

Uncovering interactions with Random Forests

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Random Forests

- >> ensembles of decision trees
 - >> diverse trees trying to solve the same problem
- >> used frequently for:
 - >> prediction (knowledge of model less important)
 - >> feature selection (prediction less important)

RF interactions: prior art

>> online official RF manual

>> Lunetta, et al. (2004)

>> Bureau, et al. (2005)

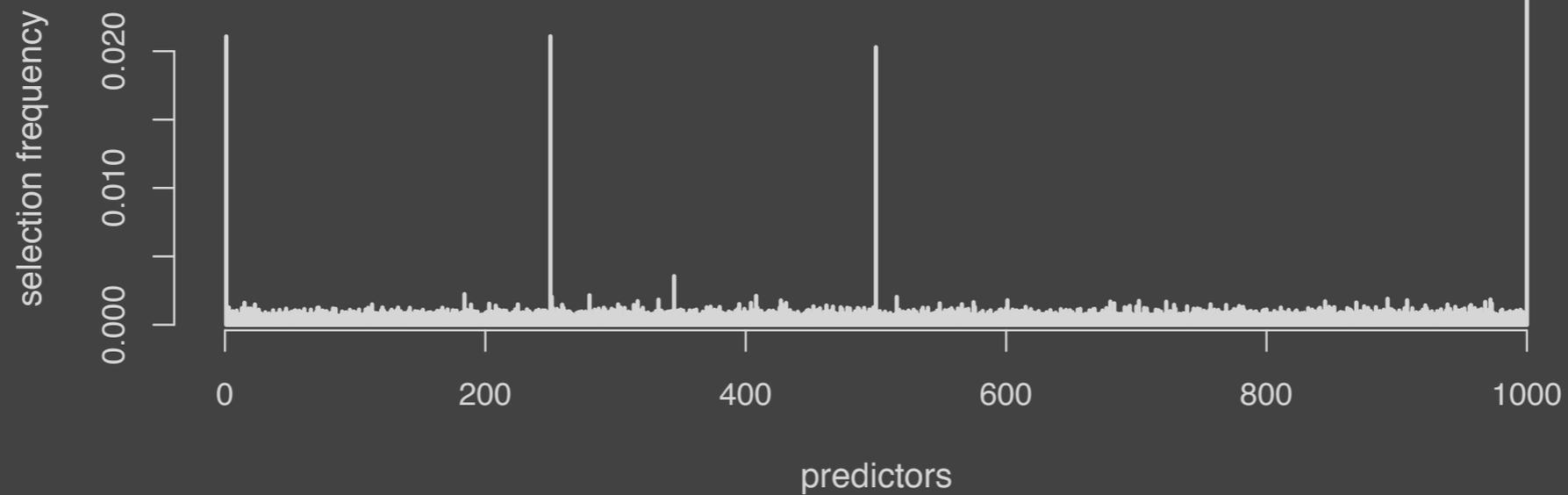
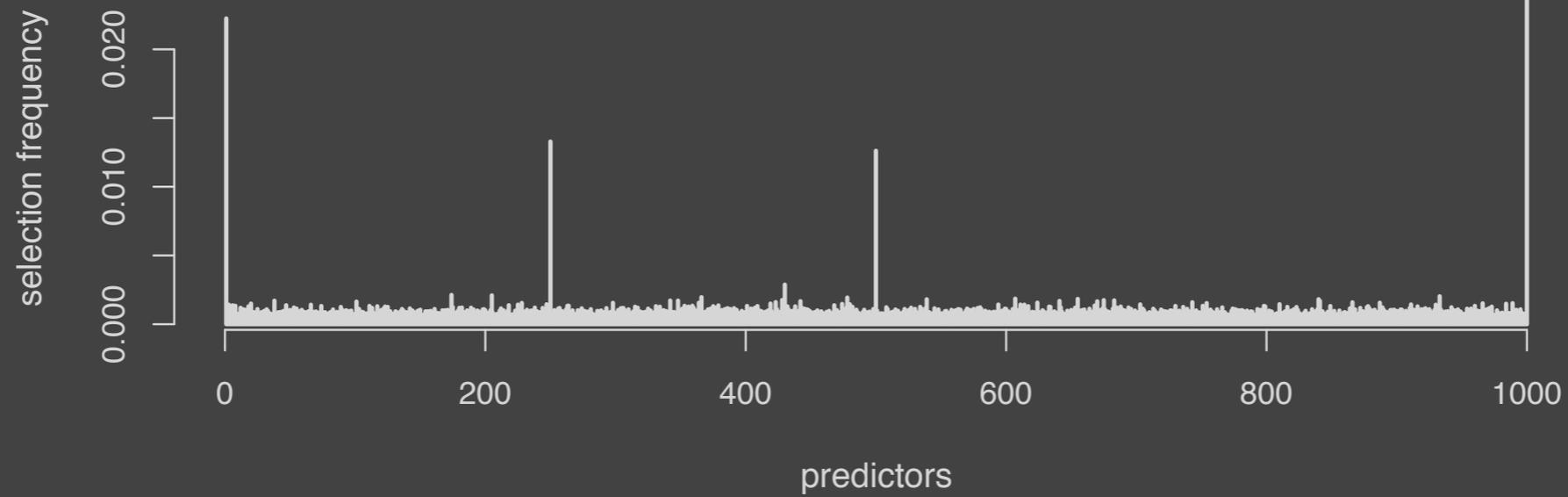
>> pairwise permutation importance

