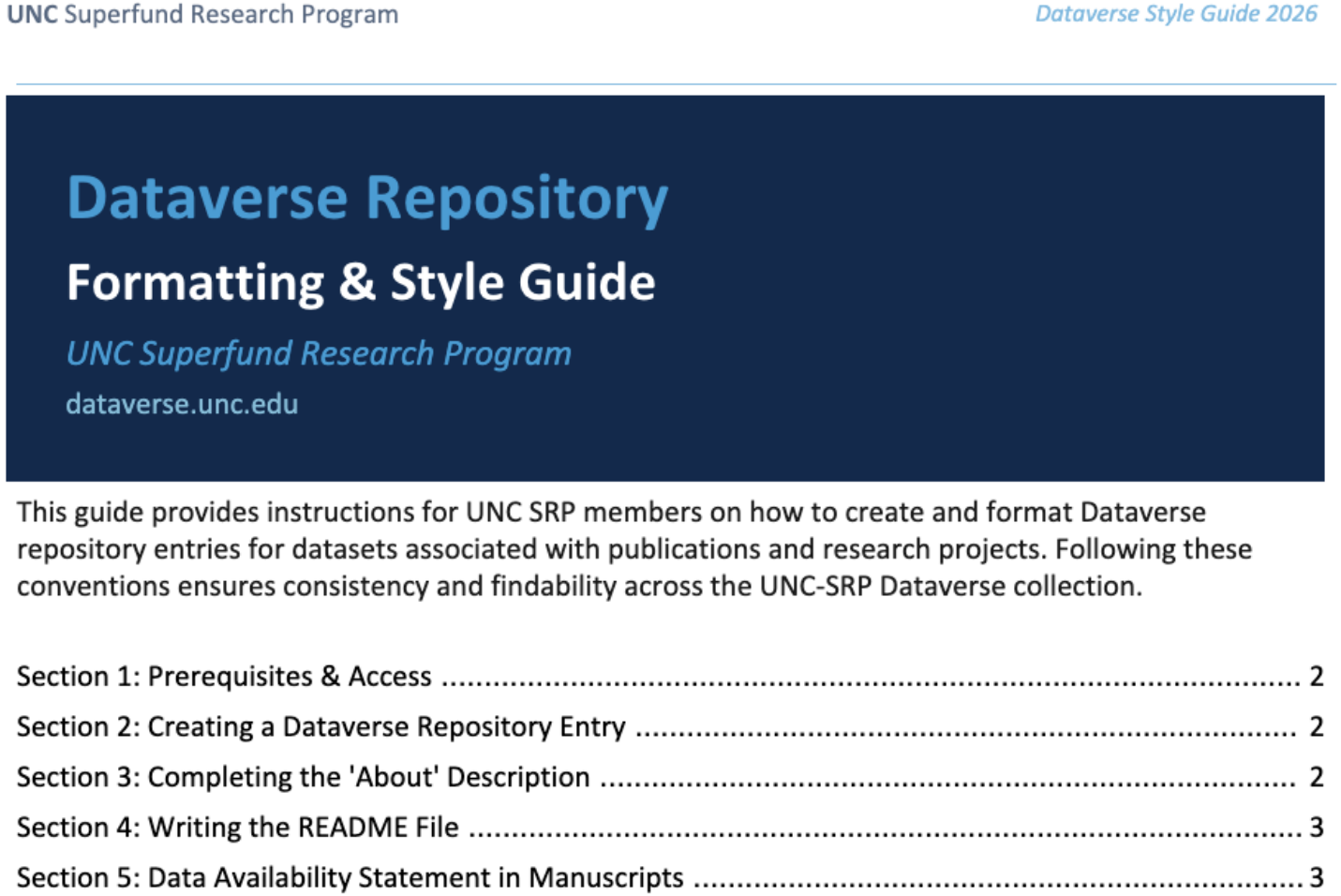


Consist text in 'About'

Data Management & Sharing

Training disseminated to UNC-SRP trainees and PIs through a dedicated style guide + hands-on workshops

- Dataverse as well as other data repositories relevant to UNC-SRP research (e.g., GEO, PRIDE, MassIVE, etc)



