Transcriptomics from Space: Linking Remote Sensing to Tree Gene Expression to Monitor Forest Responses to Water Availability

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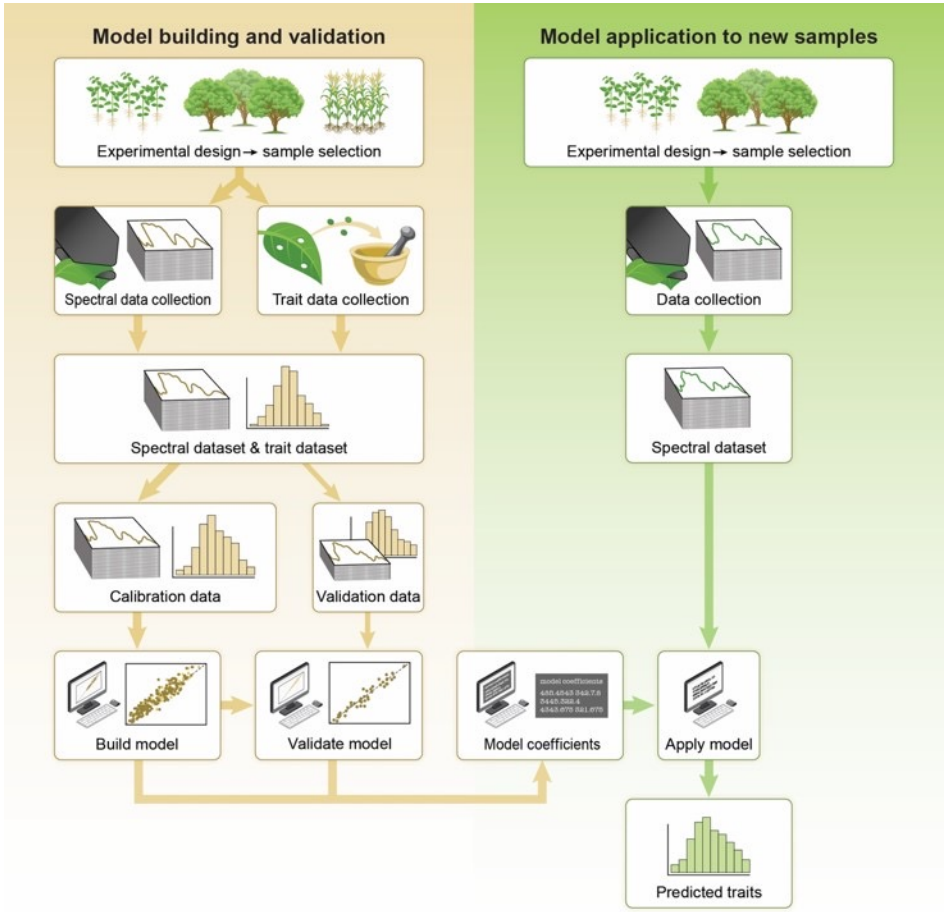
Expanding the Bounds of Spectral Functional Biology

Can richer and more dynamic assays of plant function be linked to spectral data?

