Session S:

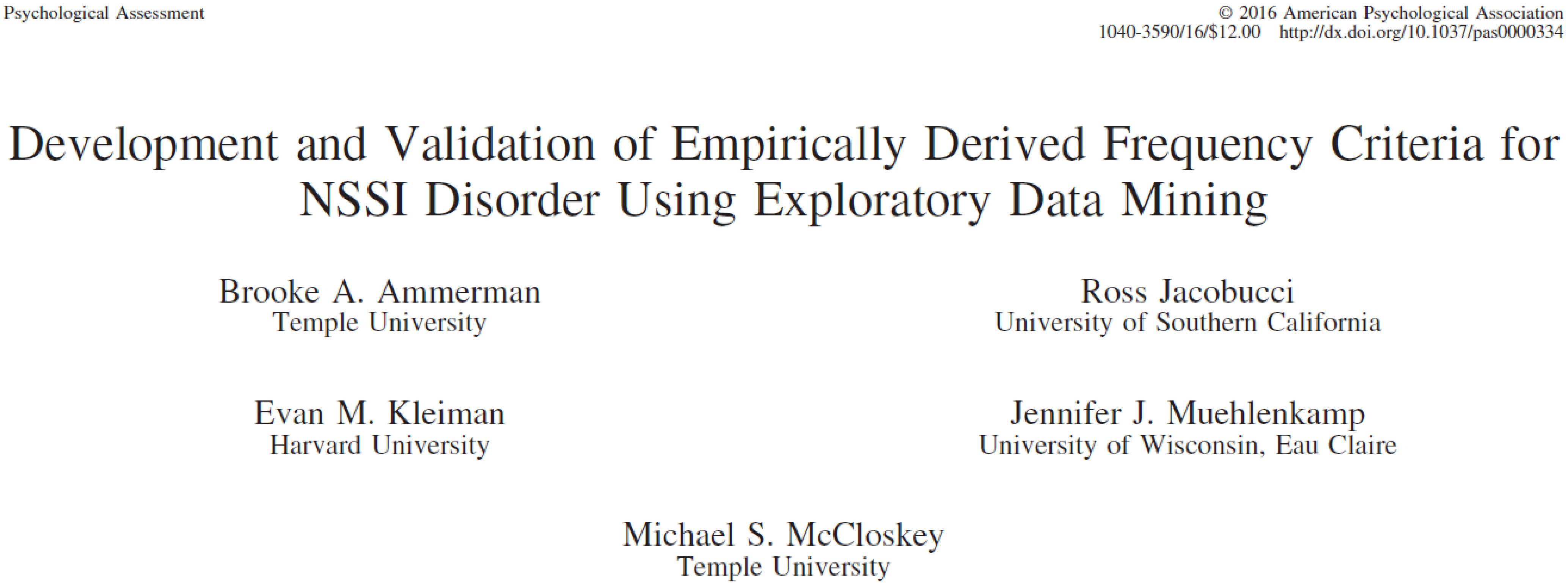
Lecture – SEM Trees

ATI Staff

Arizona State University

Summer 2016

Motivating Example



Psychological Assessment

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Development and Validation of Empirically Derived Frequency Criteria for NSSI Disorder Using Exploratory Data Mining

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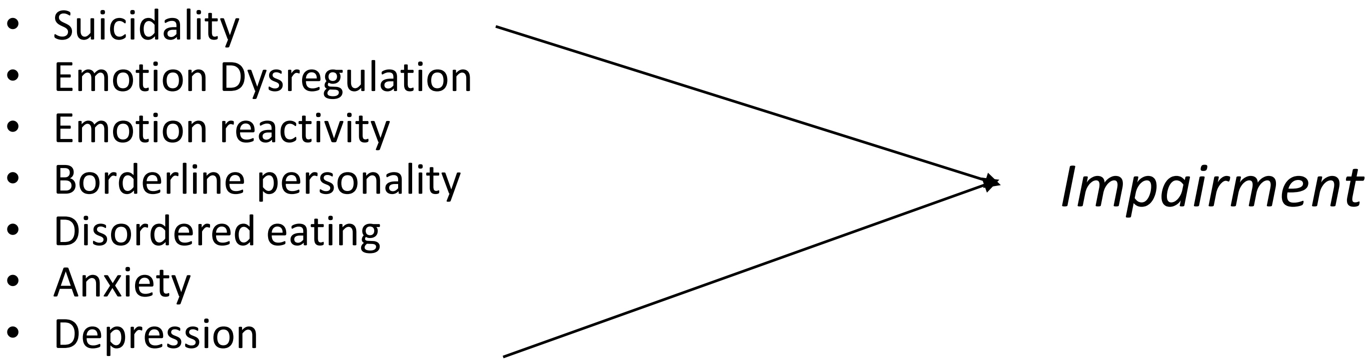
Goal of Analysis

- To find clinically meaningful sub groups of non-suicidal self-injury (NSSI)
  - Cutoffs for DSM-V Criteria
  - Current cutoff = 5 NSSI acts in past year
    - Workgroup for disorder stated this is an “arbitrary cutoff”
- Have measure of how many times participants self-injured in last year
  - “Have you ever, intentionally or on purpose, hurt yourself in the following ways, without the intention of killing yourself?”
- Outcome
  - One-factor Factor Analysis consisting of:



    - Suicidality
    - Emotion Dysregulation
    - Emotion reactivity
    - Borderline personality
    - Disordered eating
    - Anxiety
    - Depression

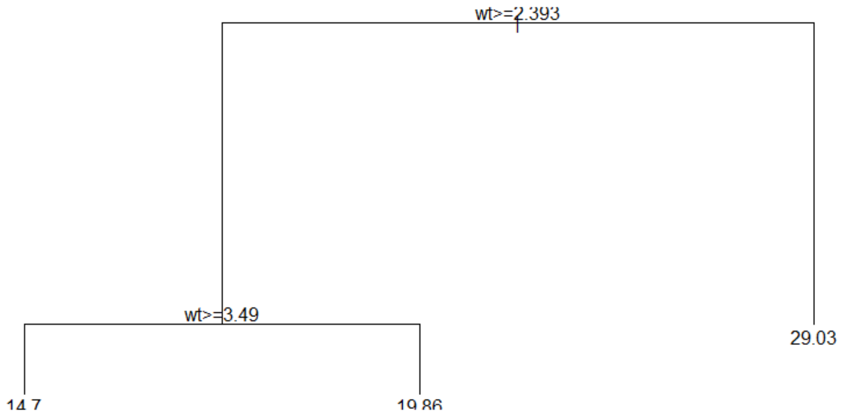
Impairment

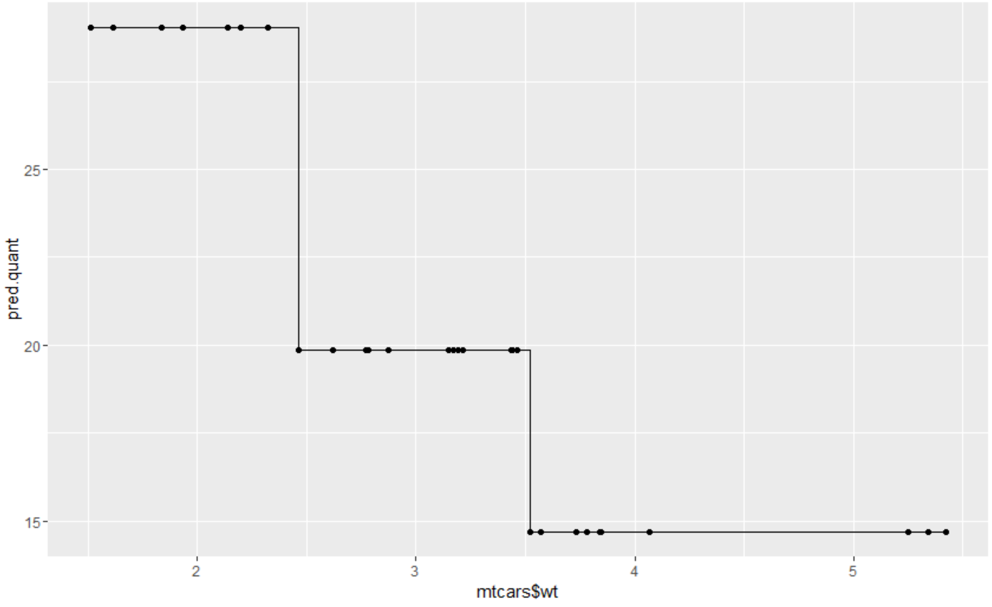
Decision Trees for Groups

Decision Trees for Groups

- As mentioned in previous presentations, Decision Trees (DTs) are non-linear models for predicting categorical or continuous outcomes

```
library(rpart);library(ggplot2); quant.out <- rpart(mpg ~ wt, data=mtcars); plot(quant.out);text(quant.out)

pred.quant <- predict(quant.out); qplot(mtcars$wt,pred.quant,geom=c("step","point"))
```





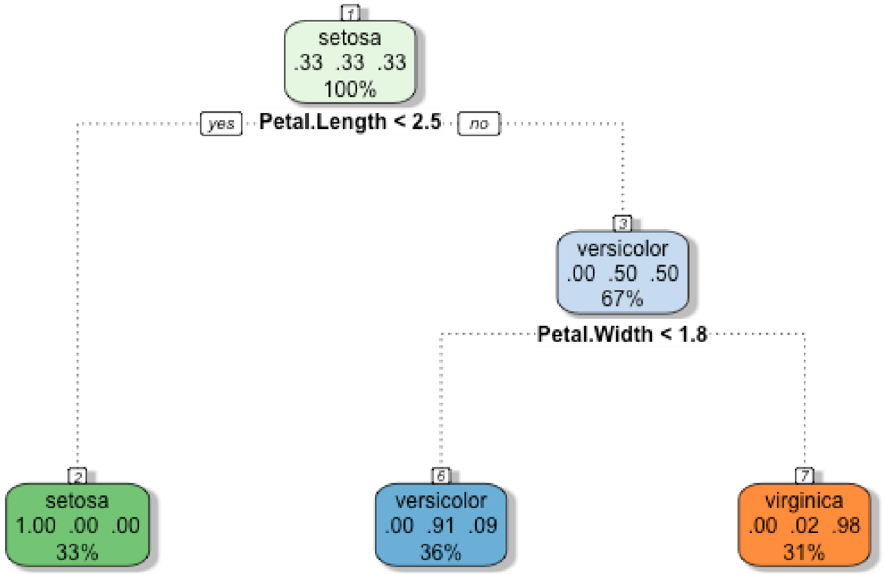
DTs for Groups Cont’d

- Most applications in Data Mining don’t involve people
  - The stepwise prediction for DT applies to groups as well
- Variable(s) you want to create groups with:
  - Predictor (one or more; categorical or continuous)
    - Categorical: Testing whether the levels of the variable are significantly different
    - Continuous: Looking for groups of people based on values of variable(s)
- Variable(s) you care about relationship with groups
  - Outcomes (one or more; categorical or continuous)

