RANDOM FORESTS OF FORESTS:
integrating data sources to combat illegal logging

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RANDOM FORESTS: AN OVERVIEW

integrating data sources to combat illegal logging

1. A moment to state the obvious
2. Random Forests
3. Integrating data
4. Concluding remarks

1. A MOMENT TO STATE THE OBVIOUS…

identifying the taxonomic and geographic source of wood is challenging

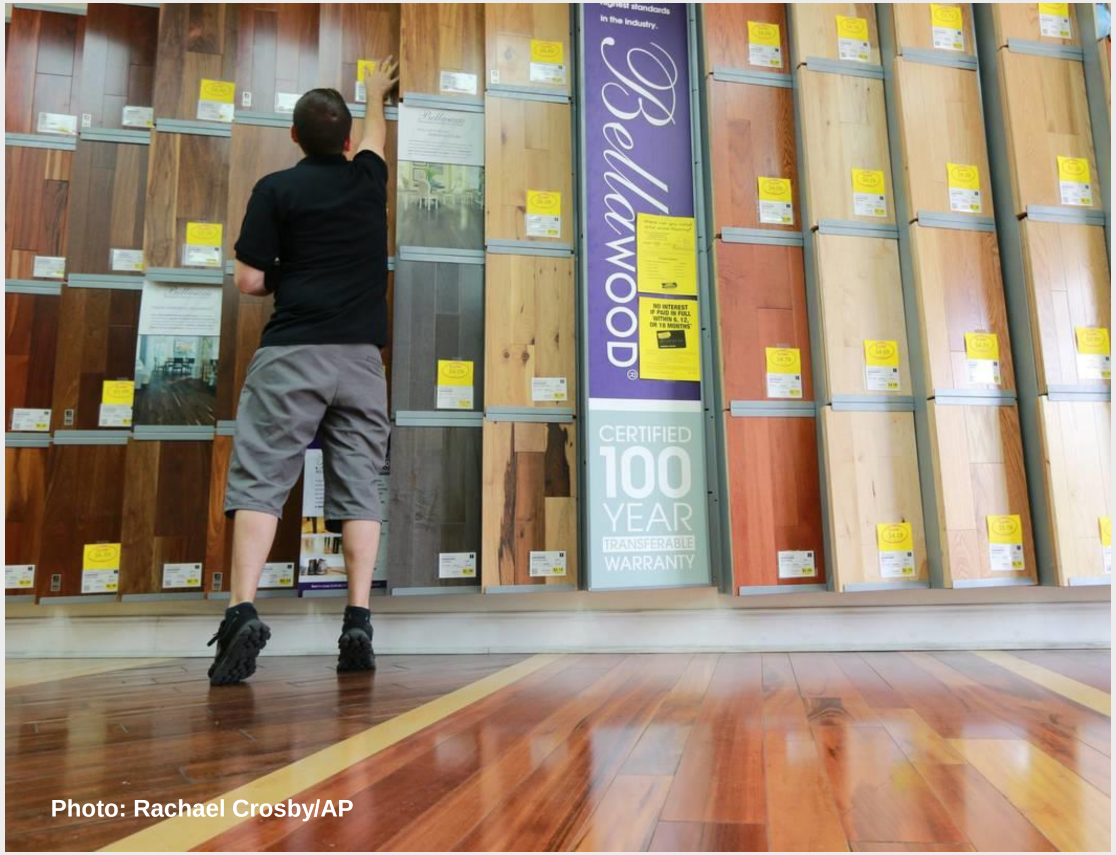
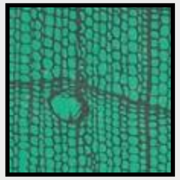


Photo: Rachael Crosby/AP

- Trees are genetically complex
- Trees are long lived, and have overlapping generations
- Trees share genetic information over long temporal and geographic spans
- Genetic complexity influences metabolic and anatomic traits, and these influence taxonomic complexity