Phenotype

Phenome &
Exposome

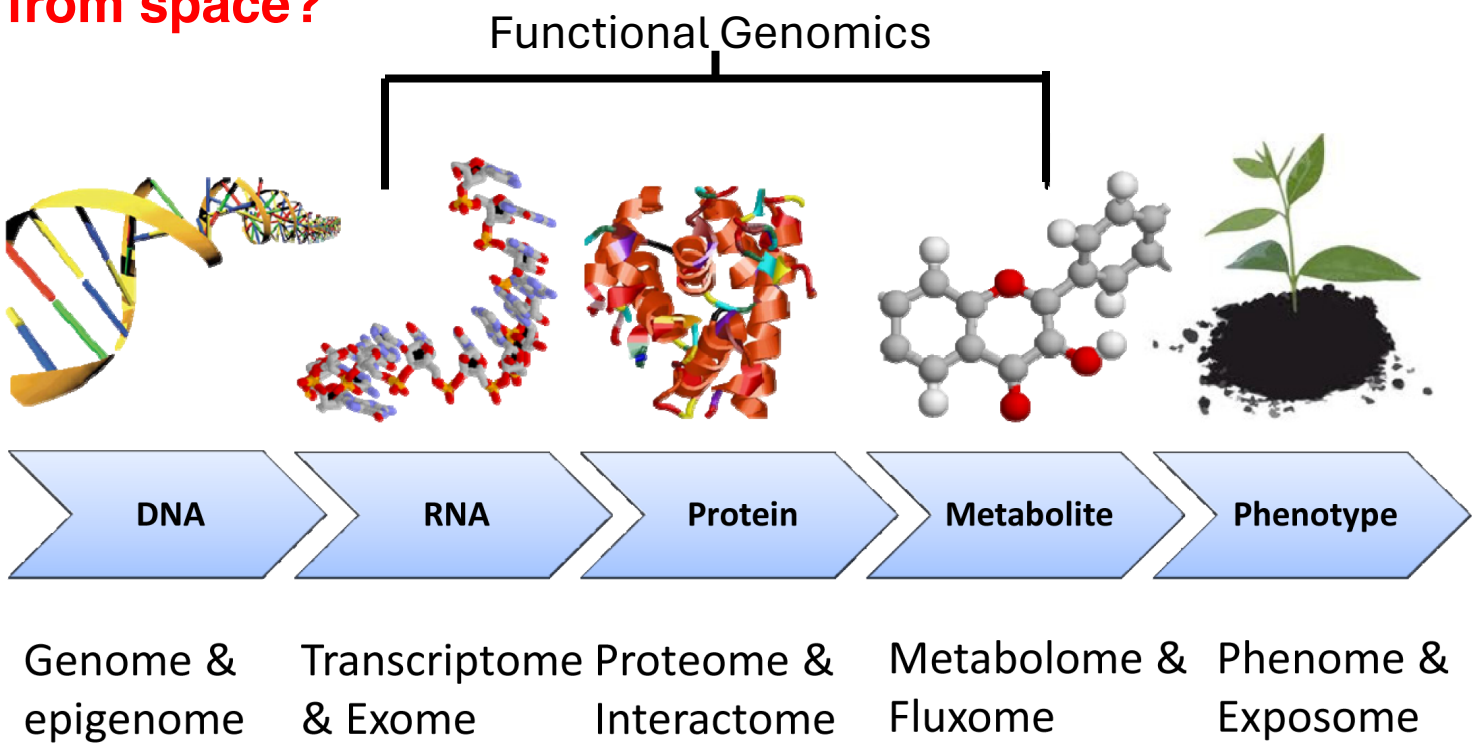


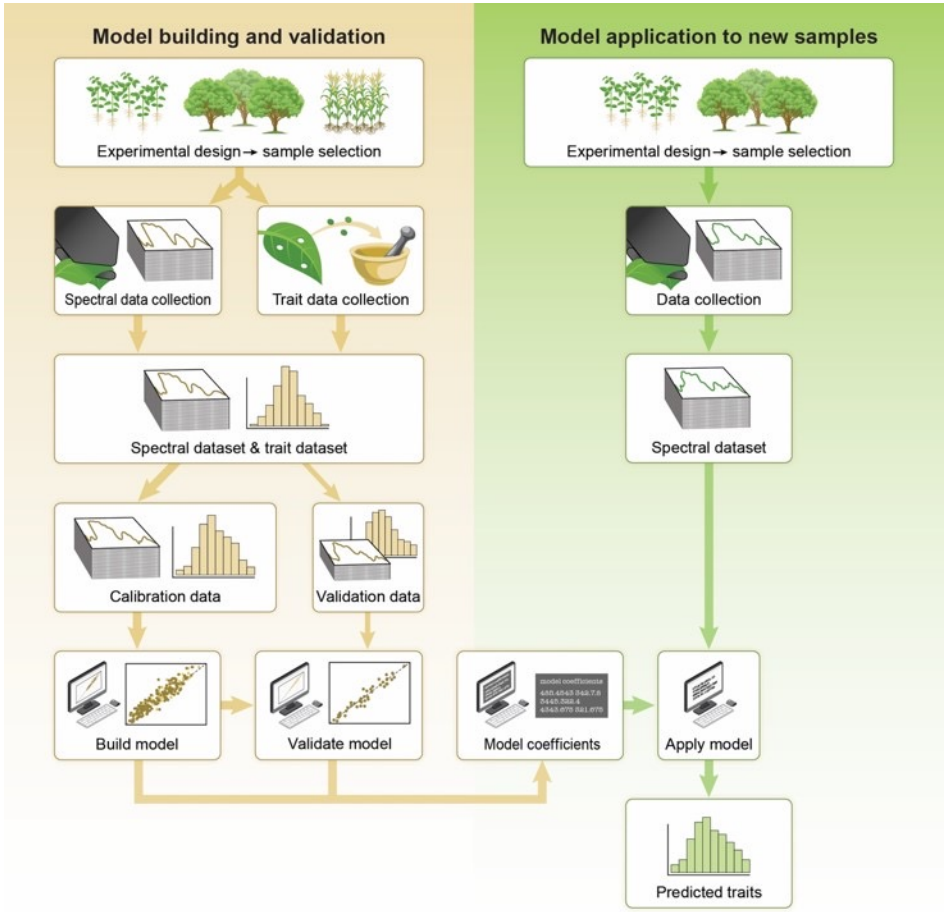
Burnett et al. 2021

Expanding the Bounds of Spectral Functional Biology

Can we predict the expression of thousands of functions?

Can we study transcriptomics from space?





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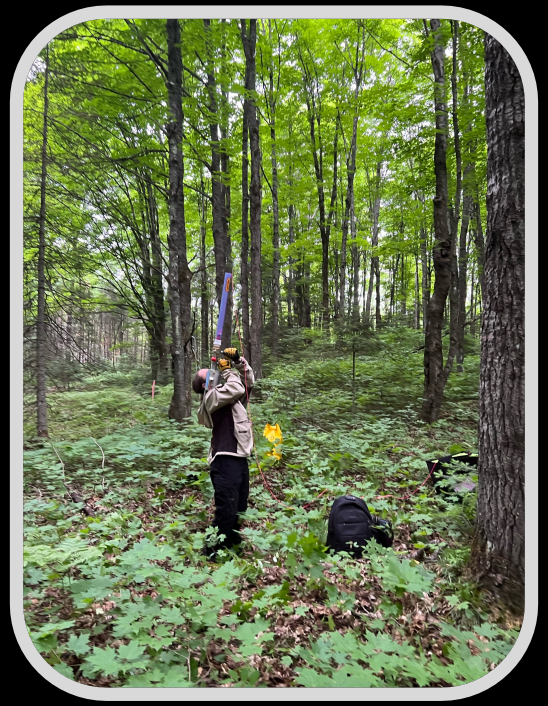
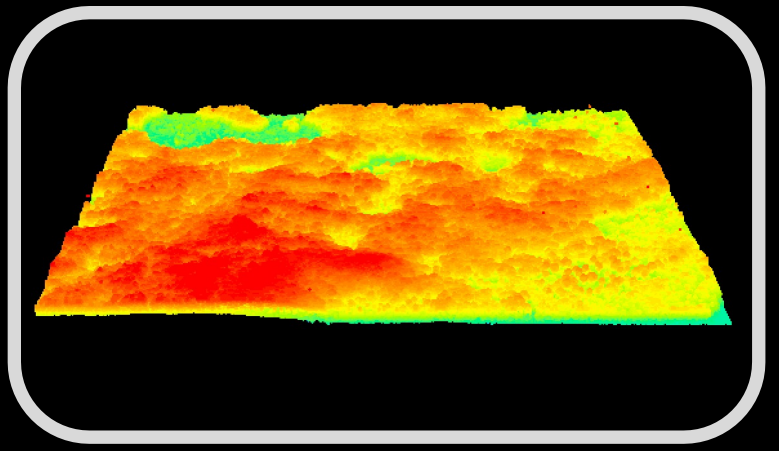
Objectives

Establish the relationships between drought, spectral signatures and gene expression in the greenhouse