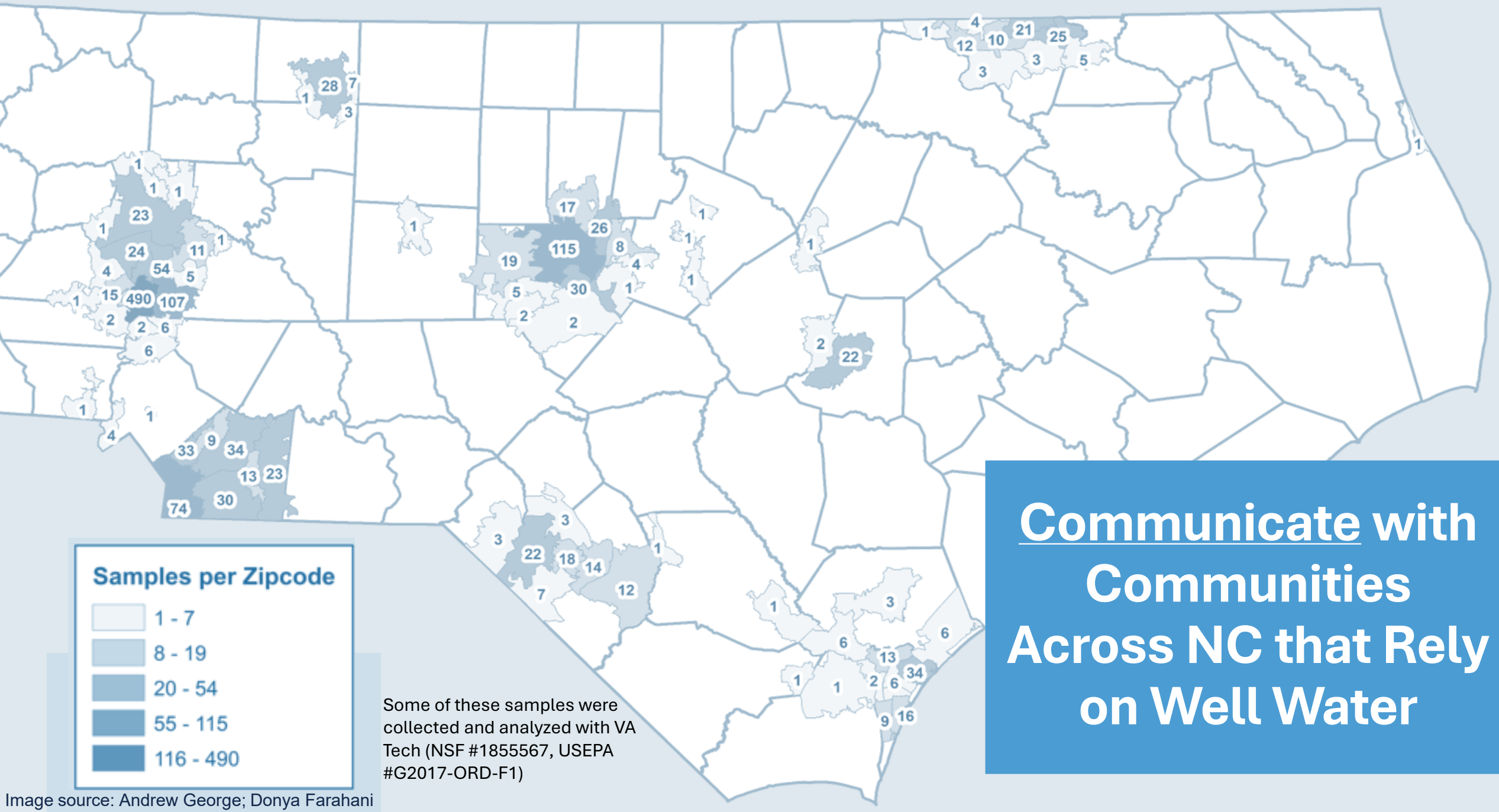
Community Engagement Core

The UNC SRP Community Engagement Core prevents and reduces exposure to contaminated well water in NC communities