ADDRESSING THE CHALLENGE

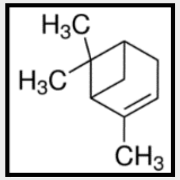


- Anatomy

  Cellular (rays, vessels); color; scent

- Genetics

  Organelle genomes; nuclear SNPs



- Chemicals

  Metabolites; spectra

$\delta^{14}N$

- Stable isotopes

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Discussion

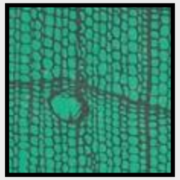
Forensic timber identification: It's time to integrate disciplines to combat illegal logging

CrossMark

Eleanor E. Dormontt[a], Markus Boner[b], Birgit Braun[c], Gerhard Breulmann[d], Bernd Degen[e], Edgard Espinoza[f], Shelley Gardner[g], Phil Guillery[h], John C. Hermanson[i], Gerald Koch[j], Soon Leong Lee[k], Milton Kanashiro[l], Anto Rimbawanto[m], Darren Thomas[n], Alex C. Wiedenhoeft[o], Yafang Yin[p], Johannes Zahnen[q], Andrew J. Lowe[a,*]

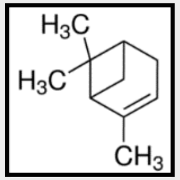
DATA INTEGRATION (?)

multiple methods = yes



Machine vision; classification trees; phylogenetic trees

Classification trees; 'barcode' phylogenetic trees; spatial-genetic interpolation

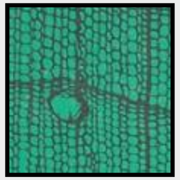


Least squares; discriminant analysis (linear; kernel; quadratic)

$\delta^{14}N$

Least squares; discriminant analysis; k-nearest neighbor

integration = ?



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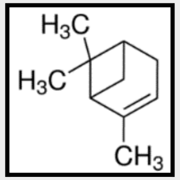

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$\delta^{14}N$

→ Data mining, machine learning, neural nets

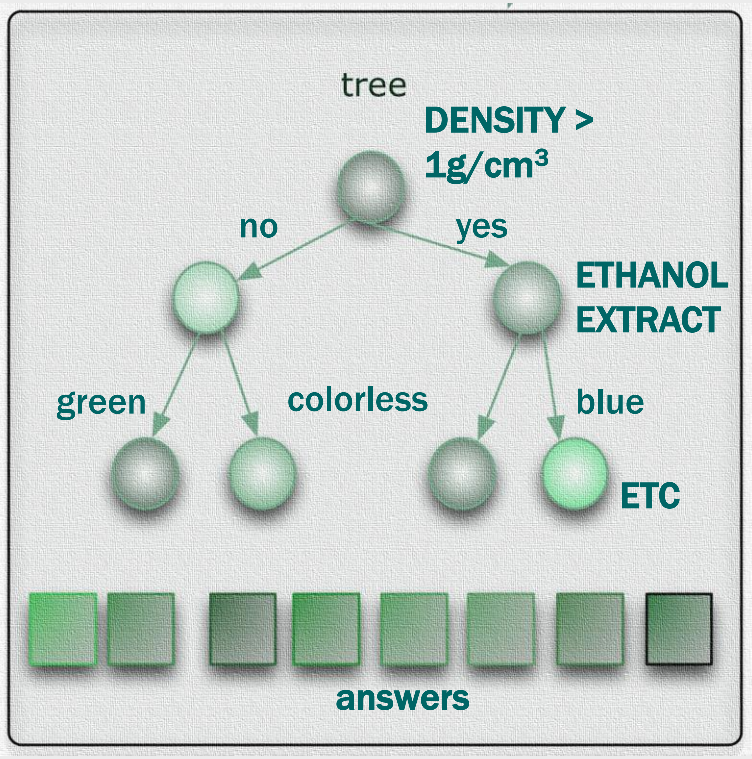
2. RANDOM FORESTS

a.k.a., “the best ‘black box’ method ever invented…”