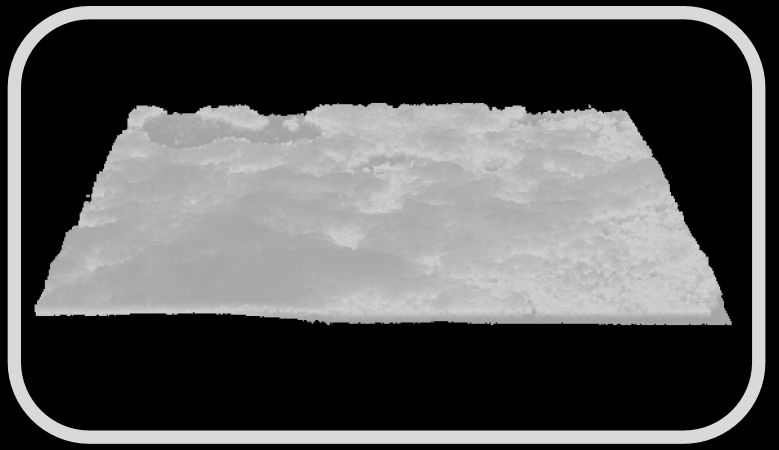




Prediction of gene expression for sub-plots in the two forest dynamics plots throughout the growing season.

Field validation of predictions by collecting spectral and gene expression data from individuals in the sub-plots throughout the growing season in 2 years.

Objectives



Greenhouse Study

Completed in Summer of 2023

15 focal species

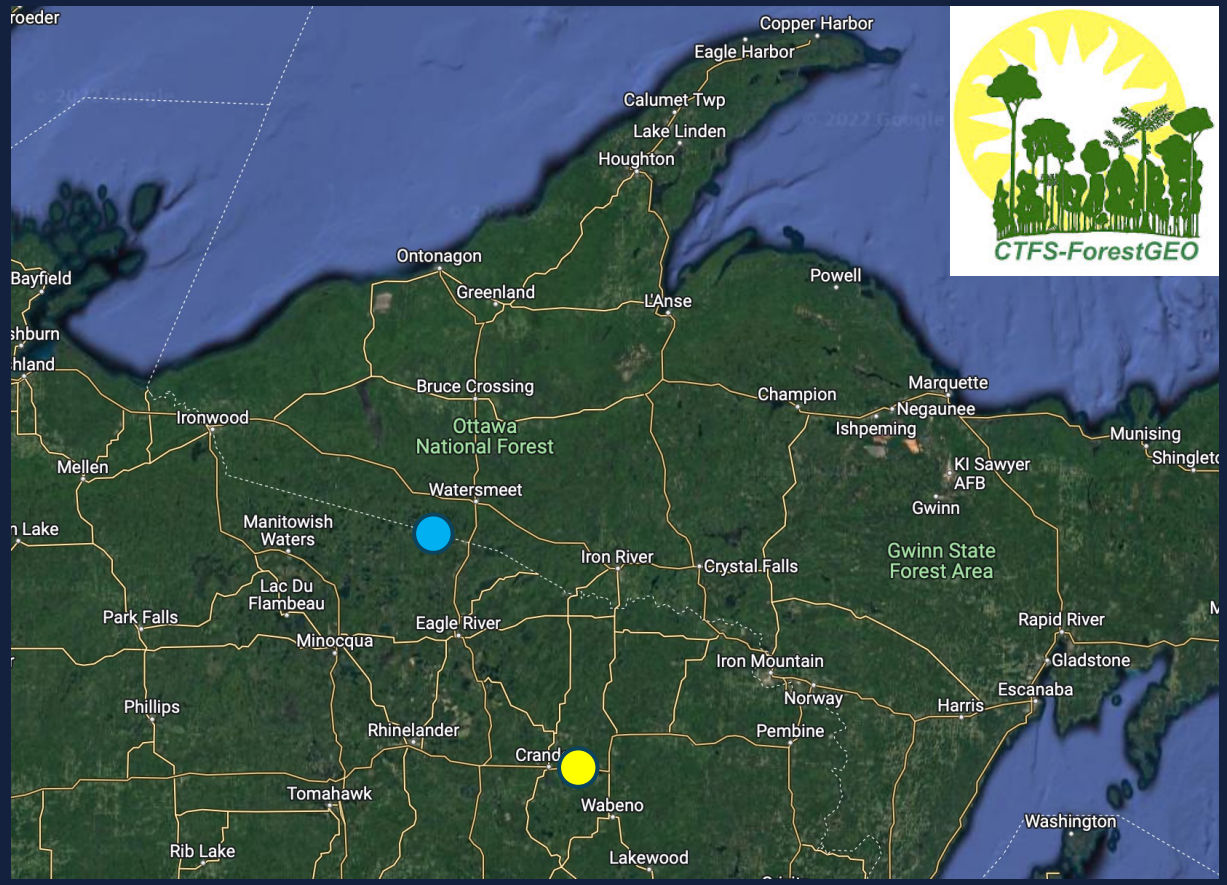
Control & Drought Samples

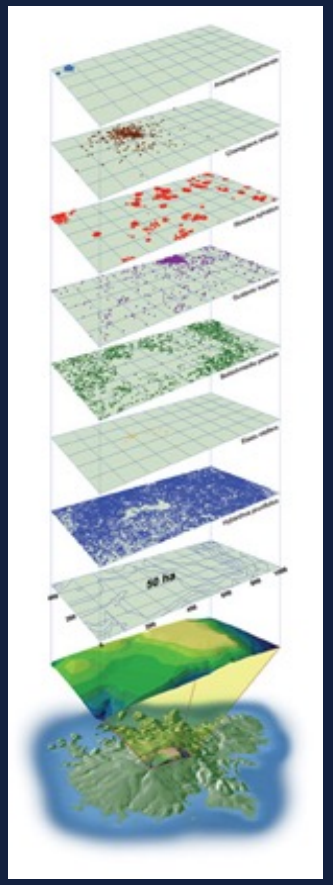
Physiologically Monitored

Spectral Reflectance via an ASD

RNAseq (beginning)