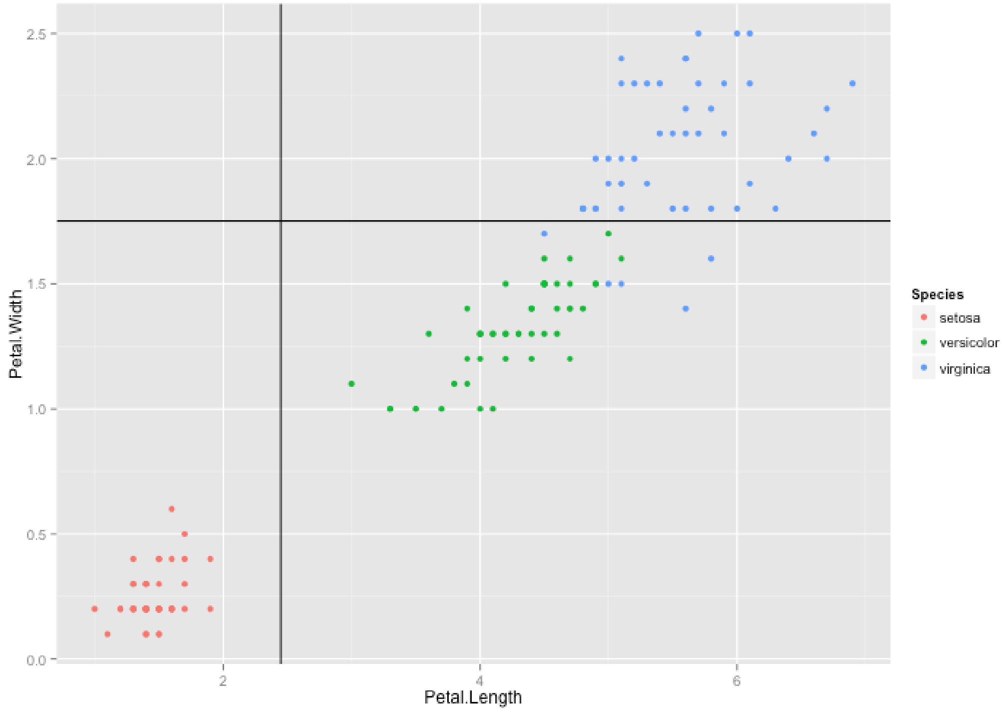
DT for Groups: Traditional Way

- Not people, but flowers!
- **Petals = Predictor**

```
library(rpart);library(ggplot2);library(rattle);attach(iris)
fit2 <- rpart(Species ~ Petal.Length + Petal.Width, data =
iris,control=rpart.control(maxdepth=2))
fancyRpartPlot(fit2)
p <- qplot(Petal.Length,Petal.Width,colour=Species); q <- p +
geom_vline(xintercept=2.45)
q + geom_abline(intercept=1.75,slope=0)
```



Rattle 2014-Dec-04 11:03:19 RJacobucci

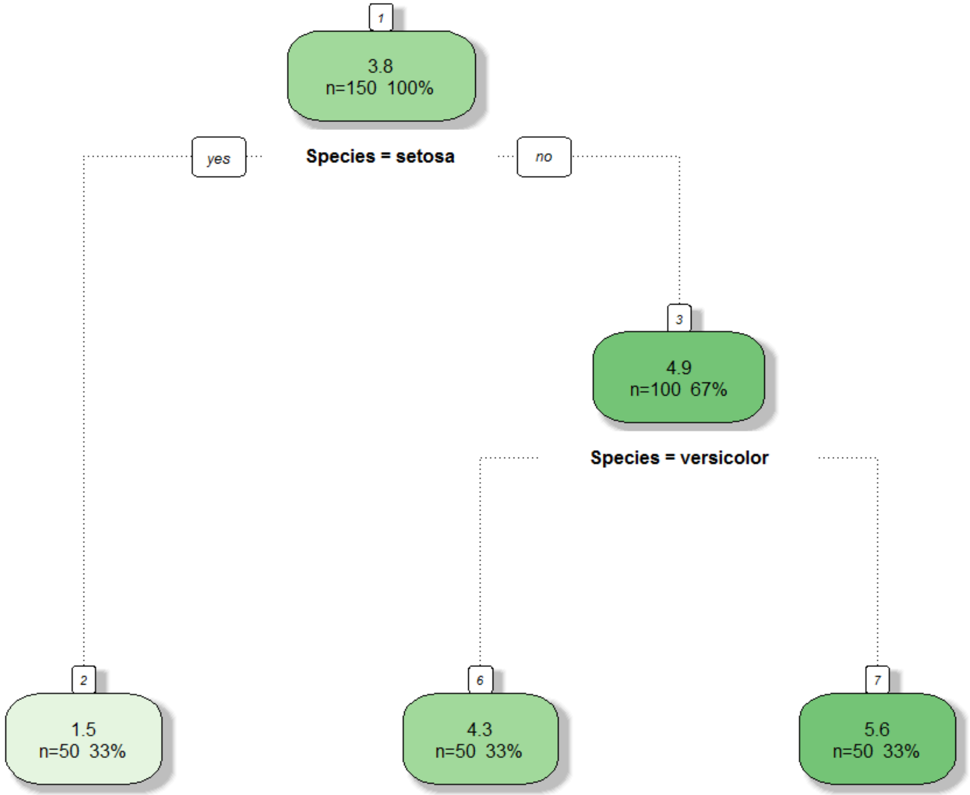


Now, instead of predicting group members, we are searching for groups *within* the predictors.

DT for Groups: Switch Predictors & Outcomes

- **Flower = Predictor**
- Test whether the groups are significantly different

```
library(rpart);library(ggplot2);library(rattle);attach(iris)
fit2 <- rpart(Petal.Length ~ Species, data =
iris,control=rpart.control(maxdepth=2))
```



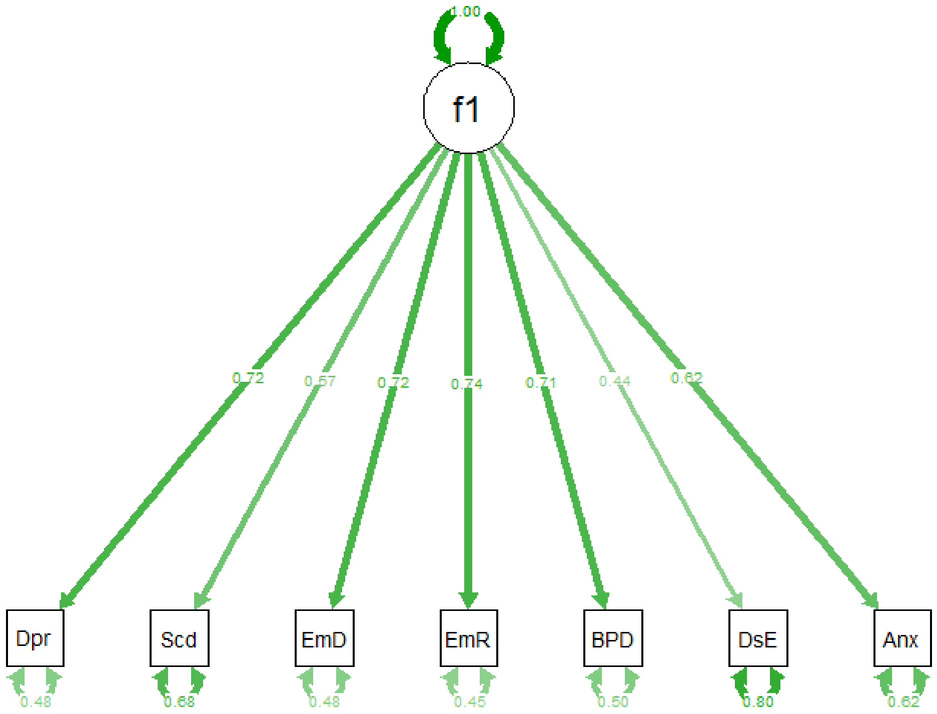
Rattle 2016-Jun-03 06:59:13 RJacobucci

DT for Groups Cont’d

- Many times we have variables that we might want to create subgroups based on
  - Income → find cutoffs for low, middle, high SES groups
  - Have continuous test scores and find cutoff for admission criteria
    - i.e. only accept those > 160 on GRE
- Which group has biggest differences on outcome?
  - Gender or Ethnicity a more “important” grouping in relation to supporting Clinton or Trump?
- Want to find interactions between groups to create further subgroupings
  - Females in low SES prefer Trump while females in high SES prefer Hillary
- Often times limited by only using 1 variable as an outcome
  - Where multivariate DT methods come in
    - E.g. multivariate boosting or SEM Trees

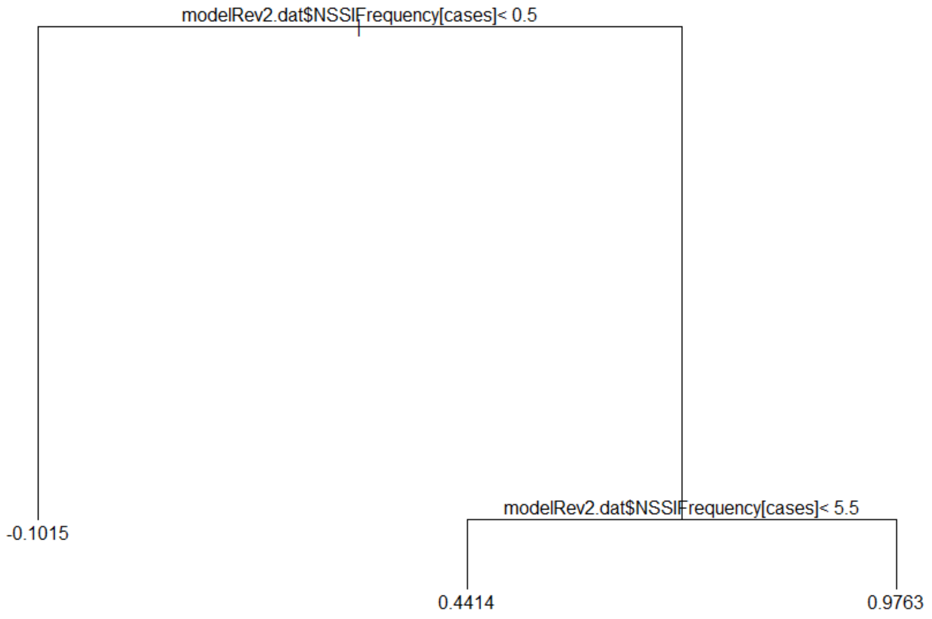
DTs and NSSI

- We want to find subgroups of people based on the number of times they self-injures
- In relation to:
  - A summed score
  - A factor score