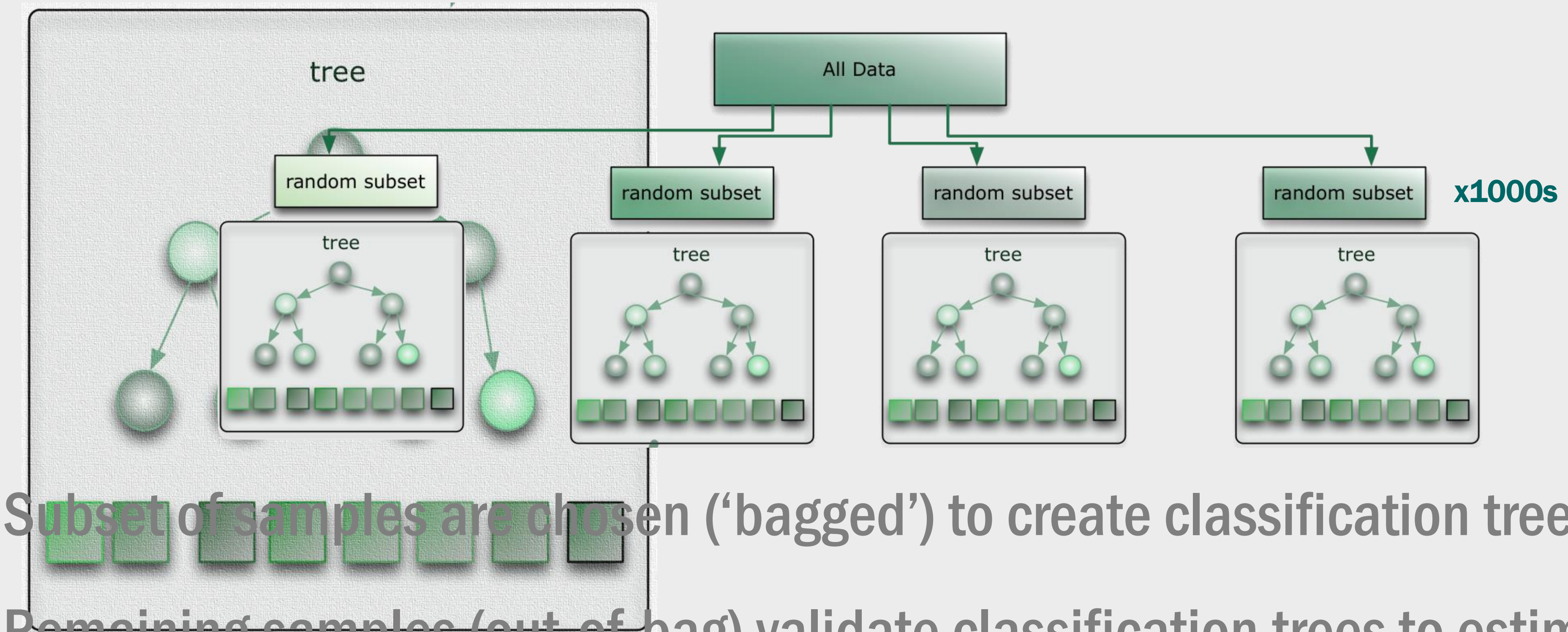
A versatile ensemble method – combines many models into one

- Can be used for simple or complex classification problems
- Handles large data sets, missing data, nearly any kind of data
- Directly identify features important in classification prediction

ONE CLASSIFICATION TREE



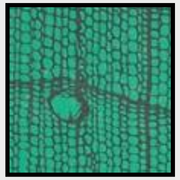
MANY RANDOM TREES = A ‘FOREST’

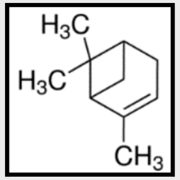


- Subset of samples are chosen (‘bagged’) to create classification trees
- Remaining samples (out-of-bag) validate classification trees to estimate error
- Classification model determined by ‘voting’ from all trees in the forest
- BONUS! Classification variables are ranked by ‘importance’ to the model

3. INTEGRATING DATA: DOUGLAS-FIR

what species can we choose?