Study Sites



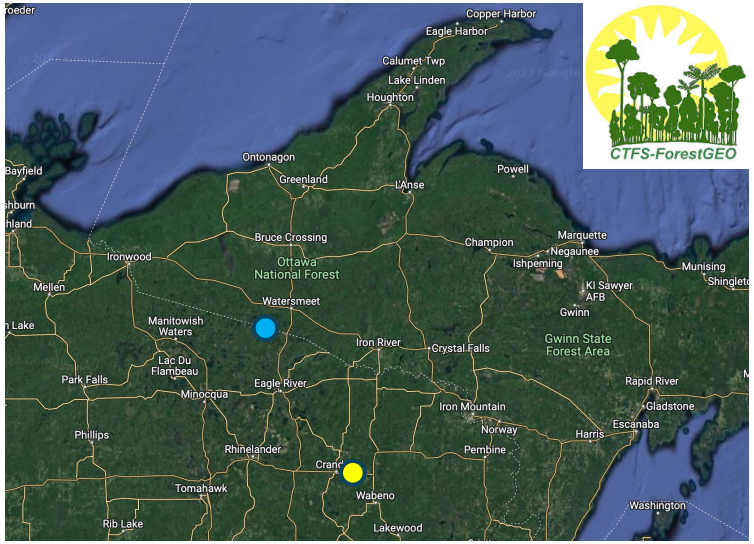


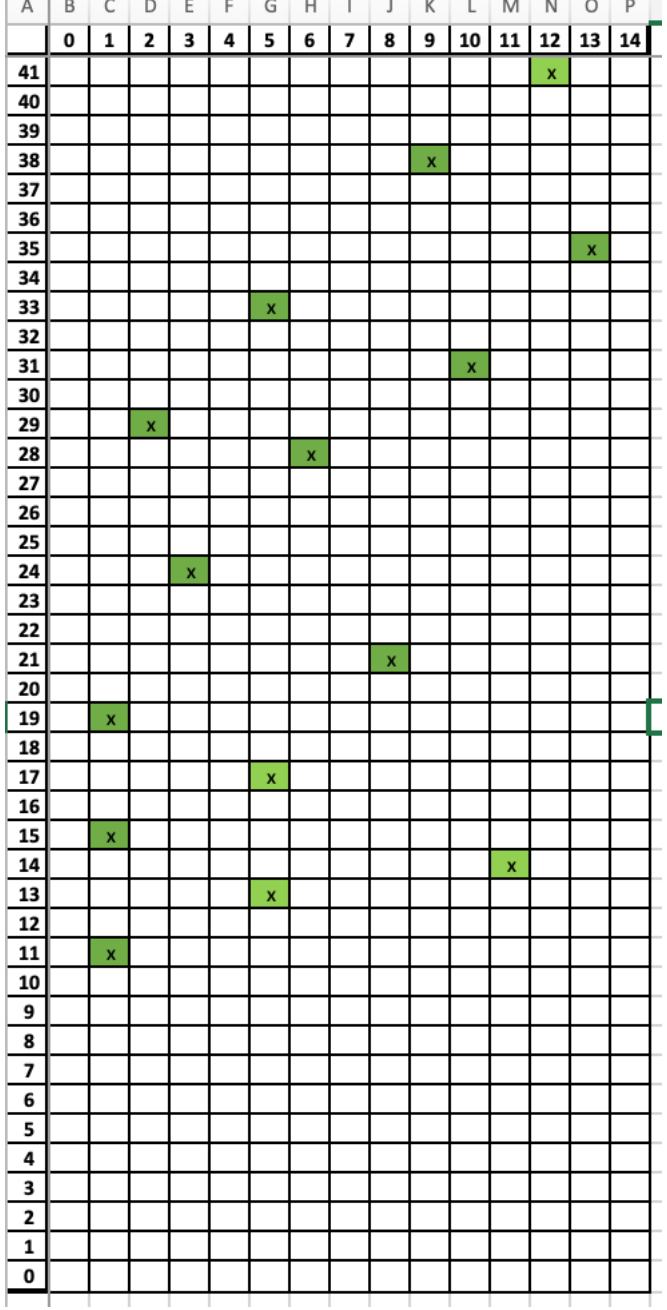
Study Sites – Left) The location of the Wabikon Lake (Yellow Dot) and UNDERC (Blue Dot) Forest Dynamics Plots. **Right)** A diagram of the data layers collected in a typical forest dynamics plot – topography and the distribution and diameter of every individual tree with a diameter 1cm or greater. Plots are re-censused every years in order to track changes in species distributions and diversity and individual growth and mortality.

Field Collection 2023

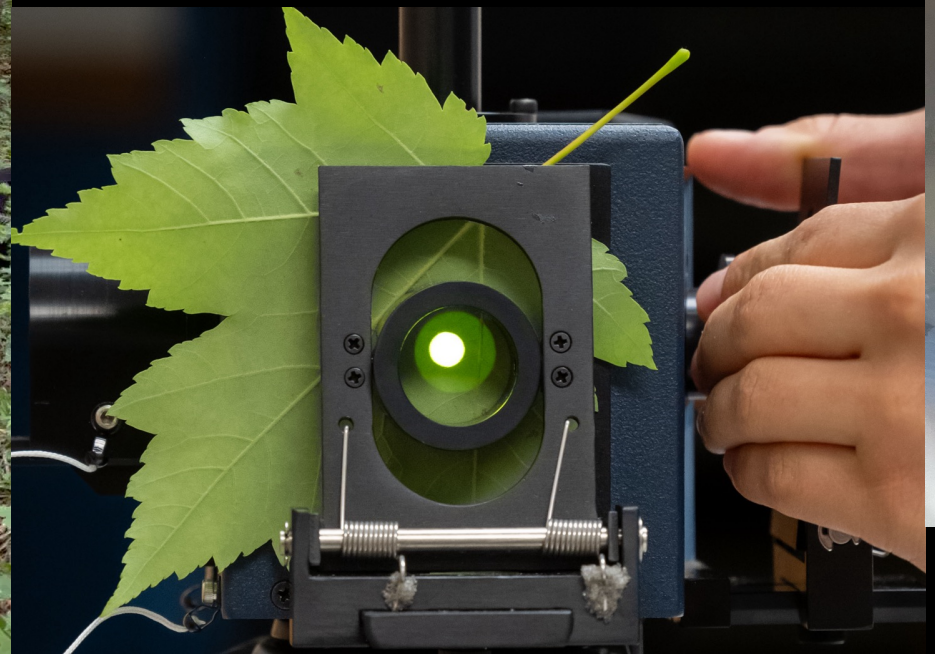
- 2 sites (UNDERC & Wabikon)
- 15 plots/site
- 9 trees/plot
- 2 sampling periods
- 135 samples/site/period
- 2 years (2023 & 2024)