>> Mao and Mao (2008)

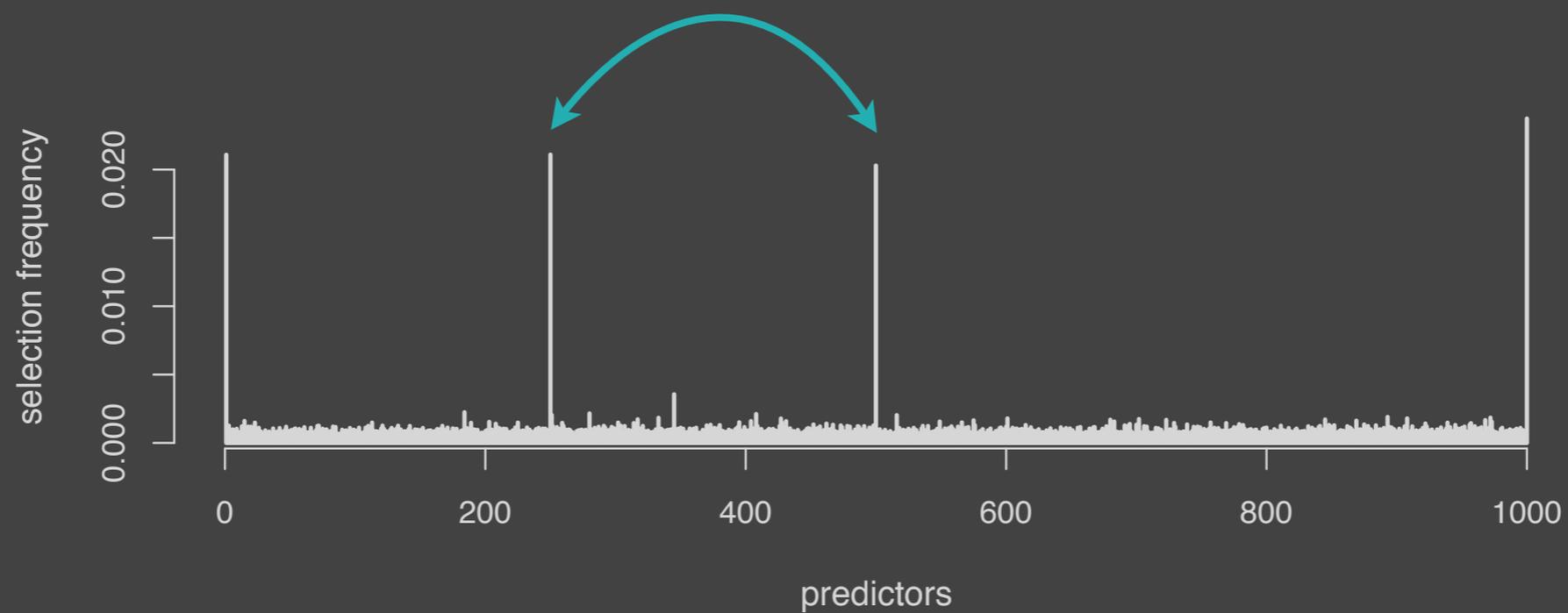
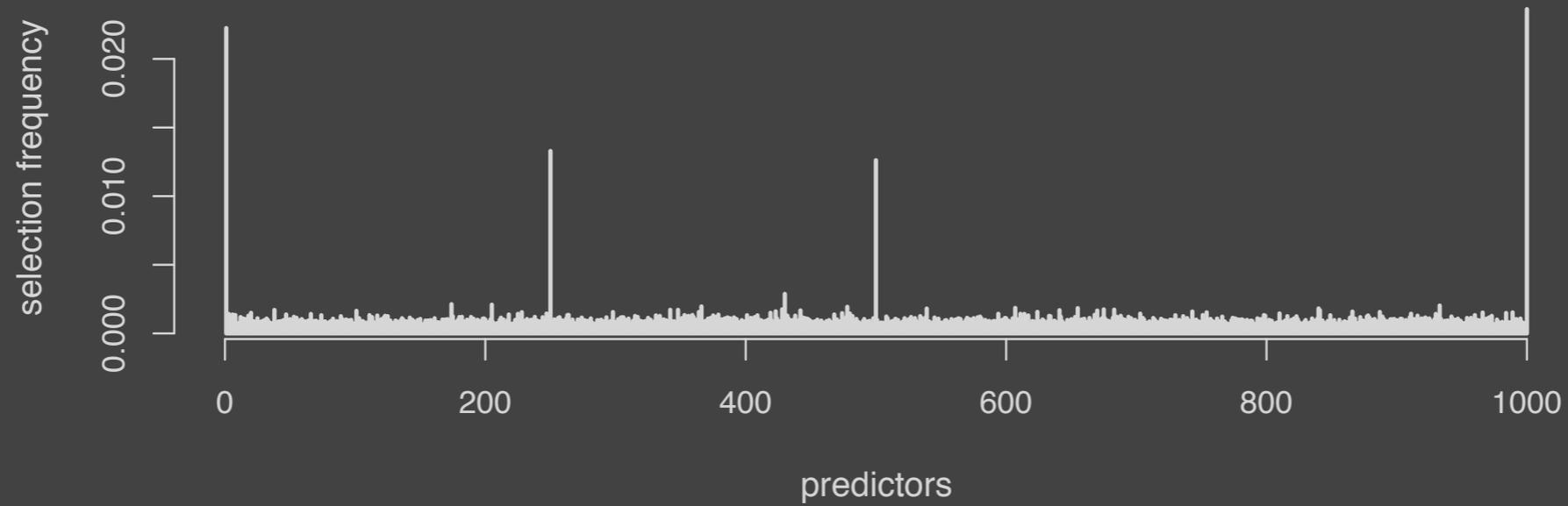
>> Jiang, et al. (2009)