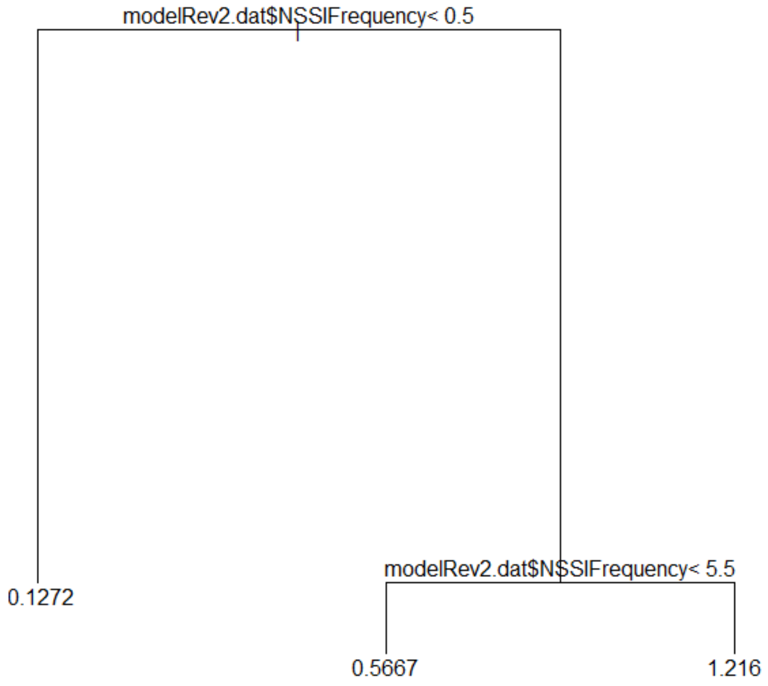


DTs and NSSI cont’d

NSSI → Summed Score


modelRev2.dat$NSSIFrequency[cases]< 0.5
modelRev2.dat$NSSIFrequency[cases]< 5.5
-0.1015
0.4414
0.9763

NSSI → Factor Score


modelRev2.dat$NSSIFrequency< 0.5
modelRev2.dat$NSSIFrequency< 5.5
0.1272
0.5667
1.216

So What Did We Learn?

- Cutoffs for NSSI Frequency Criteria should be:
  - Between 0 & 1
  - Between 5 & 6
- The DT results give us three groups with those cutoffs
- But what does this actually mean?
  - People w/ NSSI value of 0 have a deviation between their actual and predicted factor score that is significantly smaller than between their actual scores and predictions for any other group, including assuming every is in one group
  - More technically, putting people into groups decreases the RMSEA

SEM Trees & NSSI

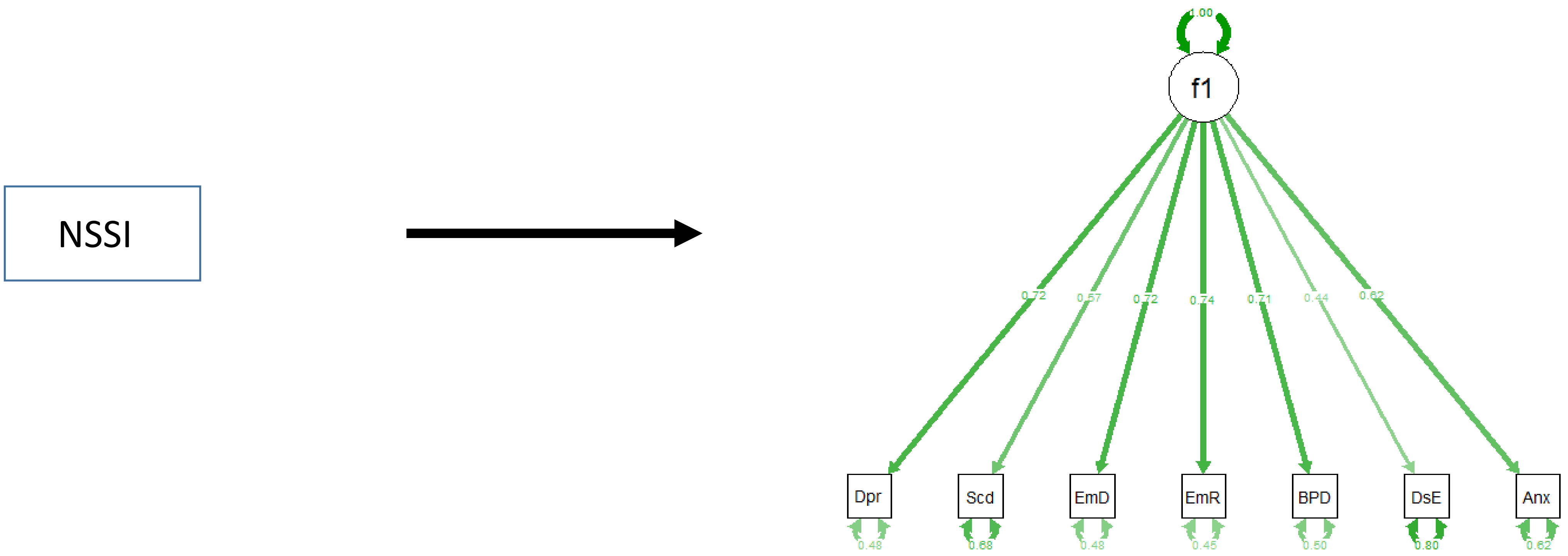
When We Can’t Reduce the Outcome to a Single Value

- Need SEM Trees or other multivariate model (Multivariate Boosting or others)
- Instead of reducing our outcome to a single variable we can use:
    - Means of multiple variables
    - A confirmatory factor model
    - Latent growth model
    - Autoregressive model
    - Etc.

SEM Trees

Predictor

Outcome



SEM Tree Cont’d

- Different than just including a covariate in the model
- In SEM Trees, the covariates predict the *model fit*
    - Not just the latent variable
- In predicting the fit of the model, you are indirectly predicting differences in each of the model parameters
    - i.e. factor variance, mean, loadings ….
    - In other words: If you change the model parameters then you change the model fit

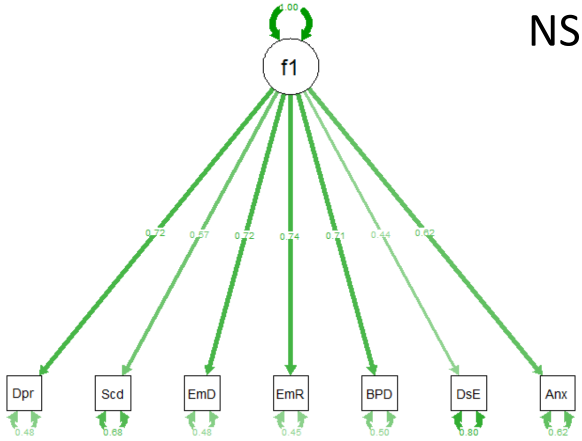
SEM Trees Algorithm

- In our NSSI example, the NSSI variable has integer values ranging from 0 to 1000
- If a covariate is an integer in SEM Trees, the model tests groups at every value:
  - 1. Fit of multiple group model with groups of people with values of 0 and 1-1000
    - Get model fit
  - 1. Fit of multiple group model with groups of people with values of 0 or 1 and 2-1000
    - Get model fit

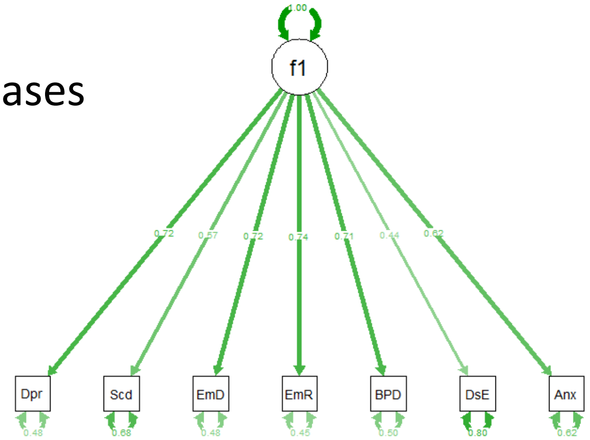
SEM Trees Algorithm Cont’d

- At each tested split, the model becomes

People w/
NSSI = 0

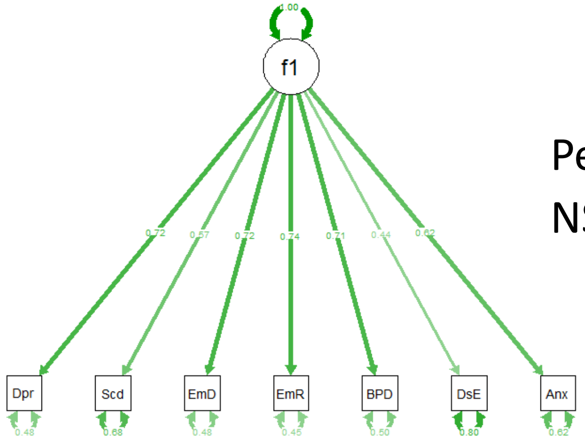


All cases



VERSUS

+



People w/
NSSI > 0

SEM Trees Algorithm Cont’d

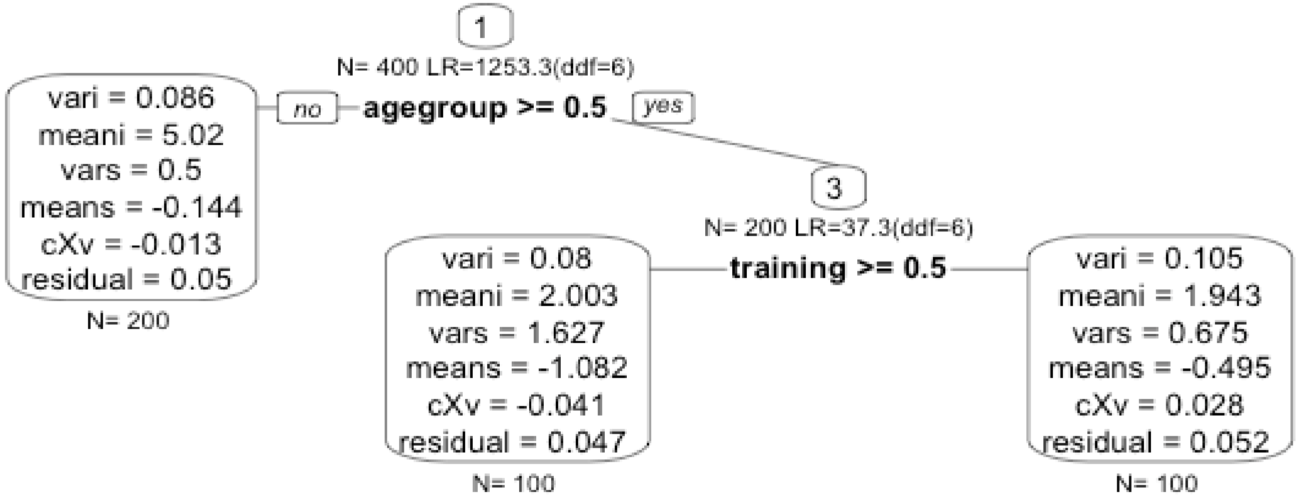
- Fitting the SEM in each group results in a separate fit
  - LL (log-likelihood) for each model
  - Model parameters are now group specific
- This can be compared using the likelihood ratio test
  - Is $LL_{all} <^{*} LL_{NSSI = 0} + LL_{NSSI = 1\text{-}1000}$
    - * Fit will always be better in multiple group model, but about <u>significance</u>
    - Larger LL is better (less negative)
    - 2 times the difference between models is a chi square distribution
      - Df = number of parameters of multiple group model minus parameters of no group model