- 540 samples collected in 2023
- Leaf spectral reflectance via ASD
- Leaf traits
- RNAseq (ongoing)

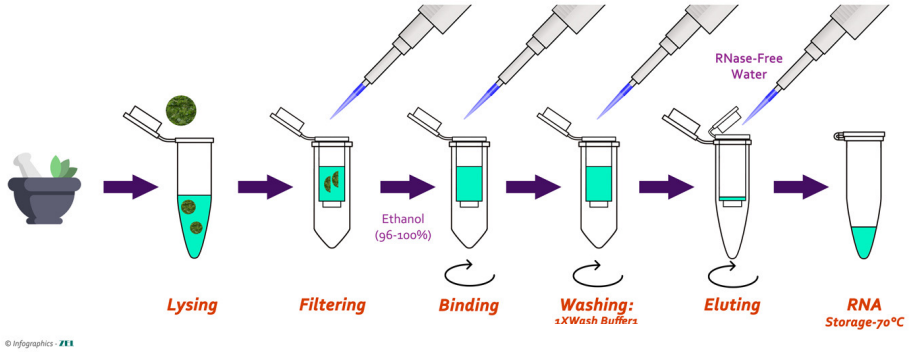




Wabikon Lake Forest Dynamics Plot



Lab & Informatics Work



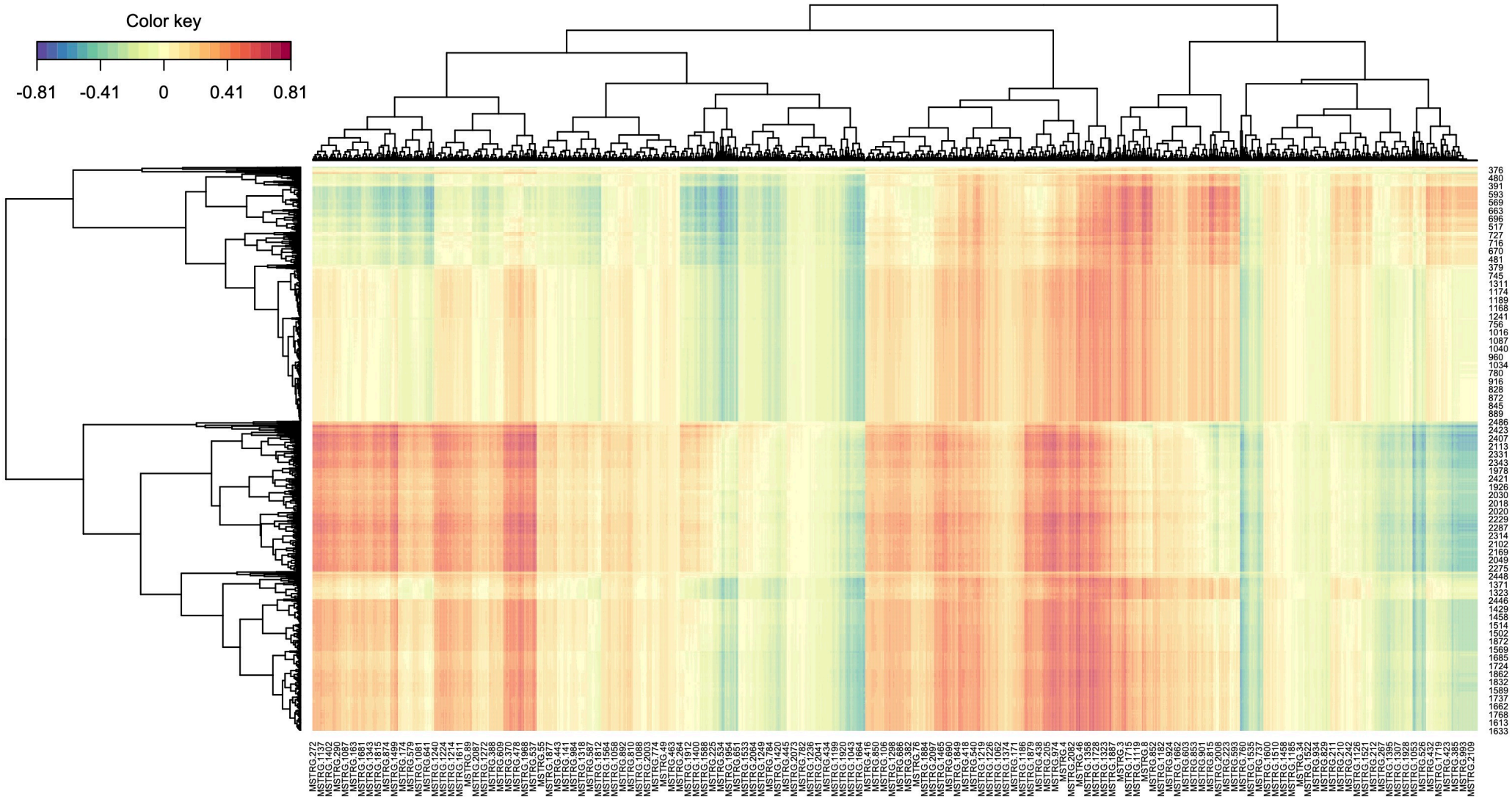
Qiagen RNA extraction via QiaCube
Illumina RiboZero+ custom kits

Illumina HiSeq X (2x150bp ; ~6Gb)