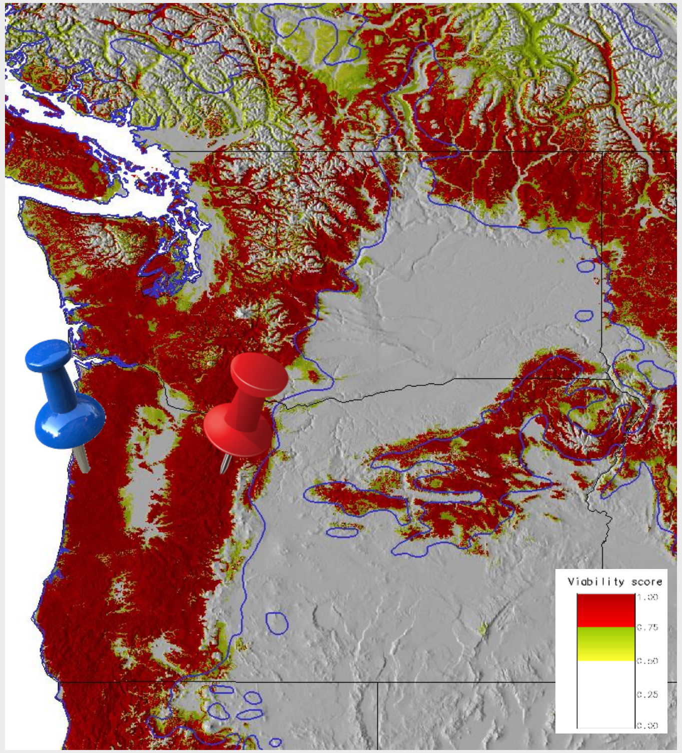




$\delta^{14}N$

- Easy to obtain
- Large geographic, climatic range, with continuous and patchy distributions
- Wealth of knowledge on D-fir

INTEGRATING DATA: PILOT STUDY

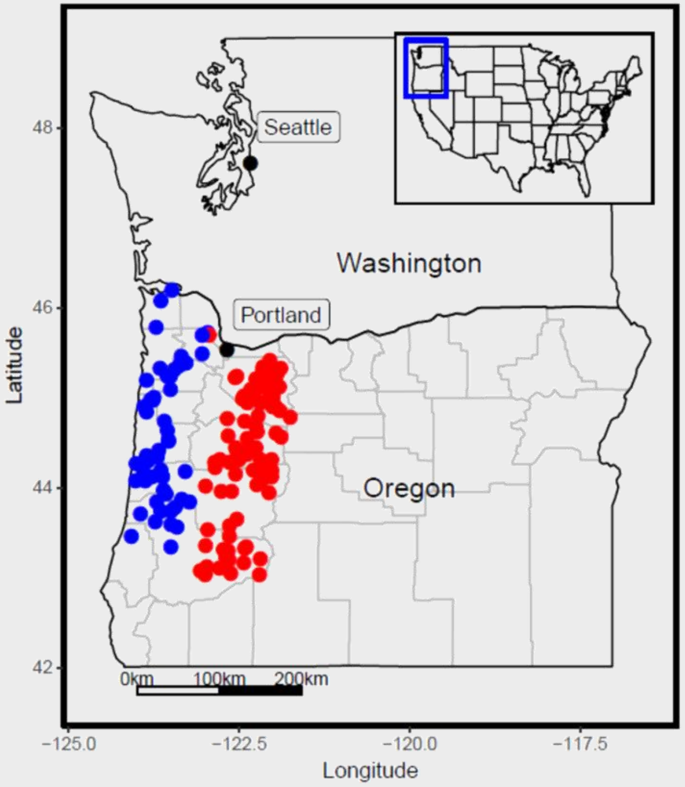


PNW REGION D-FIR

Q: can we identify tree source as coast v. cascade?