SEM Trees Algorithm Cont’d

- If the covariate is an integer (& ordinal), tests every possible group in sequence
    - 0 vs. 1-1000, 0-1 vs 2-1000, 0-2 vs 3-1000 etc…
- Same thing if numeric (continuous; i.e. 0.324)
    - Will test every value in sequence, so may be better to round first
- If categorical (factor), one vs. the rest scheme
    - If 5 categories, 15 possible splits
        - Computationally intensive
- Once a best split is determined:
    - Move down one level to start over searching for an additional split
    - Continues until:
        - No longer improves model fit
        - Reaches other stopping criterion
            - Too small N in a node
            - A priori set maximum depth (# of groups)

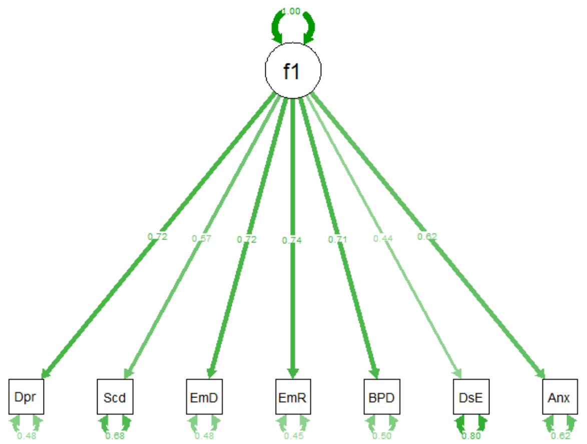
SEM Trees Algorithm Cont’d

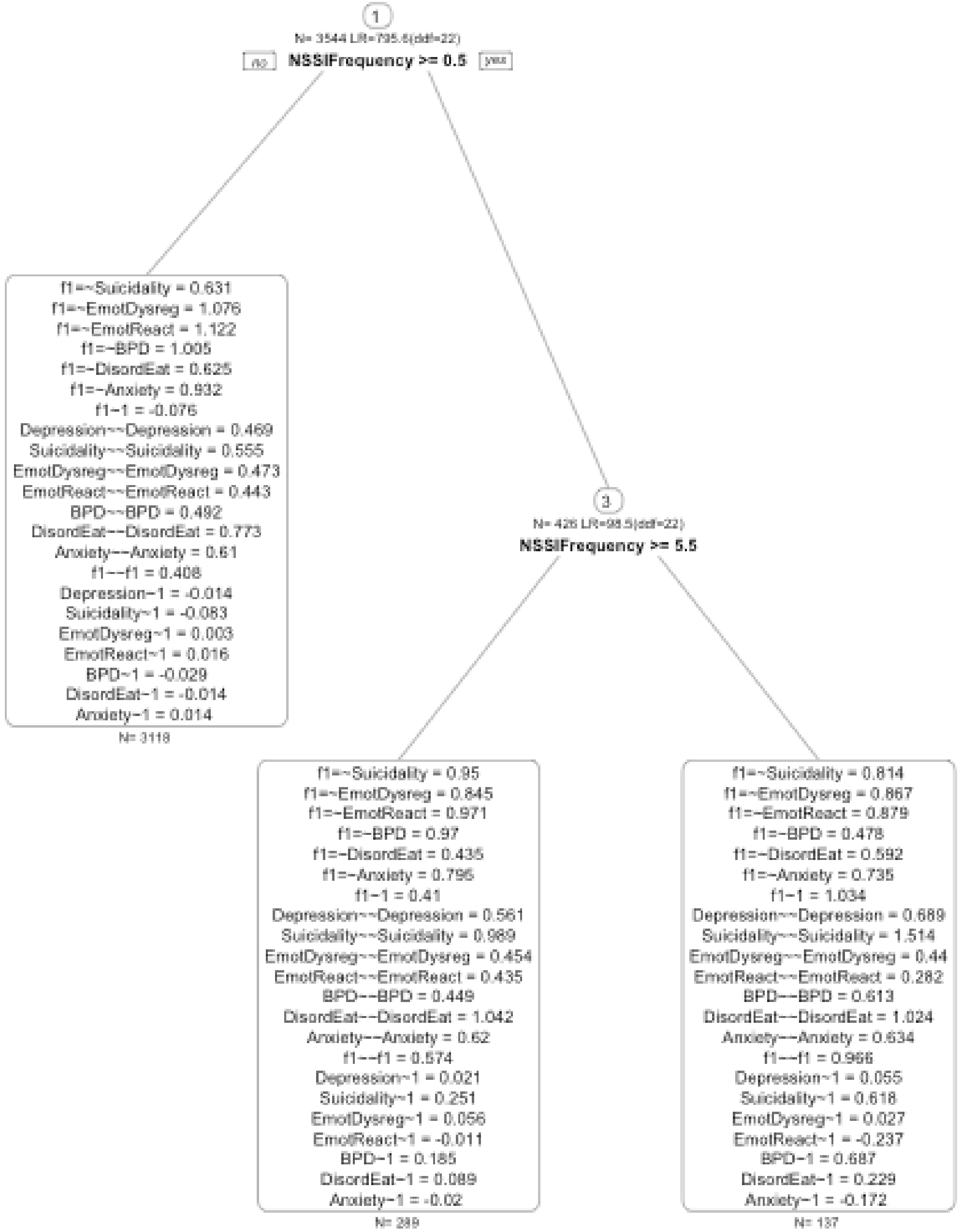
- Just like DT, SEM Trees can create a large tree
- Say the first split is between 0 & 1
- Next level, test splits on other variables
- Example:
  - Second split occurs at agegroup = 1 & between training 0-1
  - No further split for agegroup = 0



SEM Trees & NSSI

- Use a one factor CFA as the outcome
- Came up with the same splits as with DT

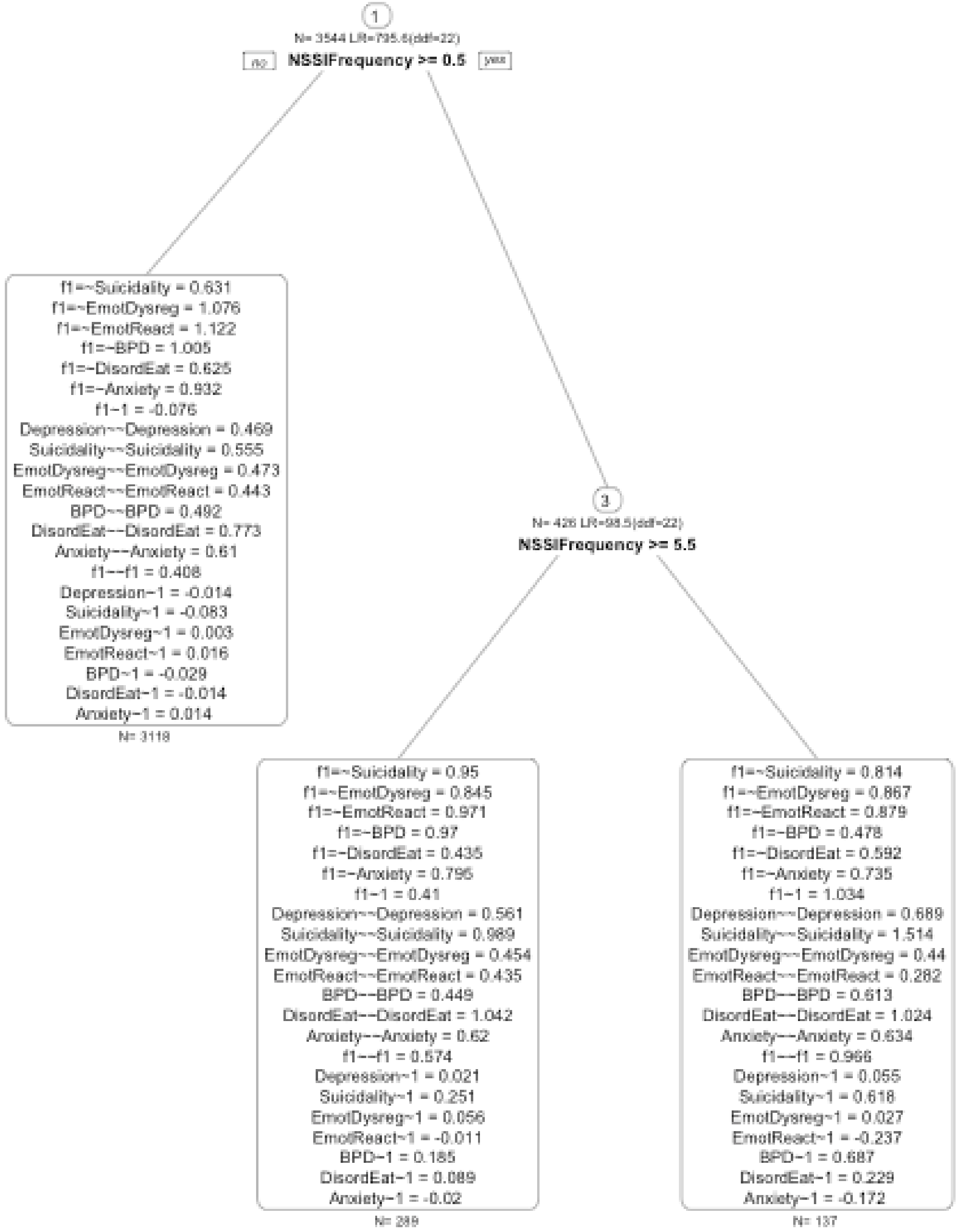




```
N= 3544 LR=795.6(df=22)
NSSIFrequency >= 0.5

f1=~Suicidality = 0.631
f1=~EmotDysreg = 1.076
f1=~EmotReact = 1.122
f1=~BPD = 1.005
f1=~DisordEat = 0.625
f1=~Anxiety = 0.932
f1~1 = -0.076
Depression~~Depression = 0.469
Suicidality~~Suicidality = 0.555
EmotDysreg~~EmotDysreg = 0.473
EmotReact~~EmotReact = 0.443
BPD~~BPD = 0.492
DisordEat~~DisordEat = 0.773
Anxiety~~Anxiety = 0.61
f1~~f1 = 0.408
Depression~1 = -0.014
Suicidality~1 = -0.083
EmotDysreg~1 = 0.003
EmotReact~1 = 0.016
BPD~1 = -0.029
DisordEat~1 = -0.014
Anxiety~1 = 0.014
N= 3118

N= 426 LR=98.5(df=22)
NSSIFrequency >= 5.5

f1=~Suicidality = 0.95
f1=~EmotDysreg = 0.845
f1=~EmotReact = 0.971
f1=~BPD = 0.97
f1=~DisordEat = 0.435
f1=~Anxiety = 0.796
f1~1 = 0.41
Depression~~Depression = 0.561
Suicidality~~Suicidality = 0.989
EmotDysreg~~EmotDysreg = 0.454
EmotReact~~EmotReact = 0.435
BPD~~BPD = 0.449
DisordEat~~DisordEat = 1.042
Anxiety~~Anxiety = 0.62
f1~~f1 = 0.574
Depression~1 = 0.021
Suicidality~1 = 0.251
EmotDysreg~1 = 0.056
EmotReact~1 = -0.011
BPD~1 = 0.185
DisordEat~1 = 0.089
Anxiety~1 = -0.02
N= 289

f1=~Suicidality = 0.814
f1=~EmotDysreg = 0.867
f1=~EmotReact = 0.879
f1=~BPD = 0.478
f1=~DisordEat = 0.592
f1=~Anxiety = 0.735
f1~1 = 1.034
Depression~~Depression = 0.689
Suicidality~~Suicidality = 1.514
EmotDysreg~~EmotDysreg = 0.44
EmotReact~~EmotReact = 0.282
BPD~~BPD = 0.613
DisordEat~~DisordEat = 1.024
Anxiety~~Anxiety = 0.634
f1~~f1 = 0.966
Depression~1 = 0.055
Suicidality~1 = 0.618
EmotDysreg~1 = 0.027
EmotReact~1 = -0.237
BPD~1 = 0.687
DisordEat~1 = 0.229
Anxiety~1 = -0.172
N= 137
```