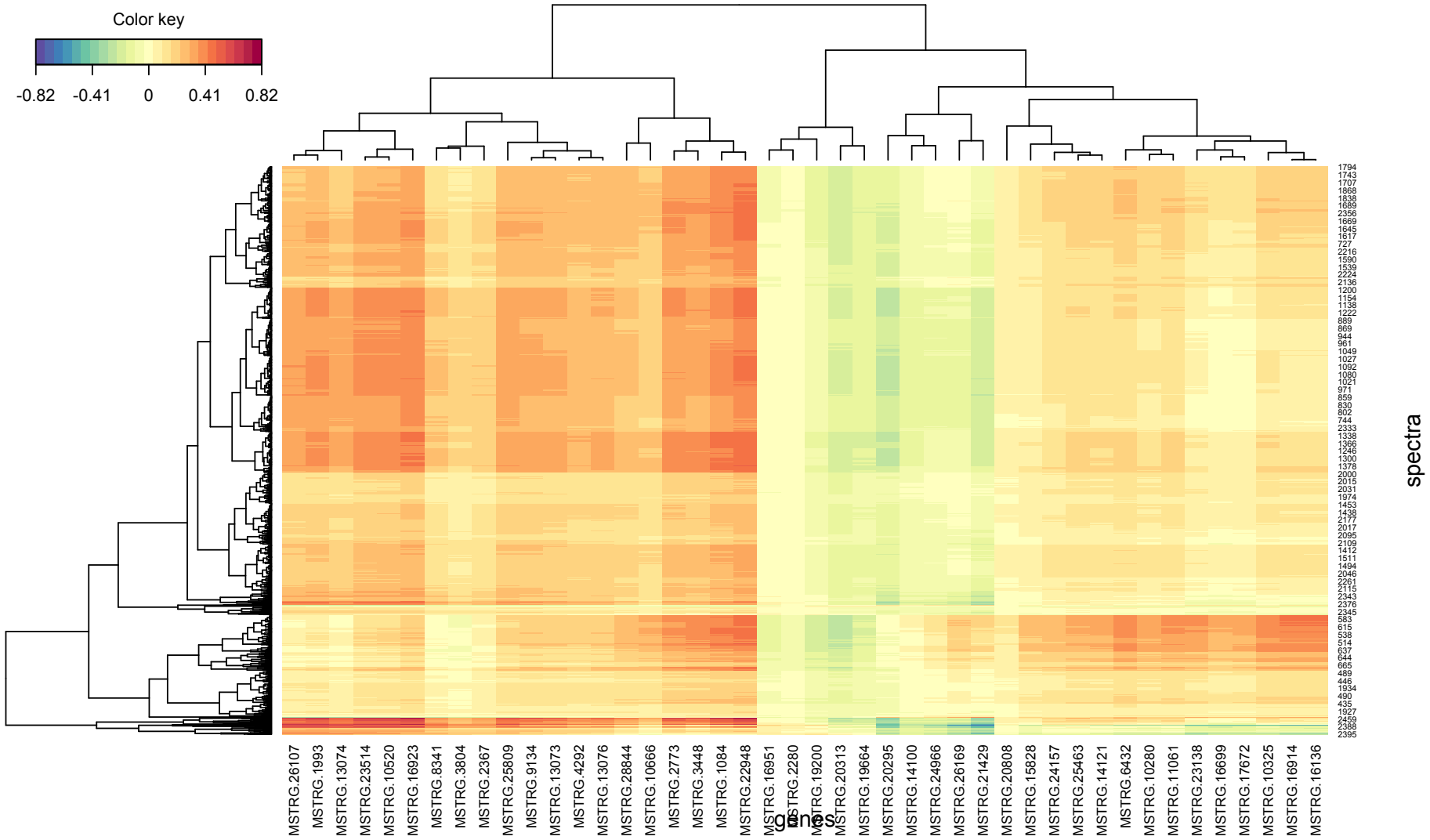
- Work completed on **40 individuals** so far (sugar maple)
- **~35k genes** per sample
- Mapped to published genome
- **Expression** of each gene characterized
- Functionally **Annotated**

- Today I will show results from Regularized Canonical Correlation Analysis (**RCC**) – common in ‘multi-omic’ analyses.

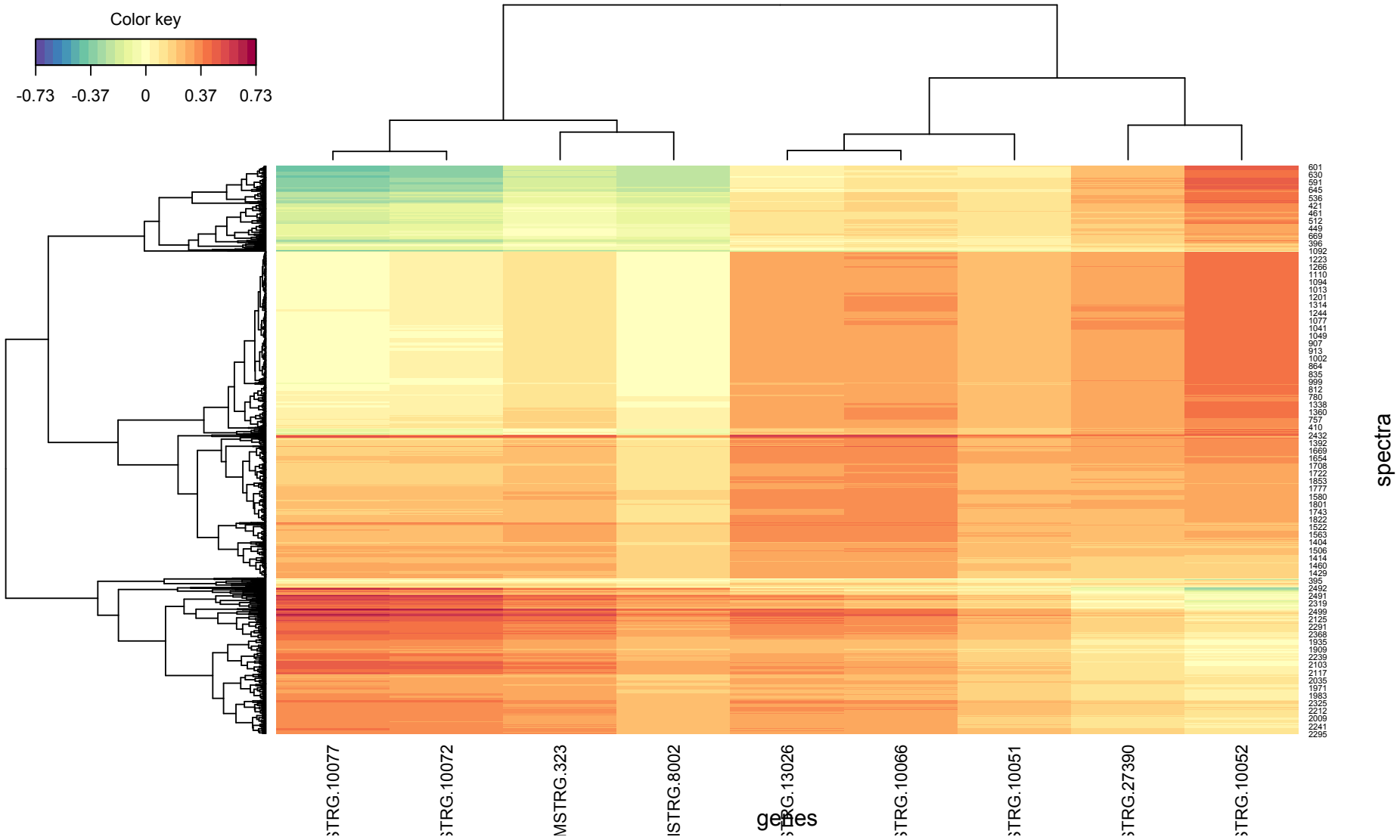
Gene expression for 1k random genes in Sugar Maple by Spectral Reflectance (RCC – regularized canonical correlation analysis)