- Genetics
- Metabolomics
- Anatomy
- Isotopes

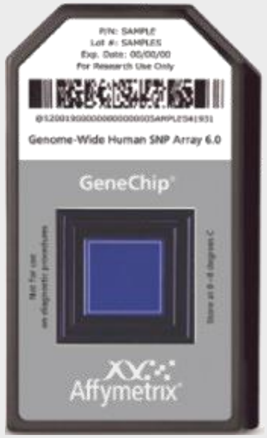
INTEGRATING DATA: GENETICS



PNW GENETICS STUDY

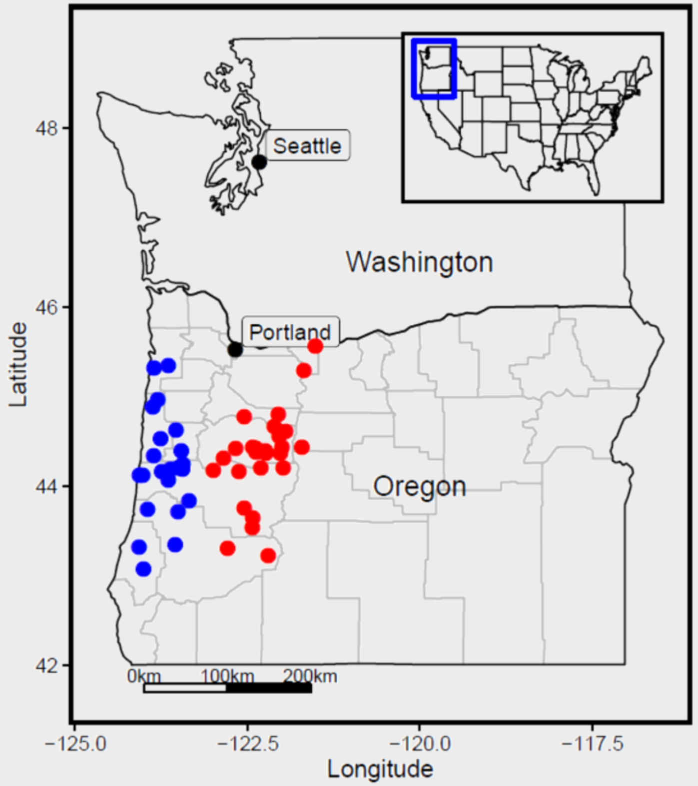
384 individuals; 141 in Oregon

51 coast 90 cascade



- Needle DNA assayed for nuclear genetic variation at 25,000 genes
- 16,467 usable Single Nucleotide Polymorphisms (SNPs)
- SNPs ranked by spatial signal; 500 'top Fst' SNPs selected
- Random Forest classification performed using 500 SNPs