SEM Trees & NSSI Cont’d

- Can investigate individual parameters to get a better clue to how groups differ
  - Factor mean increased w/ NSSI frequency
  - Most variable means increased
  - Factor variance increased



1
N= 3544 LR=795.6(ddf=22)
no NSSIFrequency >= 0.5 yes

f1=~Suicidality = 0.631
f1=~EmotDysreg = 1.076
f1=~EmotReact = 1.122
f1=~BPD = 1.005
f1=~DisordEat = 0.625
f1=~Anxiety = 0.932
f1~1 = -0.076
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Suicidality~~Suicidality = 0.555
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Depression~1 = -0.014
Suicidality~1 = -0.083
EmotDysreg~1 = 0.003
EmotReact~1 = 0.016
BPD~1 = -0.029
DisordEat~1 = -0.014
Anxiety~1 = 0.014
N= 3118

3
N= 426 LR=98.5(ddf=22)
NSSIFrequency >= 5.5

f1=~Suicidality = 0.95
f1=~EmotDysreg = 0.845
f1=~EmotReact = 0.971
f1=~BPD = 0.97
f1=~DisordEat = 0.435
f1=~Anxiety = 0.796
f1~1 = 0.41
Depression~~Depression = 0.561
Suicidality~~Suicidality = 0.989
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BPD~1 = 0.185
DisordEat~1 = 0.089
Anxiety~1 = -0.02
N= 289

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f1~~f1 = 0.966
Depression~1 = 0.055
Suicidality~1 = 0.618
EmotDysreg~1 = 0.027
EmotReact~1 = -0.237
BPD~1 = 0.687
DisordEat~1 = 0.229
Anxiety~1 = -0.172
N= 137

SEM Trees & NSSI Conclusion

- Agreement in cutoffs across methods
  - Important, as SEM Trees hasn’t been studied that much
- SEM Trees allows for a more comprehensive evaluation
  - While being able to make specific comparisons across groups
- Was able to incorporate more information into the model than if we used mixture models
  - This is not always the case in comparing mixtures and SEM Trees
  - We had a ***very*** informative covariate
- Not that difficult to program and didn’t take long to run
  - Demonstrated in Lab Session T

SEM Trees Options

SEM Trees Options

- Because there is an SEM for each group
  - Should set minimum number of cases per node of tree
    - `min.N` in `semtree.control`
- Large number of covariates?
  - Need to prevent type-1 errors (overfitting)
    - Also, large, uninterpretable tree
  - Can use Bonferroni correction or use cross-validation
  - `bonferroni = TRUE` or `method=“cv”` in `semtree.control`
- Large number of response options for covariate(s)
  - These variables are more likely to be split on
  - Correct with changing `method=“fair”`

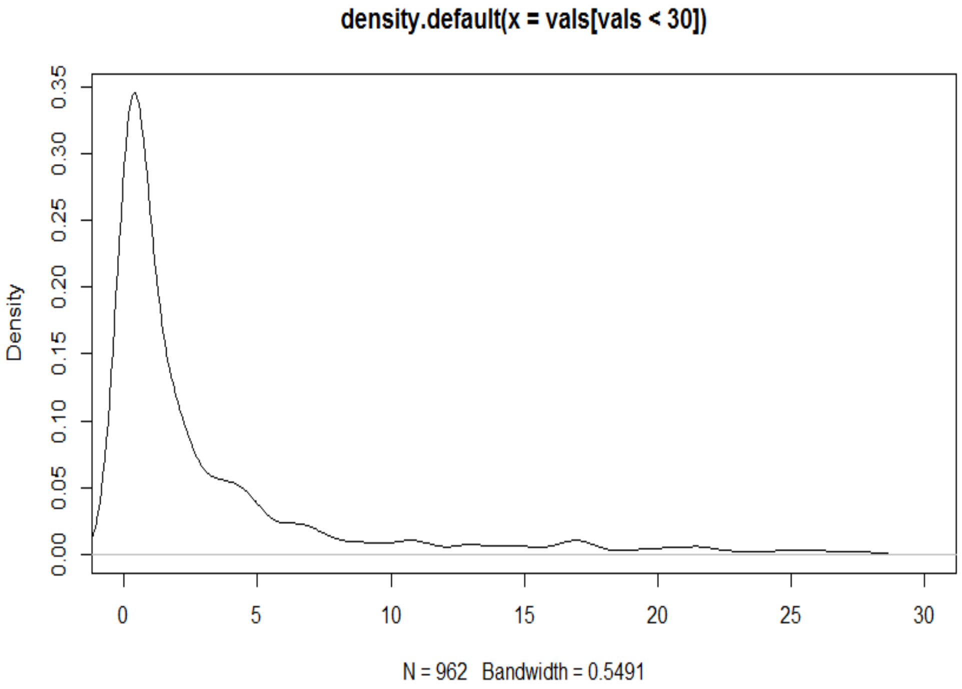
SEM Trees & Invariance

- In many contexts, it is necessary to ensure that groups are measured on the same construct
- This can either be call differential item functioning (IRT) or measurement invariance (SEM)
- This entails constraining certain parameters to be equal across groups
- Most common: constrain factor loadings
- Easy to do in SEM Trees
  - Set `invariance =` parameter names in `semtree.control`
    - Demonstrated in Lab Session T

SEM Trees vs. Mixture Models

Mixture Models

- Traditional way of doing things
  - Look for multiple underlying normal distributions underlying NSSI distribution



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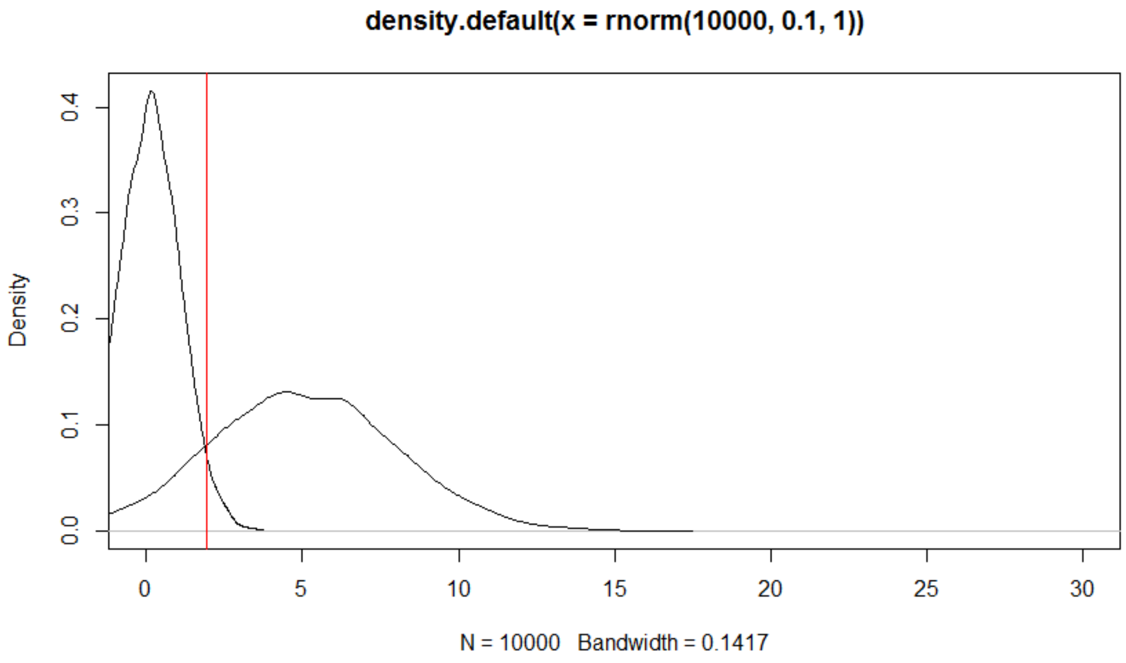
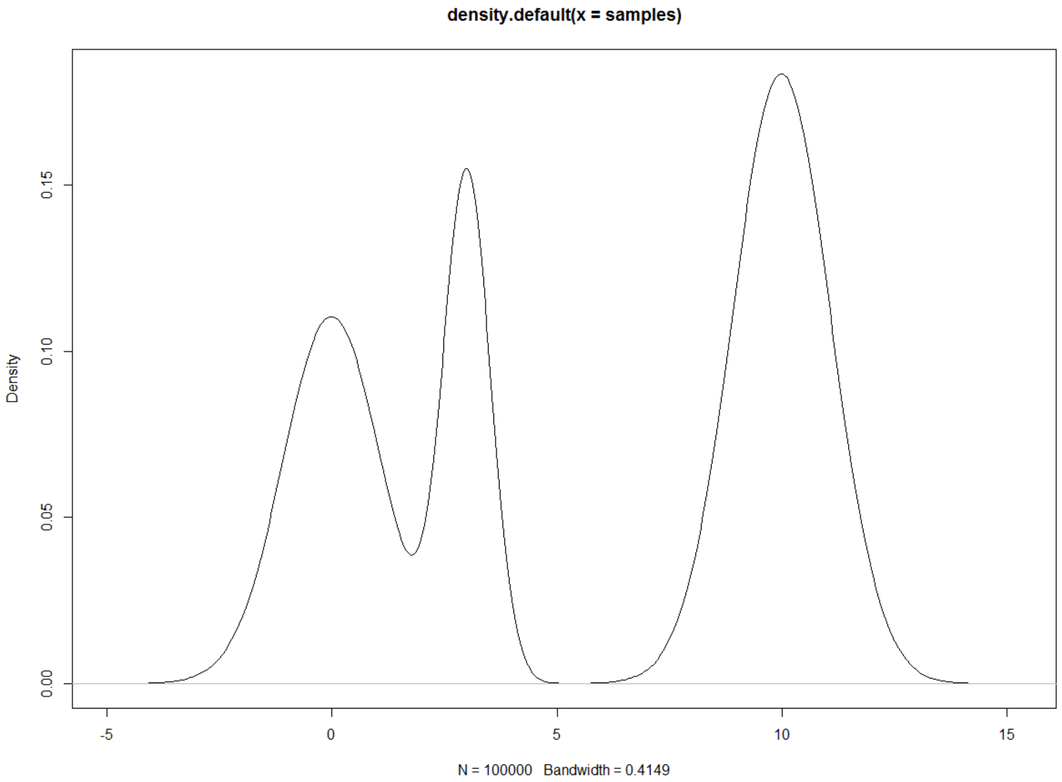