>> selection with RF Gini importance, conventional (LM-based) interaction test (up to 3-way)

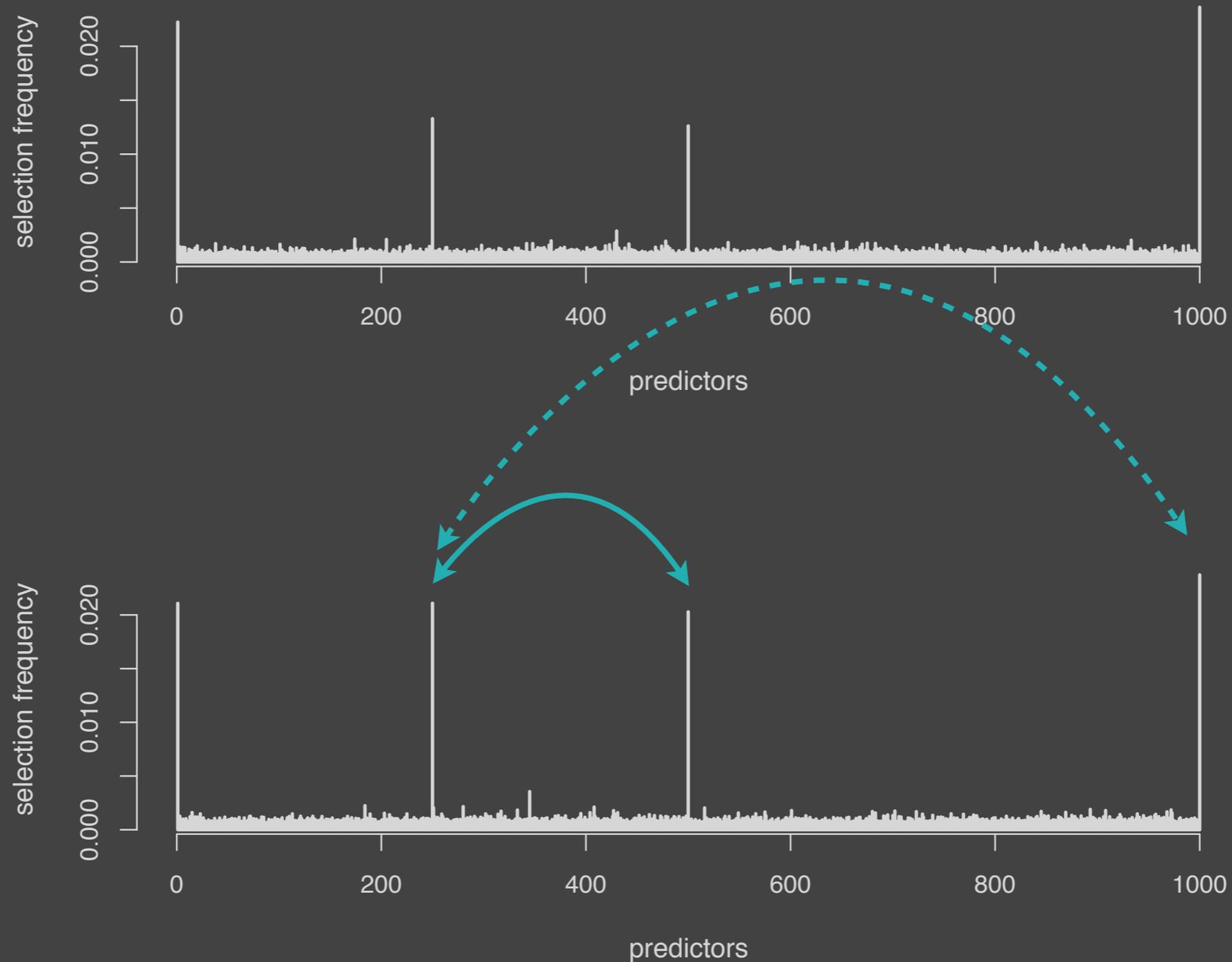
a typical problem



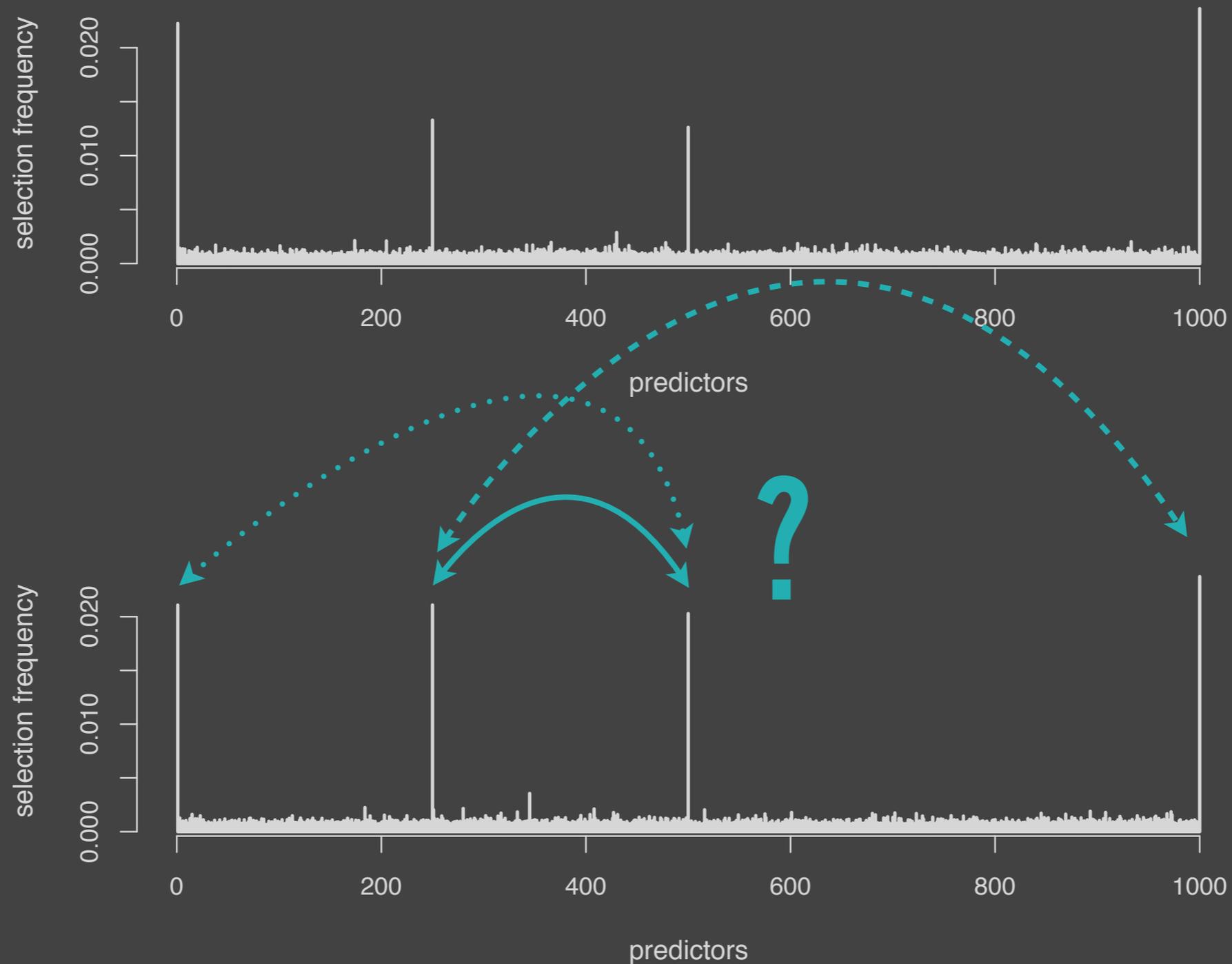