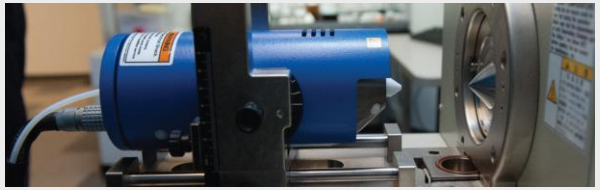
INTEGRATING DATA: METABOLOMICS



METABOLOMIC STUDY

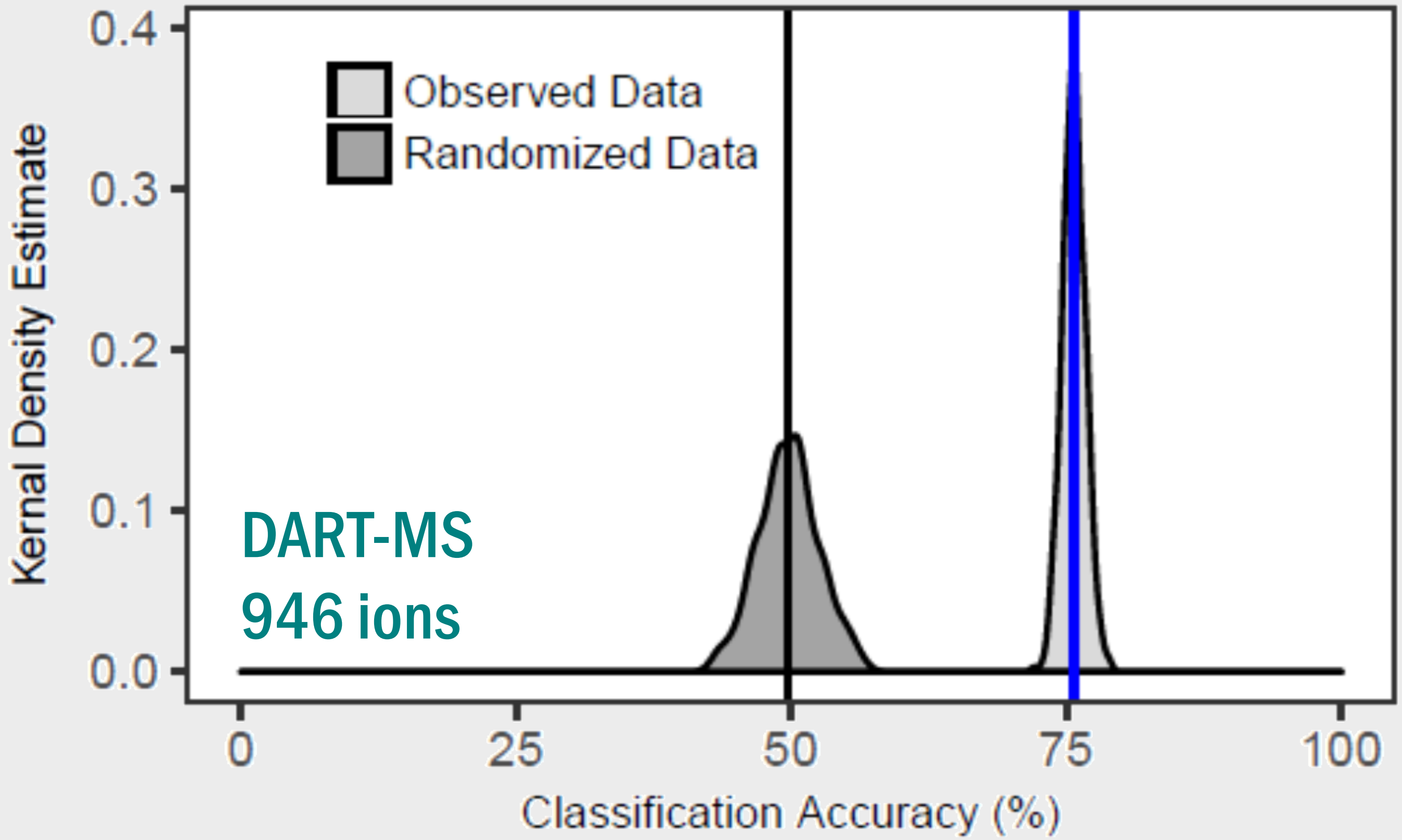
188 individuals; Oregon

86 coast 102 cascade



- Cores extracted from trees, dried
- Heartwood (yrs 27-29) profiled by DART-MS
- Ion presence, abundance estimated by Mass Mountaineer™; 946 ions
- Mean profiles estimated (n=3)
- Random Forest classification performed using 946 ions

RESULTS: RF CLASSIFICATION



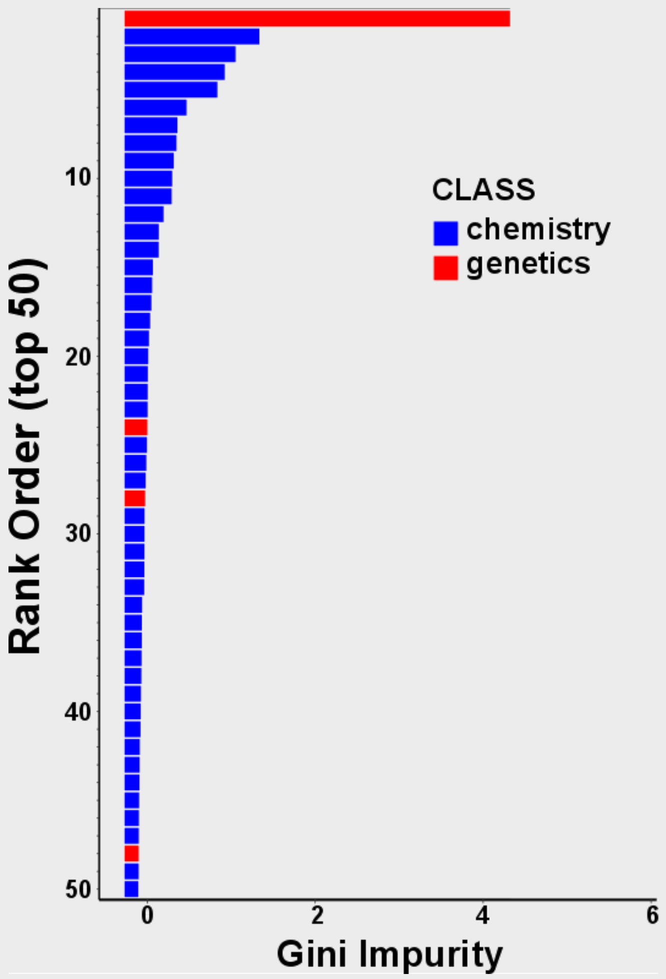
- Sanity check: randomized data accurately classified 50% of time…
- Observed classifications estimated from 500 replicates
  - *Example: DART-MS accurate 75.7% of time*