RCC of gene expression (ABA response genes) by spectral reflectance (n = 44 genes)



RCC of gene expression (drought response genes) by spectral reflectance (n = 9 genes)



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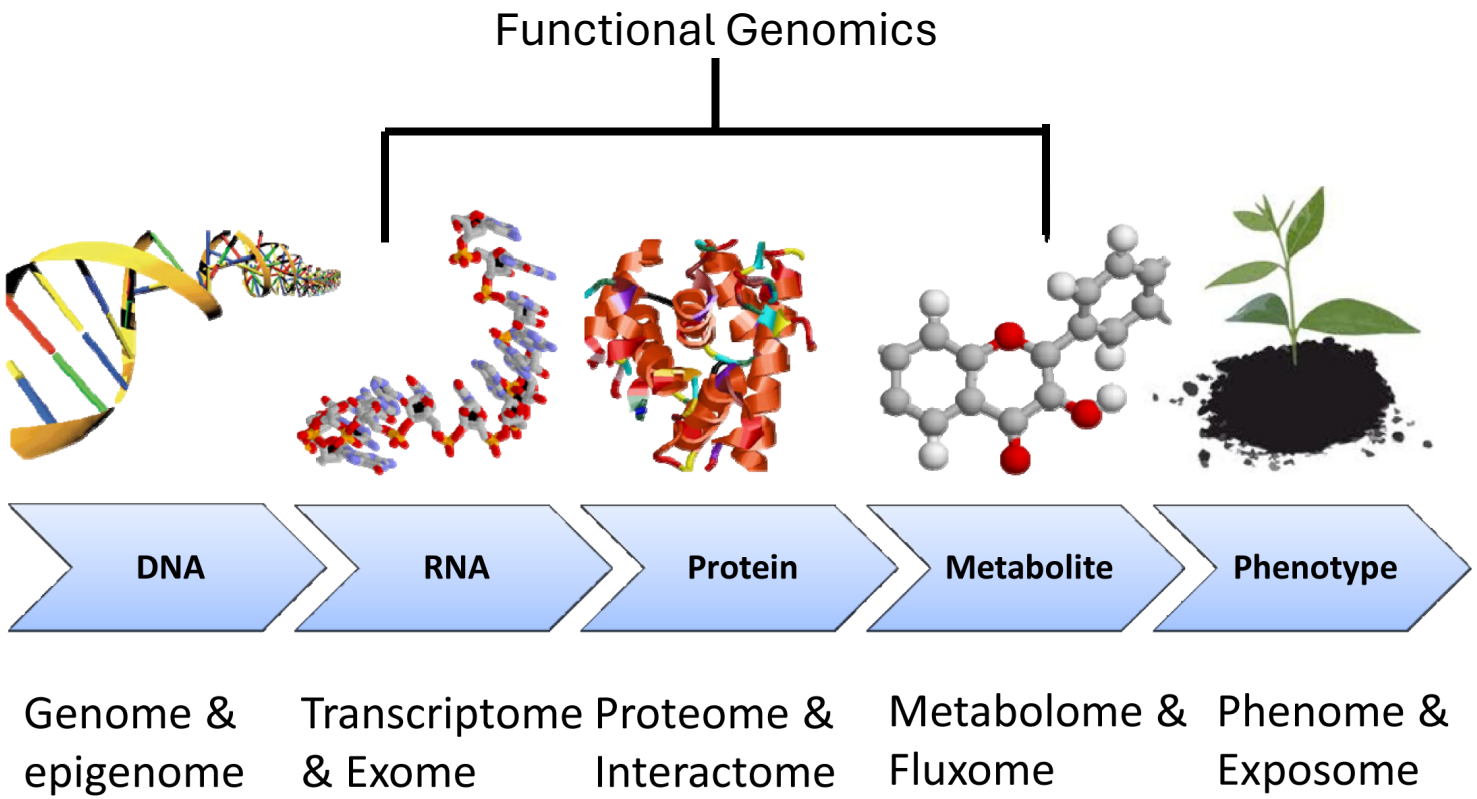