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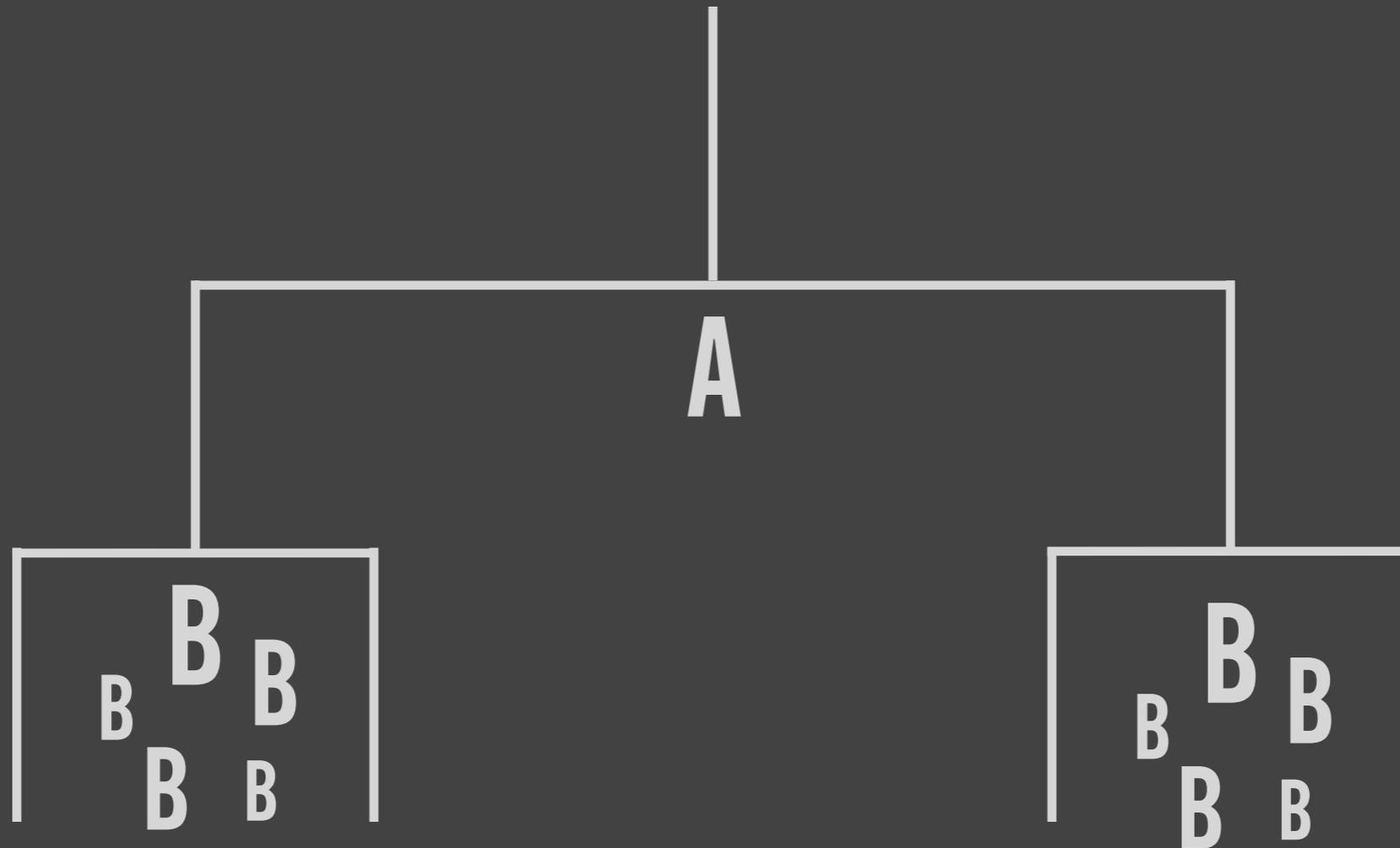