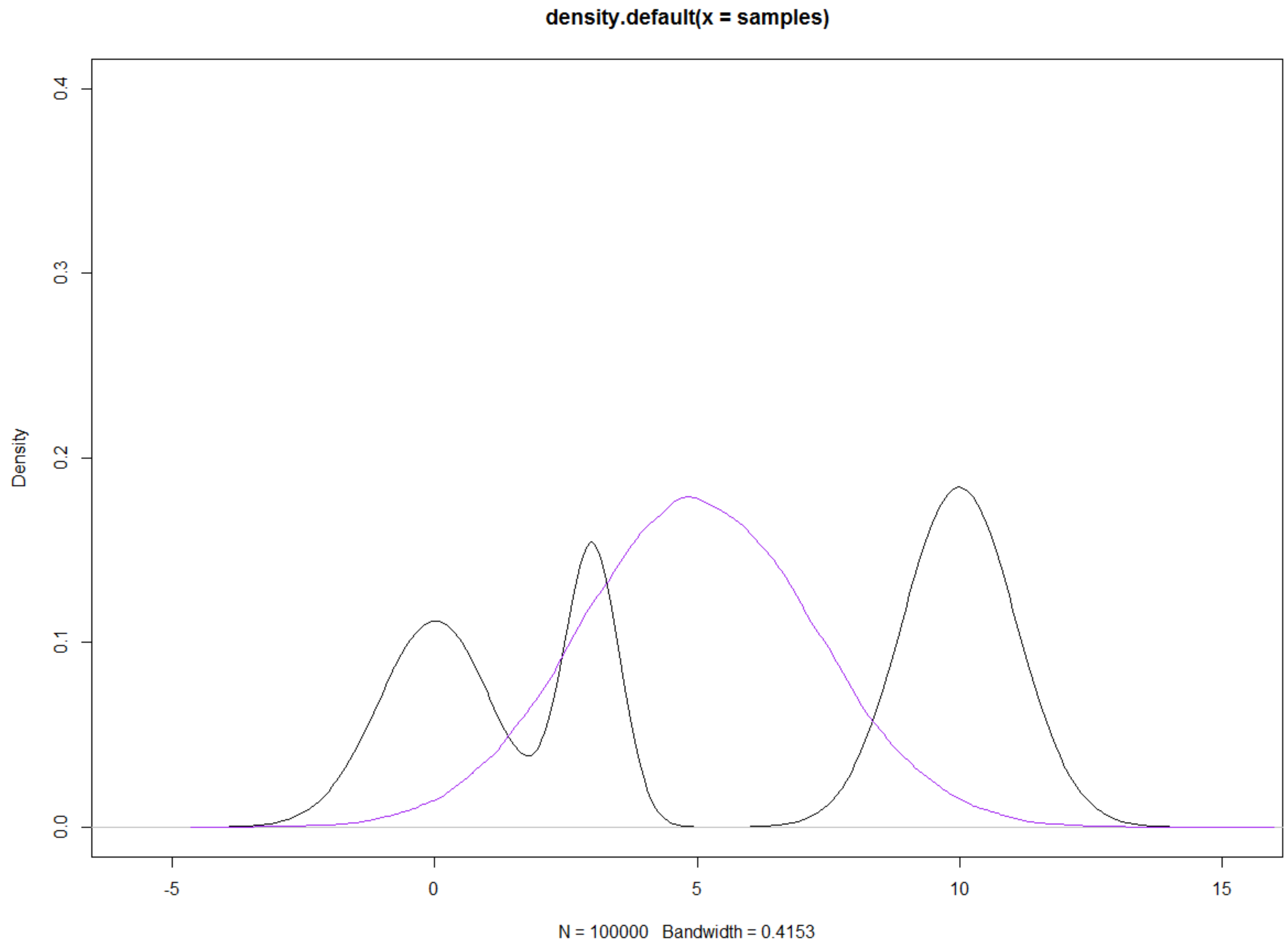
SEM Trees vs. Mixture Models

- Do very similar things, but find groups (classes) a little differently
- Let’s say we have a variable we are trying to find groups in
- Hypothetical distribution for a cognitive score variable:



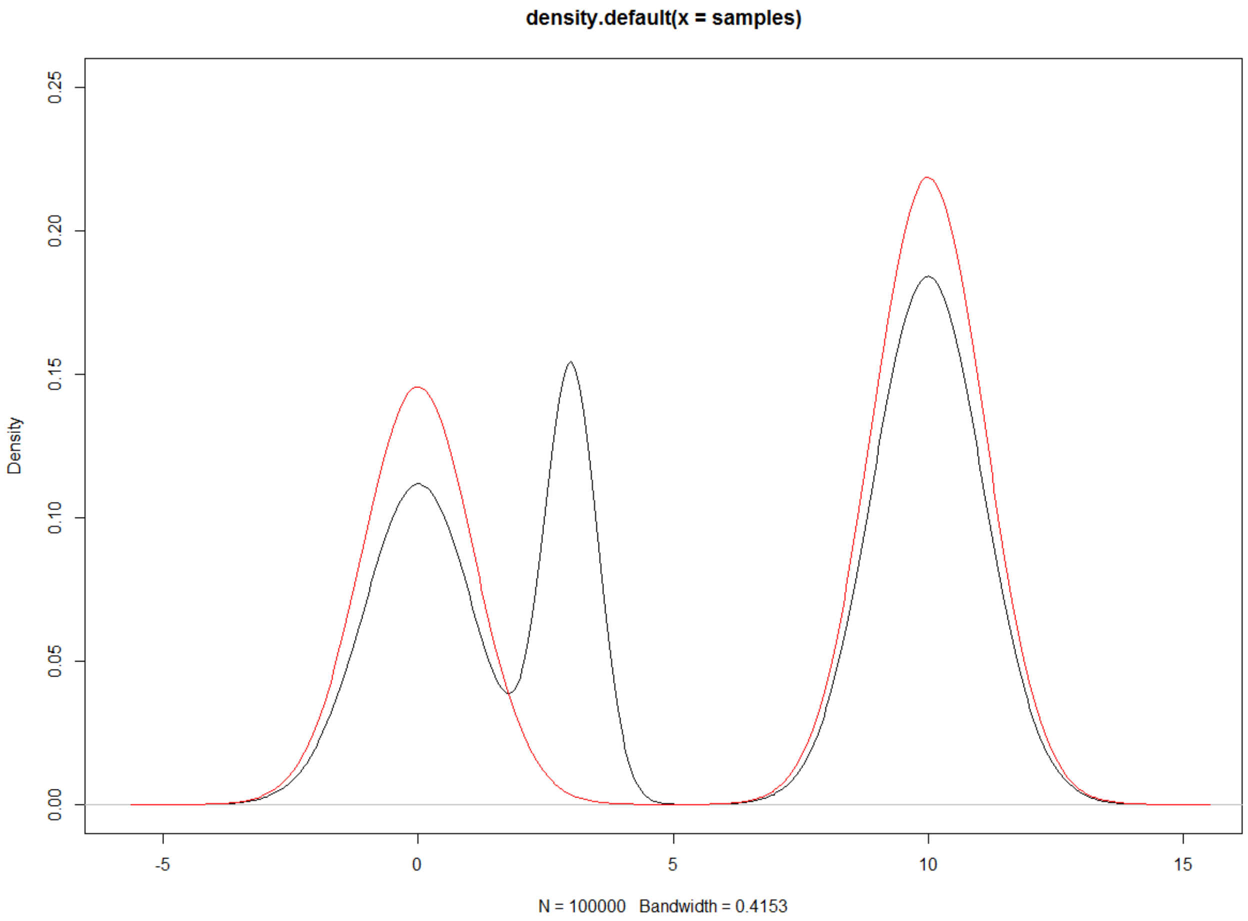
Assume Homogeneity

- Doesn’t do so well



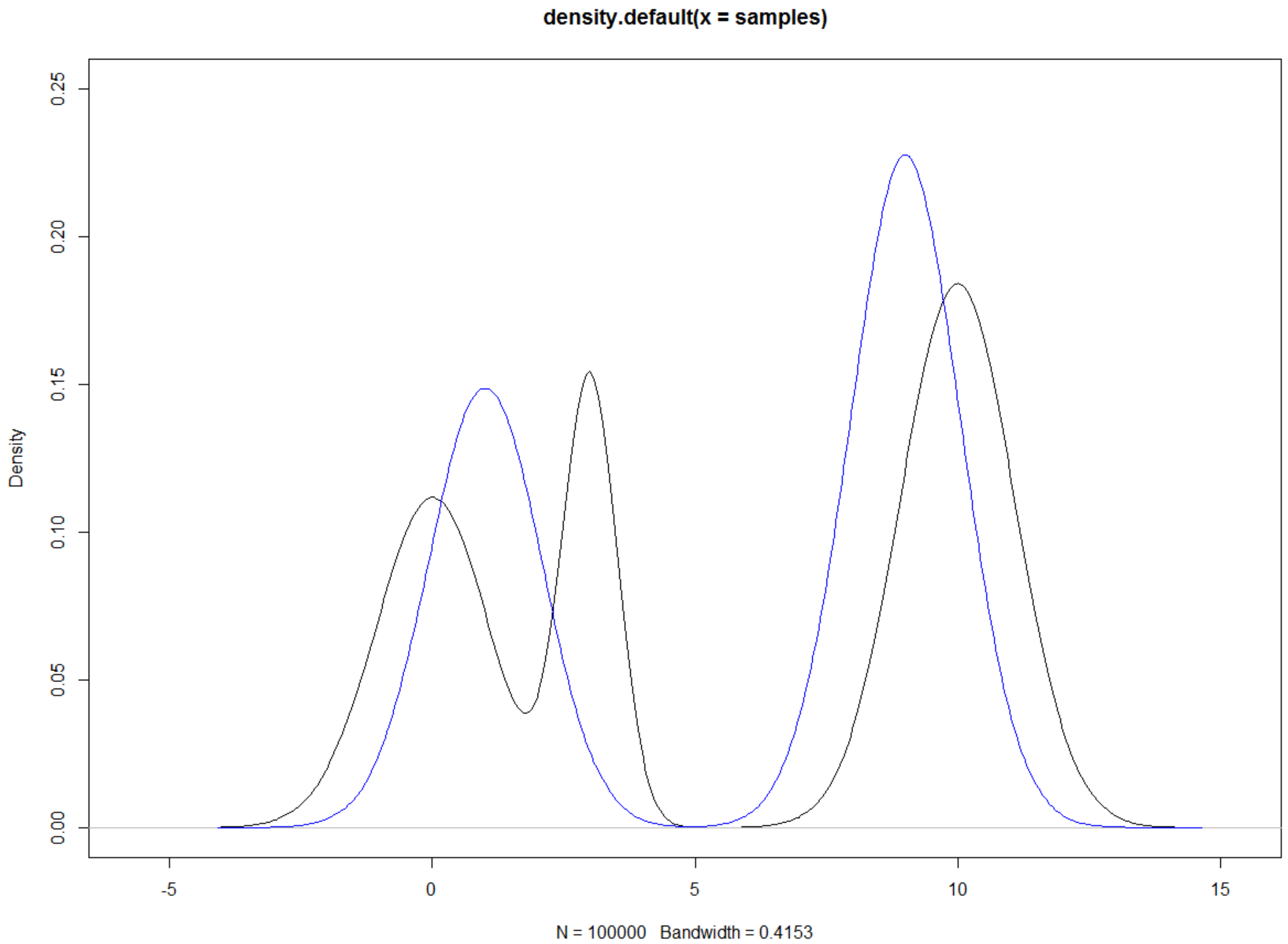
Comparison Example

- Mixture models will attempt to fit this distribution directly
- An example with 2 classes



Comparison Example Cont'd

- SEM Trees will try and fit this distribution
  - But only through splitting on the covariates
  - Meaning SEM Trees is more constrained
  - Doesn't have access to the whole search space
  - For example, the blue line could represent the distribution for a gender variable



Comparison Example Summary

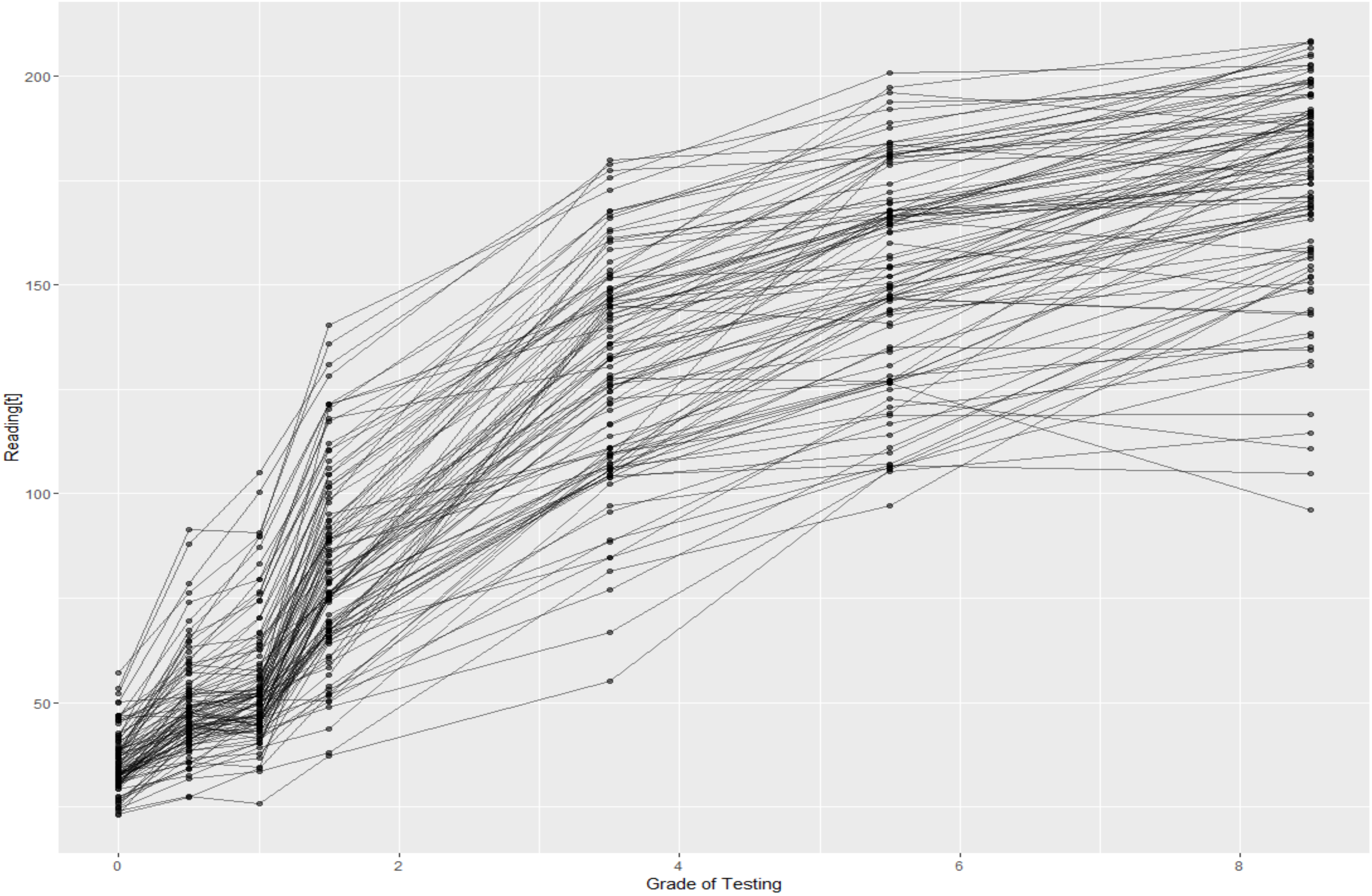
- SEM Trees requires informative covariates to split on
  - Mixtures do not
- SEM Trees may be less likely to overfit
- SEM Trees allows interactions and non-linear prediction
  - In mixtures, the classes are all at the same level, not nested or based on interactions
  - In mixtures, the relationship between class membership and auxiliary variables is constrained to be linear
- Can be very useful to test both methods and compare the resultant groups

SEM Tree vs. Growth Mixture Model

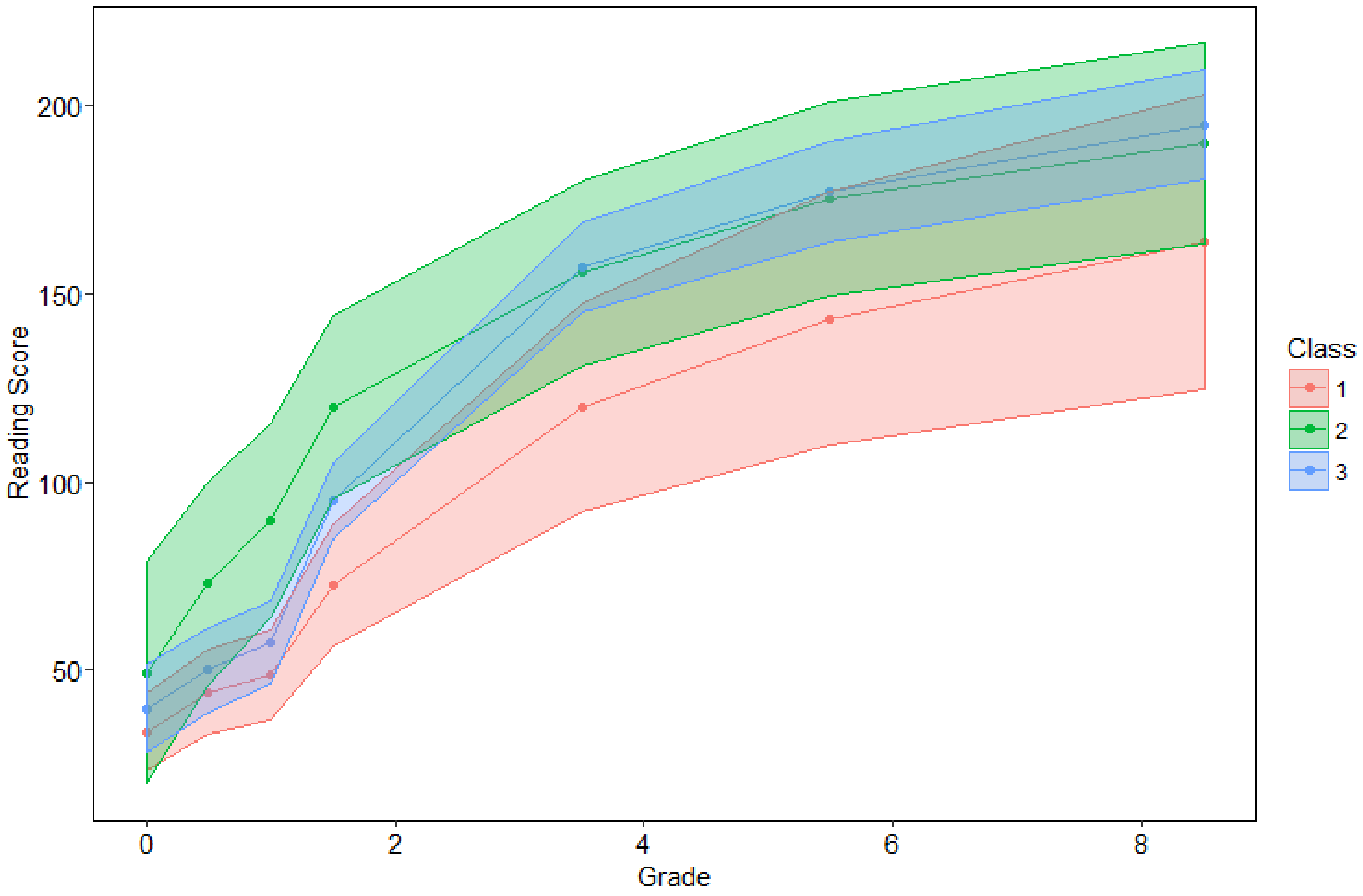
Comparison Example

- Compare differences in trajectories
  - Using a latent growth curve model
  - Change in reading from Kindergarten to 8th grade
  - Early Childhood Longitudinal Study - Kindergarten Cohort (ECLS-K) data
- Questions we are trying to answer
  - Do all children learn at the same rate or are the subgroups?
    - i.e. Late bloomers (start low, but catch up)
    - Those who start high and improve fast
  - Can other measured variables give us insight into these groups
    - Covariates include fine motor skills (*fine*), gross motor skills (*gross*), approaches to learning (*learn*), self-control (*control*), interpersonal skills (*interp*), internalizing behaviors (*int*), and general knowledge (*gk1*)