RF CLASSIFICATION ACCURACY

MODEL	INPUTS	ACCURACY
GENETICS MODEL	500 SNPs	83.4%
METABOLITE MODEL	Metabolites: 946 ions	75.7%
FULL MODEL	Genet+Metab: 500 SNPs + 946 ions	83.6 %

GENETIC & METABOLOMIC 'IMPORTANCE'

SNPs+METAB

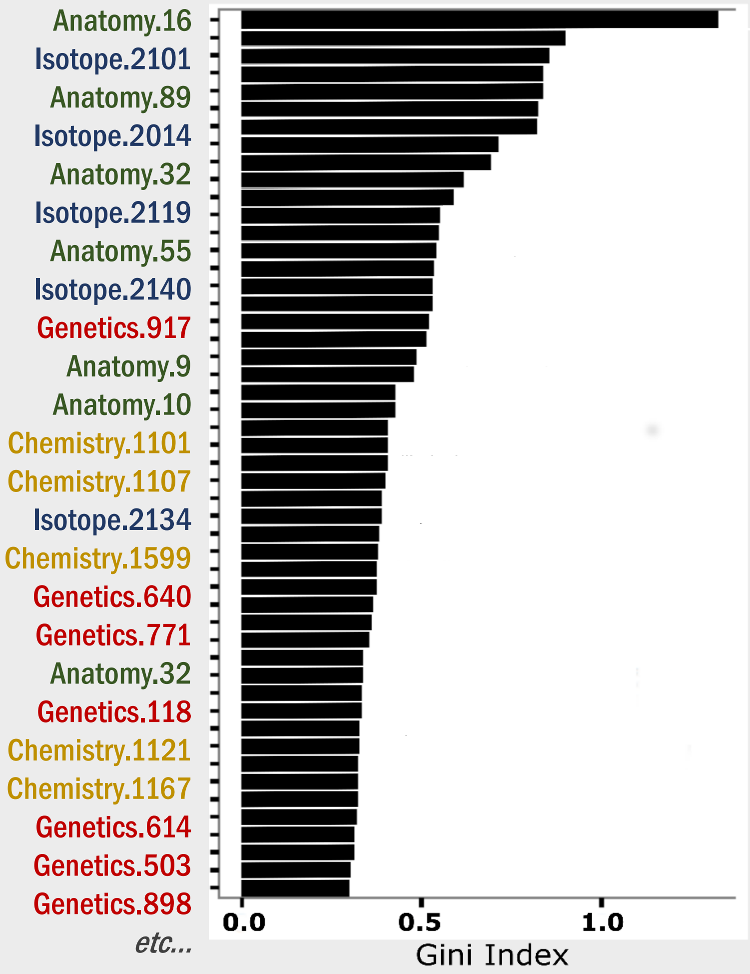


What can we learn from integrated analysis?

- Integration DOESN'T measurably improve classification accuracy (in this case)
- Integration DOES reveal contribution of genetics, metabolomics to the classification model
- Integration allows us to examine classifier 'importance' – what drives the classification?