Kathleen Gray
CEC Co-Leader
Associate Professor, UNC-CH

Andrew George
CEC Co-Leader
Community Engagement Coordinator, UNC-CH

Sarah Yelton
CEC Co-Investigator
Environmental Education Manager, UNC-CH

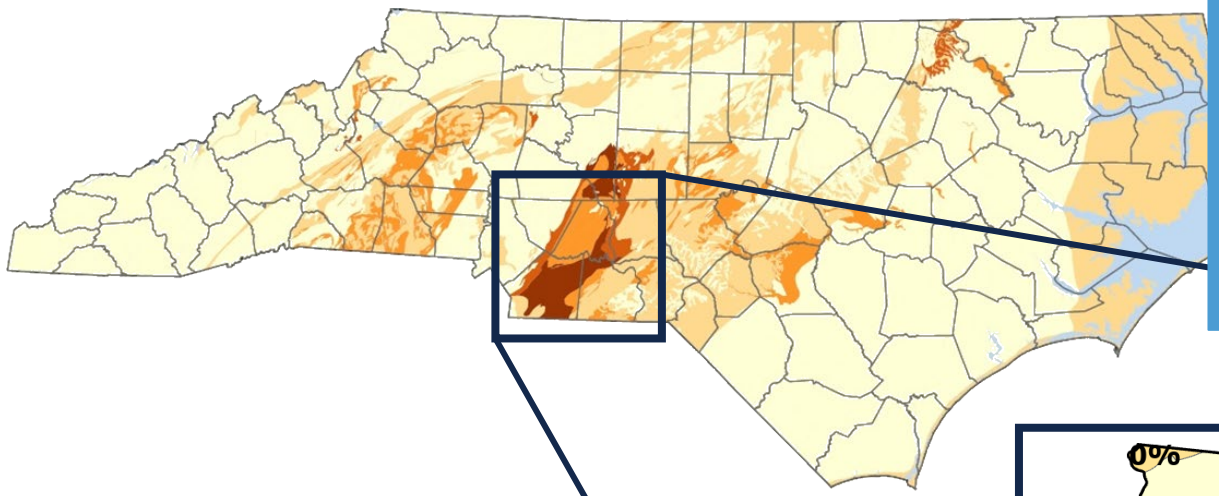


Communicate with Communities Across NC that Rely on Well Water

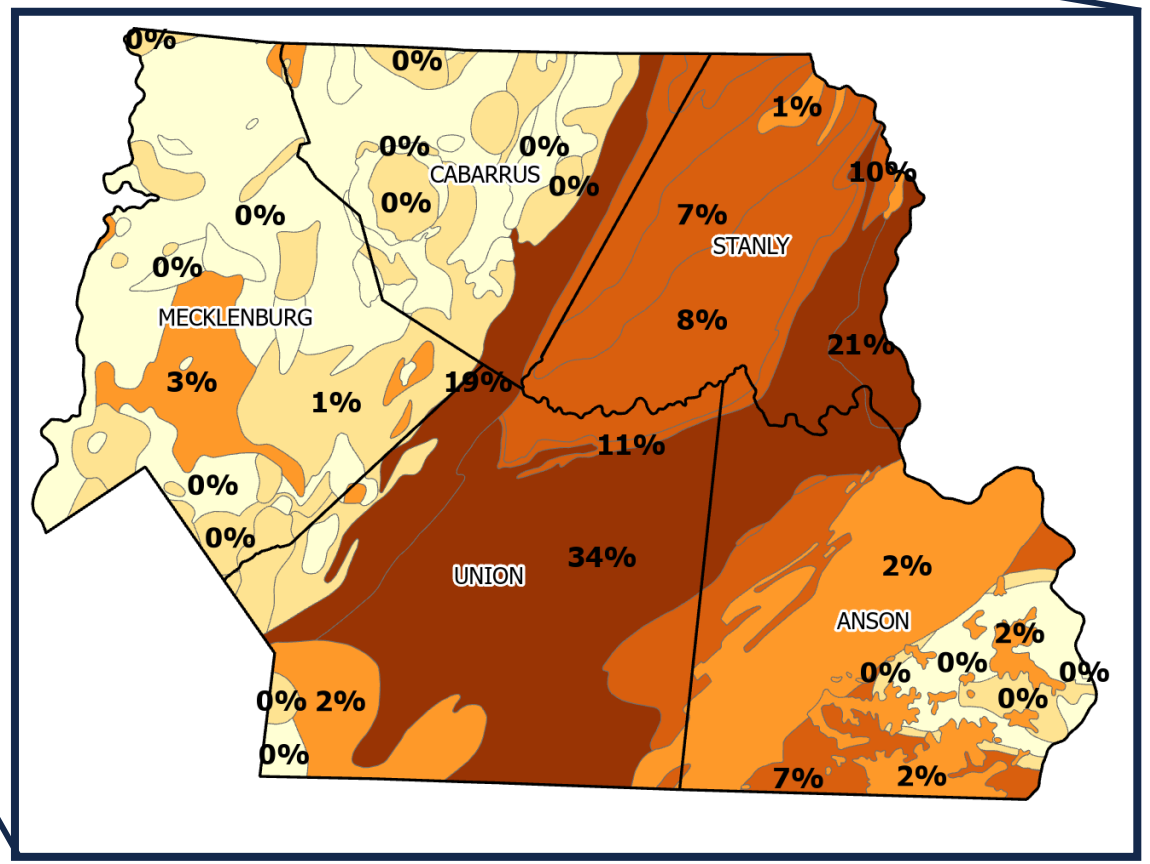
Some of these samples were collected and analyzed with VA Tech (NSF #1855567, USEPA #G2017-ORD-F1)

Image source: Andrew George; Donya Farahani

Collaborate with Researchers Across Institutions to Respond to Community Concerns



Owen Duckworth
Professor
Crop & Soil Sciences, NCSU



Collaborate with Community Leaders to Detect Contaminants, Share Results & Inform Solutions

80 participants attended report-back meeting jointly convened by UNC SRP and local health department

Image source: K. Gray

Evaluate participant experience

Image source: K. Gray

POST-HELENE WATER RESPONSE

POWR

- RESEARCH PROJECT -

Mitchell County
N=55 households
24 private, 17 public,
14 natural springs

Buncombe County
N=68 households
38 private, 30 public

Image source: K. Gray

UNC and NCSU collaborated to respond to community concerns about drinking water quality post-Helene

Image source: NC Department of Transportation

Gillings School of
Global Public Health