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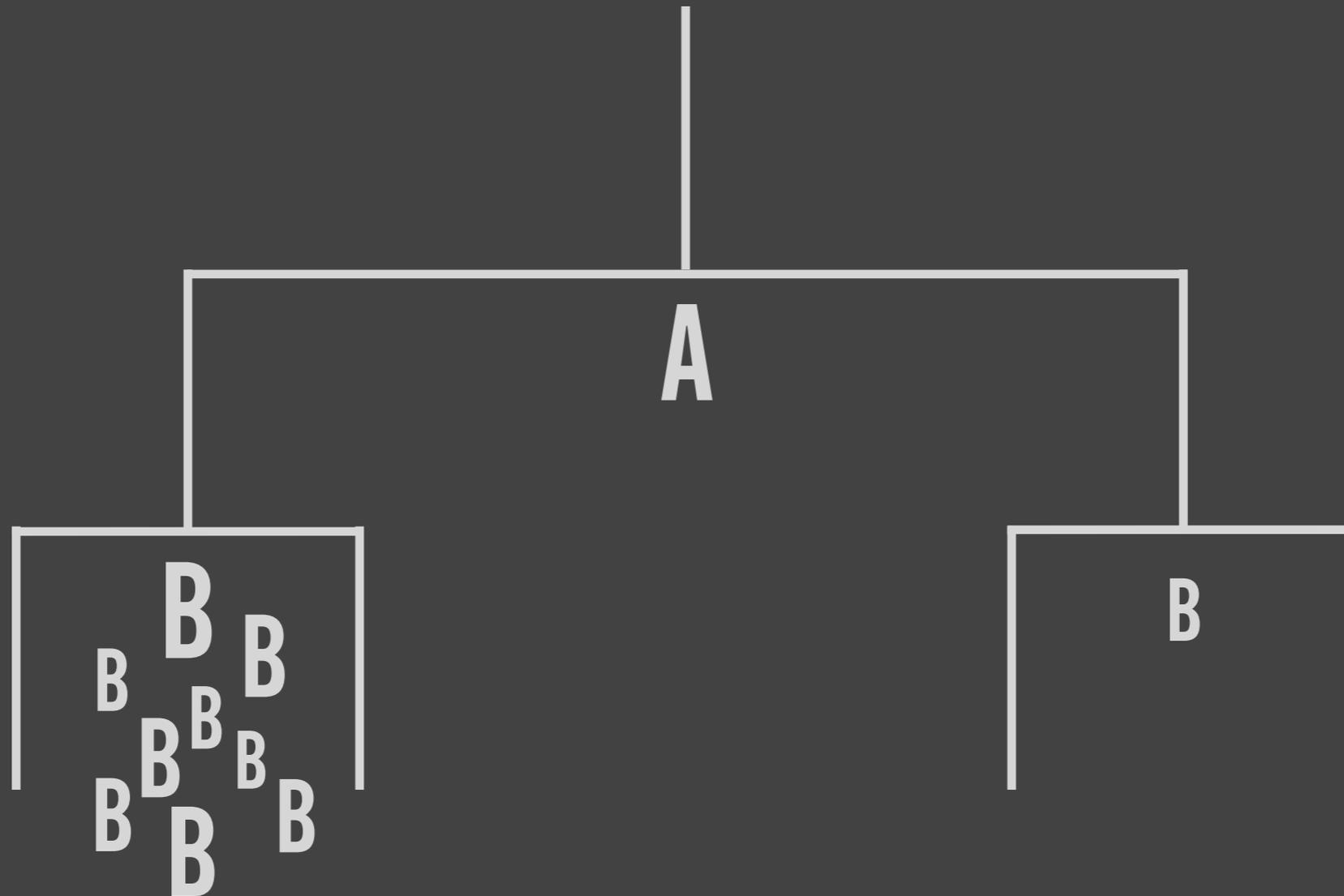
a typical problem