GENETIC & METABOLOMIC 'IMPORTANCE'

SNPs+METAB+ANAT+ISO

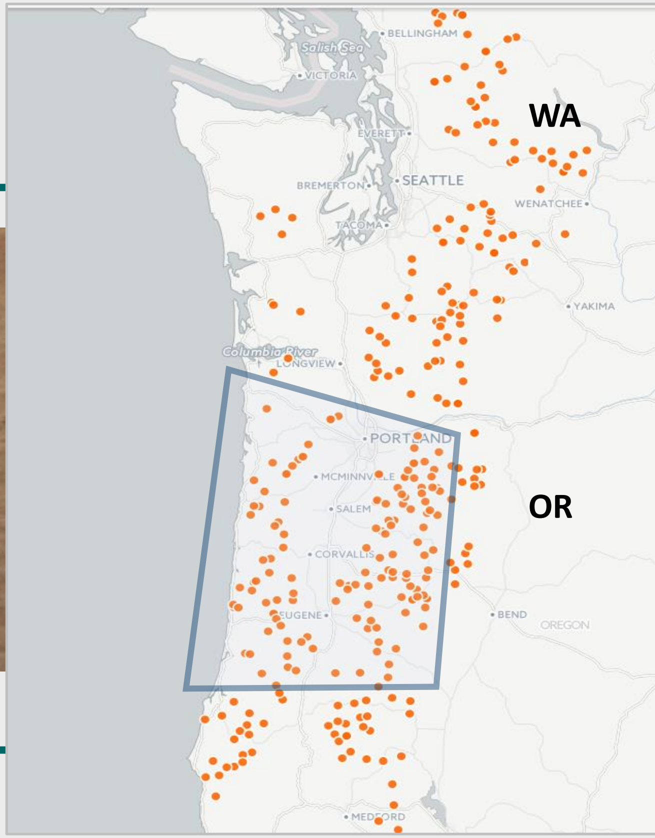


What can we learn from integrated analysis?

- Integration doesn't measurably improve classification accuracy (in this case)
- Integration reveals contribution of genetics, metabolomics to the classification model
- Integration allows us to examine classifier 'importance' – what drives the classification?
- *Imagine if you had a rich data set ....*

GENETICS + METABOLOMICS +

MODEL	INPUTS	VARIABLES
GENETIC MODEL		
METABOLITE MODEL		
ANATOMY MODEL		
ISOTOPE MODEL		
FULL MODEL		



PNW GENETIC STUDY

340 families (locations)

4. CONCLUDING REMARKS

- Integrated classification models from multiple data sources possible with Random Forests (and other algorithms)
- Gain insights into:
    - Factors responsible for classification
    - Methodological, variable importance
- Develops robust classification models

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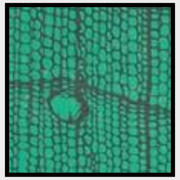
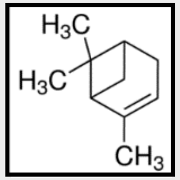


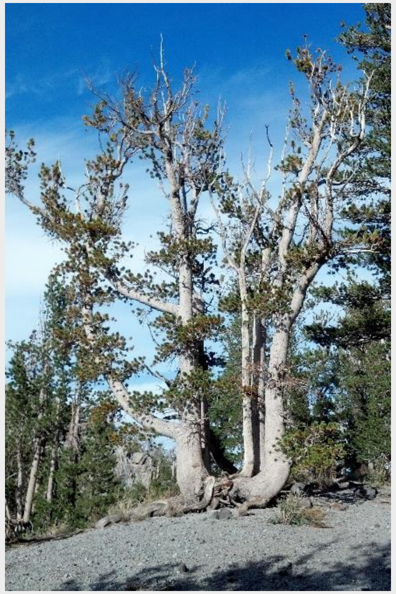


$\delta^{14}N$

CONCLUDING REMARKS

- "Field of Dreams" hypothesis: *Build it…*
- Temperate zone trees can help simulate…
  - Spatial classification
  - Taxonomic classification (e.g., White Oaks, Pines)
  - Spatial + Taxonomic classification

https://en.wikipedia.org/wiki/Oak#/media/File:Quercus_robur.jpg



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‘WE’ - DEFINED

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