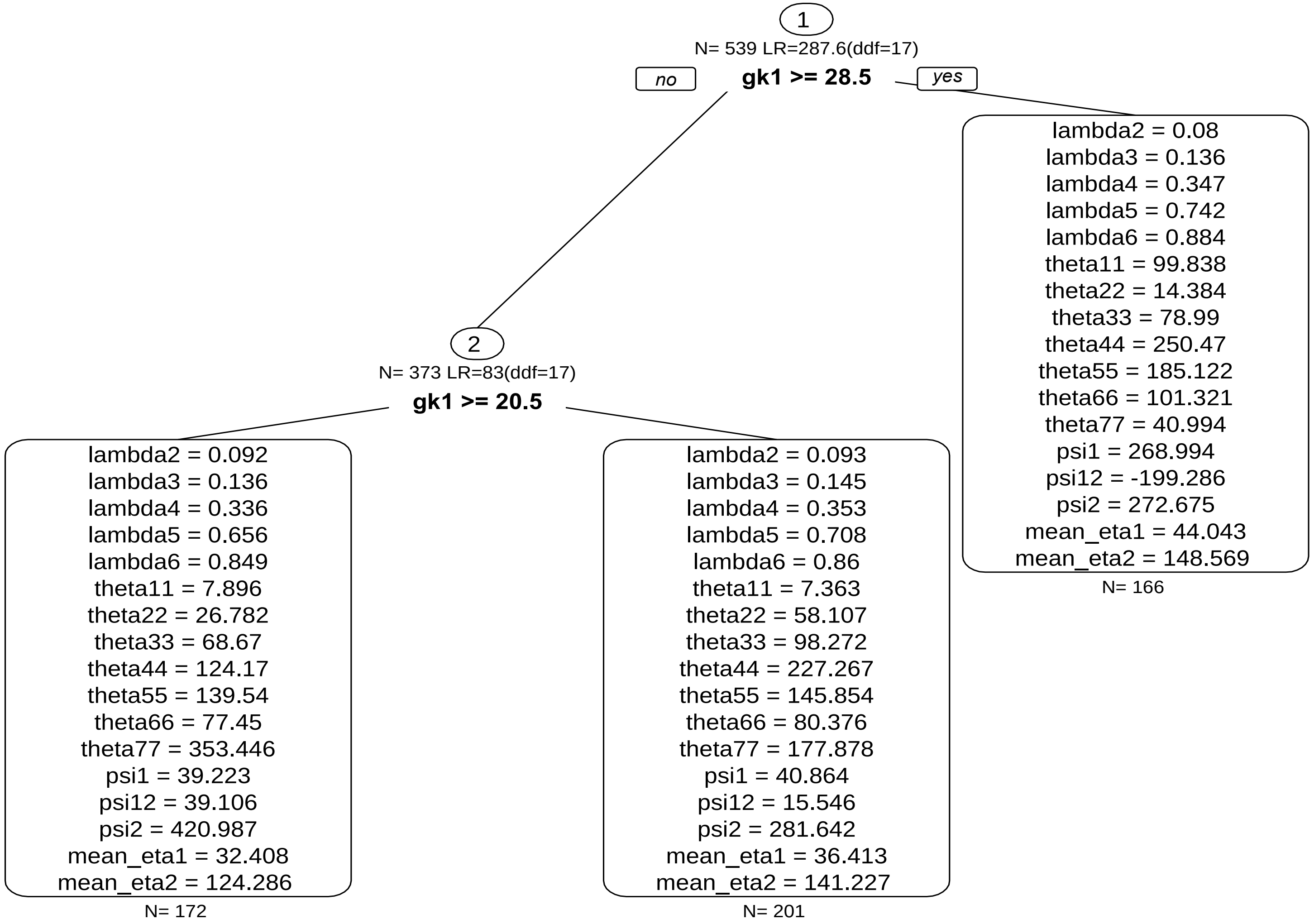
Trajectory Plot



Growth Mixture Model



Growth SEM Trees



1

N= 539 LR=287.6(ddf=17)

no

gk1 >= 28.5

yes

lambda2 = 0.08
lambda3 = 0.136
lambda4 = 0.347
lambda5 = 0.742
lambda6 = 0.884
theta11 = 99.838
theta22 = 14.384
theta33 = 78.99
theta44 = 250.47
theta55 = 185.122
theta66 = 101.321
theta77 = 40.994
psi1 = 268.994
psi12 = -199.286
psi2 = 272.675
mean_eta1 = 44.043
mean_eta2 = 148.569

N= 166

2

N= 373 LR=83(ddf=17)

gk1 >= 20.5

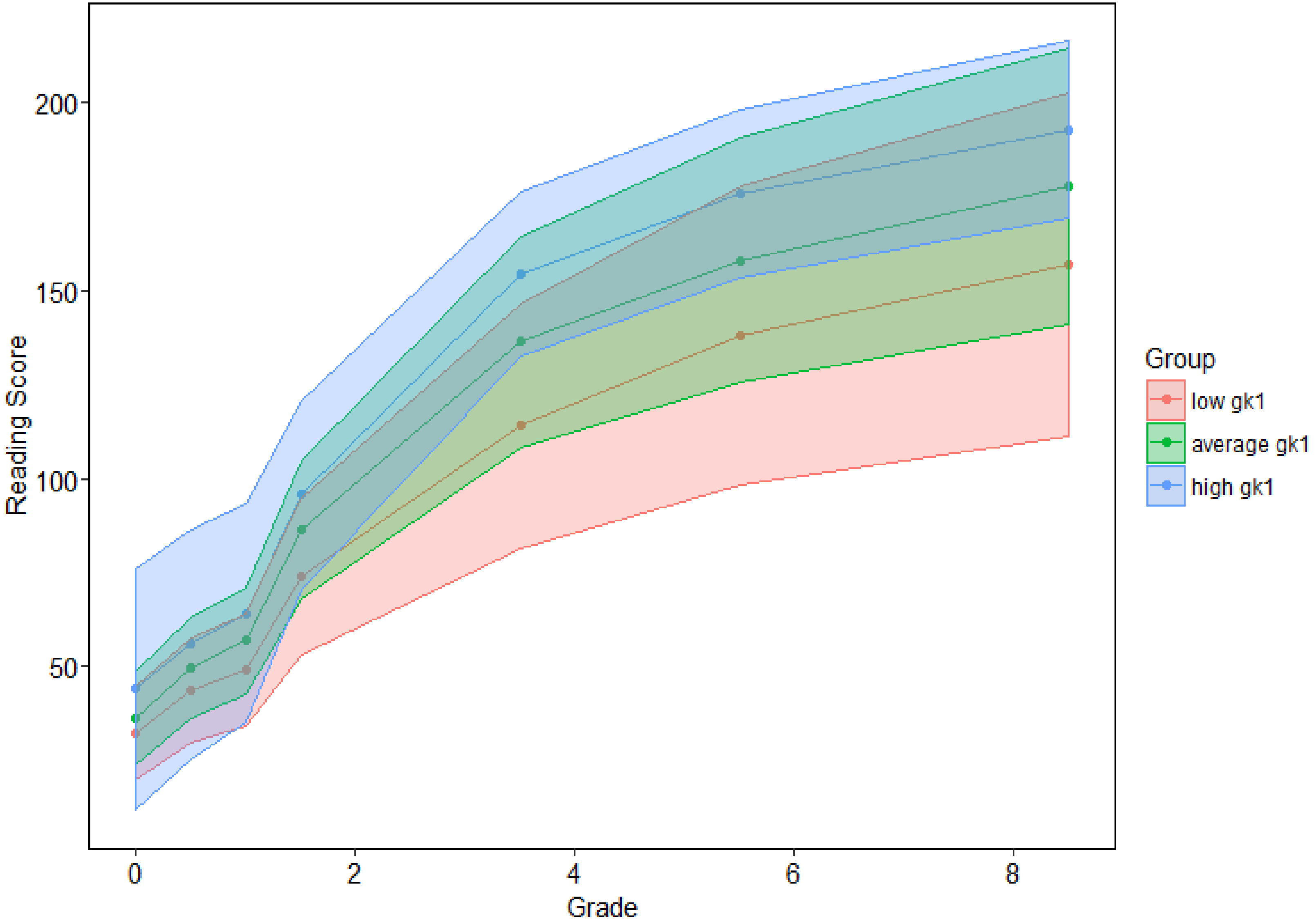
lambda2 = 0.092
lambda3 = 0.136
lambda4 = 0.336
lambda5 = 0.656
lambda6 = 0.849
theta11 = 7.896
theta22 = 26.782
theta33 = 68.67
theta44 = 124.17
theta55 = 139.54
theta66 = 77.45
theta77 = 353.446
psi1 = 39.223
psi12 = 39.106
psi2 = 420.987
mean_eta1 = 32.408
mean_eta2 = 124.286

N= 172

lambda2 = 0.093
lambda3 = 0.145
lambda4 = 0.353
lambda5 = 0.708
lambda6 = 0.86
theta11 = 7.363
theta22 = 58.107
theta33 = 98.272
theta44 = 227.267
theta55 = 145.854
theta66 = 80.376
theta77 = 177.878
psi1 = 40.864
psi12 = 15.546
psi2 = 281.642
mean_eta1 = 36.413
mean_eta2 = 141.227

N= 201

Growth SEM Trees



Comparison Example Summary

- SEM Trees split twice on the general knowledge variable
  - Was a significant auxiliary variable in Mixture Model
- SEM Trees didn’t fit as well
  - More variability within group and overlap across groups
- The Growth Mixture Model had more interesting classes
  - Class 1 caught up to Class 3 in grades 4 and 5
    - Different loadings across groups
  - SEM Trees groups really only differed in Kindergarten

SEM Trees Conclusion

- Has been extended to allow multiple trees
  - SEM Forests – analogous extension from DT → Random Forests
  - Can take a really long time to run (hours/days)
- Very new method
  - Hasn’t been tested to a large extent to set guidelines for best practices
- Can take a long time to run
  - Small model and small # of covariates can be 5 minutes
  - Large model and large # of covariates can be hours
- REMEMBER: Just because you get out a tree, does not mean that it represents real groups
  - Needs to make theoretical sense
  - Could just be the product of overfitting