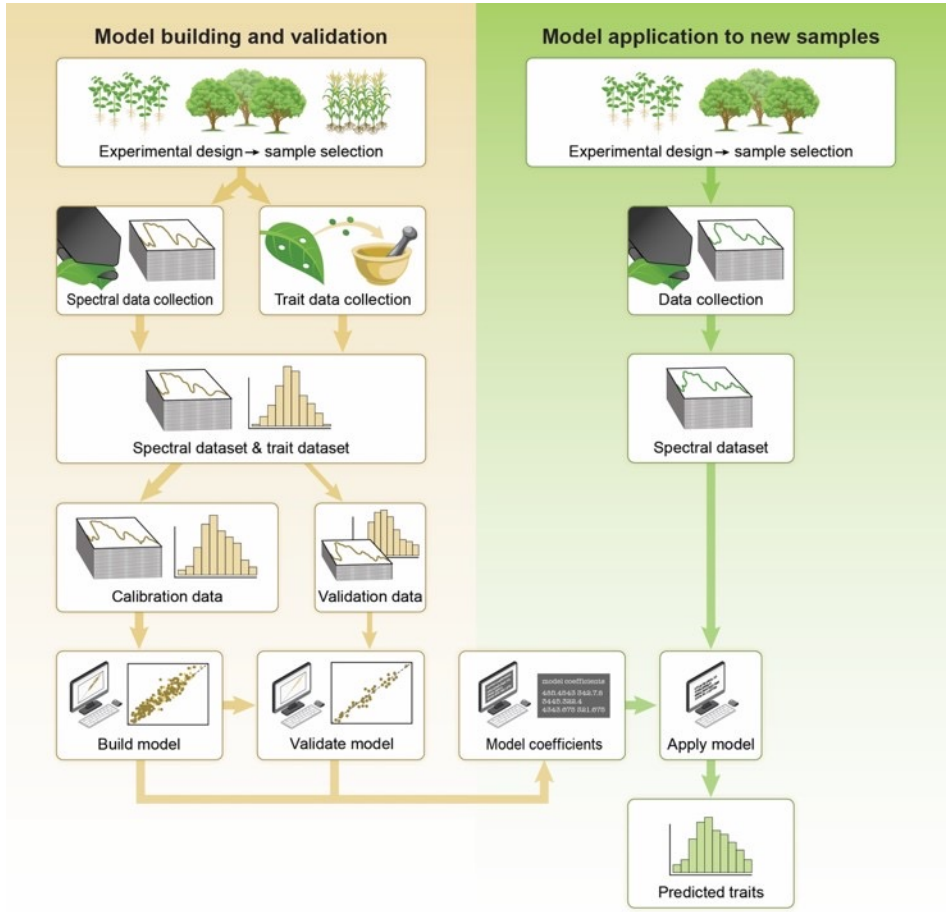

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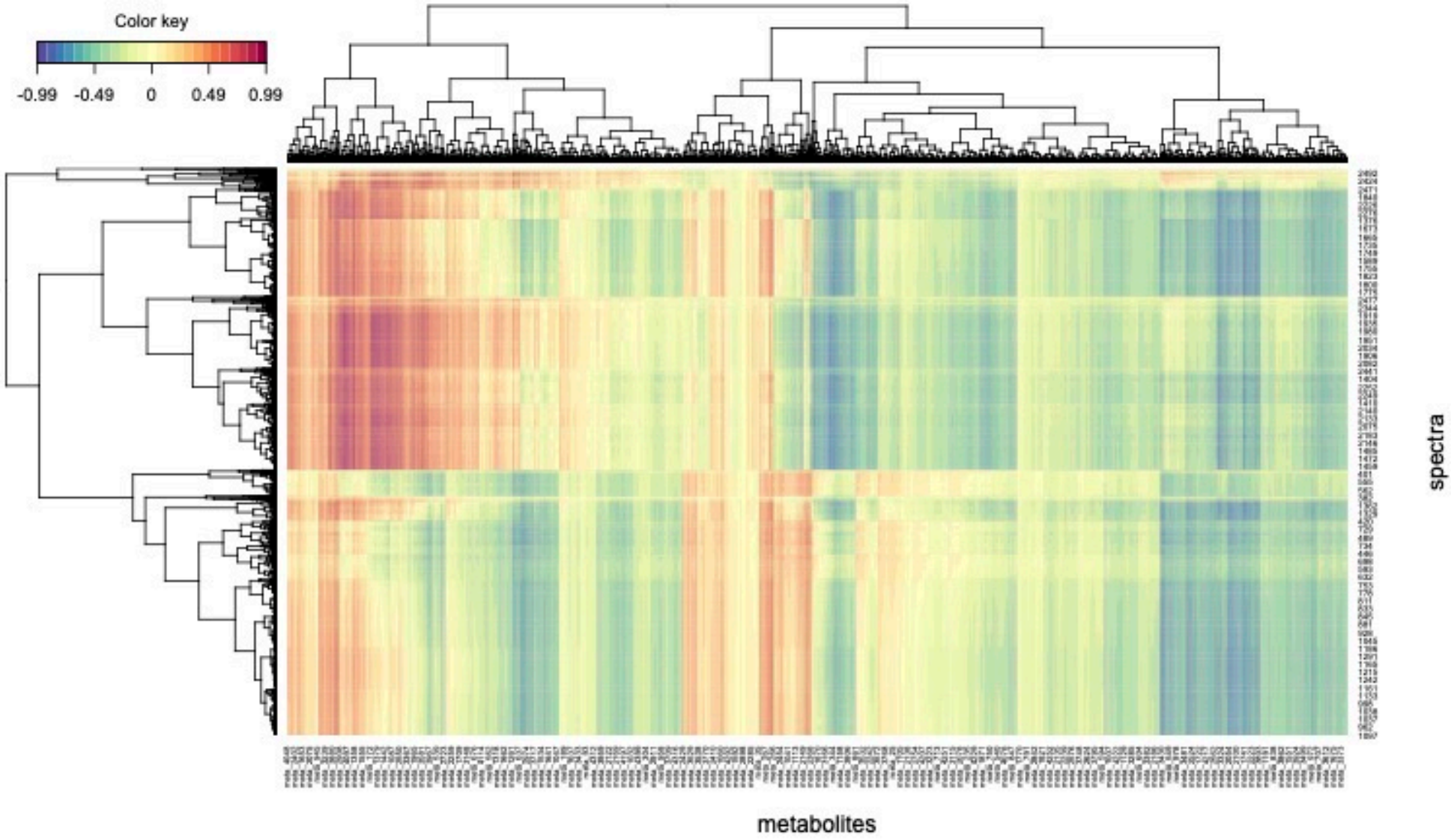
Untargeted Metabolomics – Leaf-Level Metabolite Expression by Spectral Reflectance (~5k metabolites)



Conclusions and What's Next

- Levels of ***gene and metabolite expression can be predicted upon the basis of spectral reflectance data***, but this, of course, is not the case for all genes or metabolites.
- We are ***developing the informatics pipelines*** to move from one species to many such that we can link spectral data to genes and metabolites that are shared between species
- We have ***completed ~60% of the sampling*** for this project with one more field campaign this summer (coinciding with NEON AOP at both sites)
- We aim to provide the ***first maps of gene expression on landscape scales by the end of 2024***.

Acknowledgments

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