split symmetry



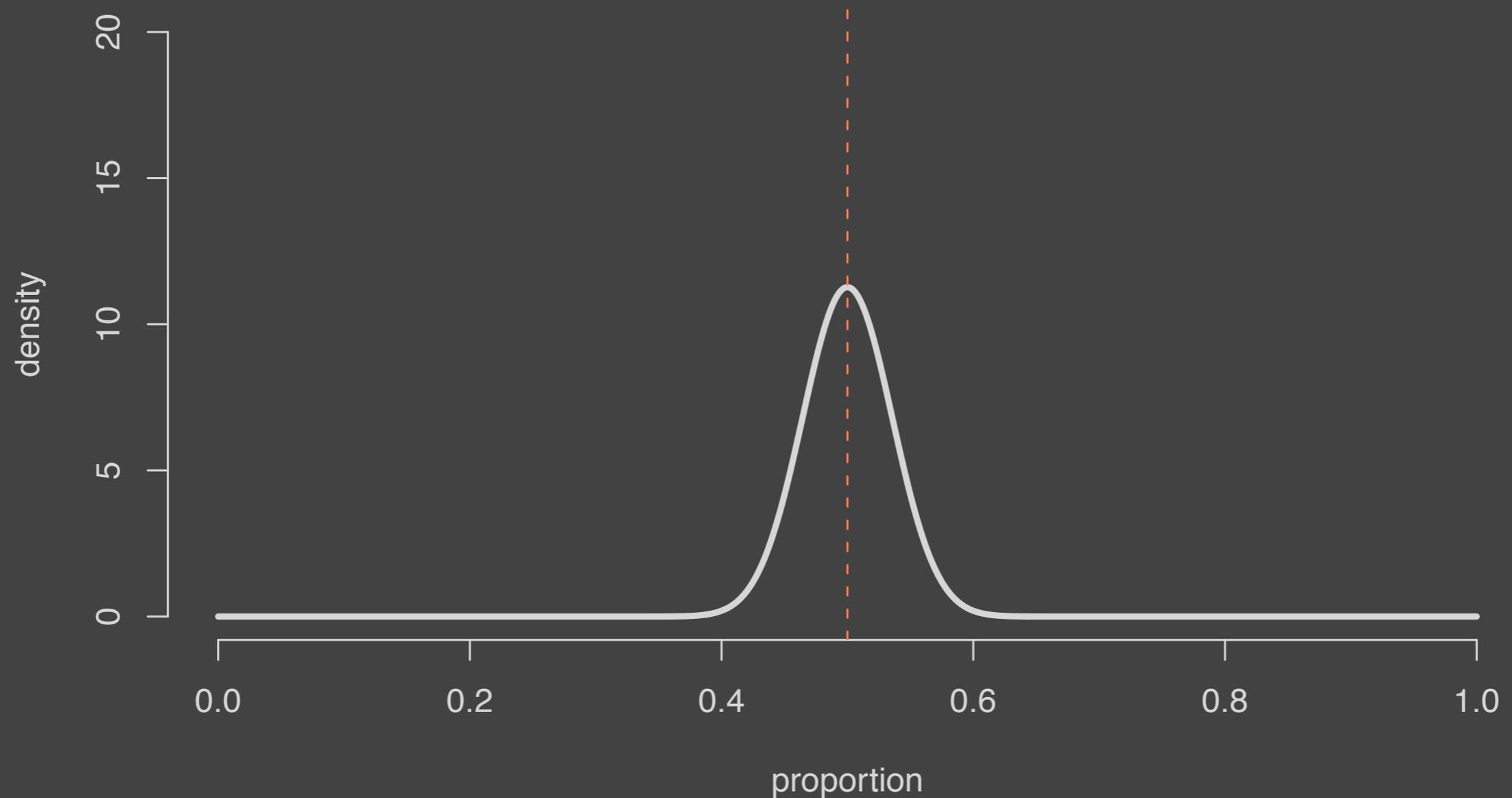
split asymmetry



testing split symmetry

- >> independence of predictors A and B:
 - >> expect B as **left daughter** 50% of the time
 - >> expect B as **right daughter** 50% of the time
 - >> the prior (a beta density) is centered around **0.5**

testing split symmetry



testing split symmetry

>> we update the **prior density parameters** with the observed left/right daughter counts:

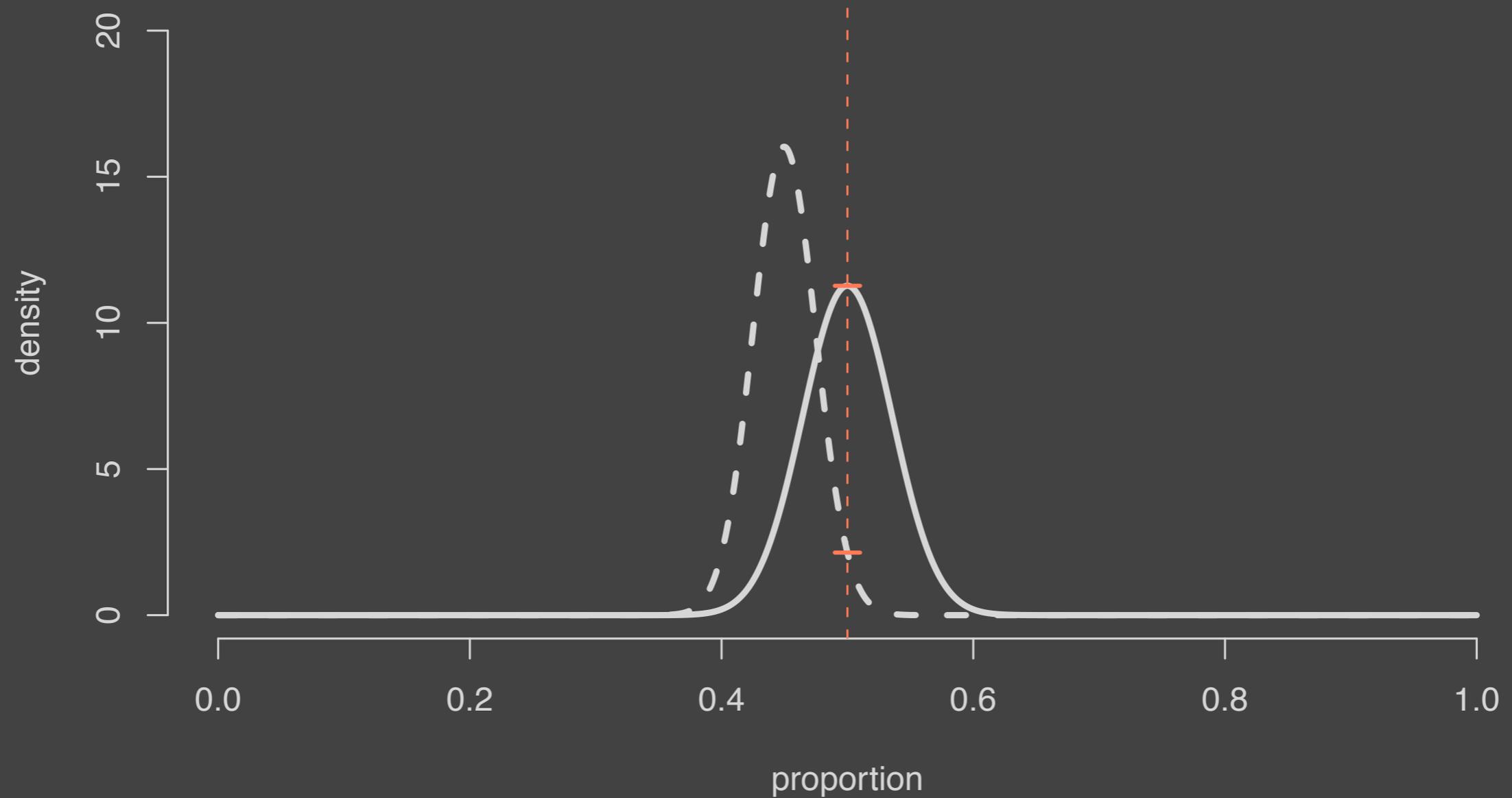
$$\gg a_{\text{posterior}} = a_{\text{prior}} + AB_{\text{left}}$$

$$\gg b_{\text{posterior}} = b_{\text{prior}} + AB_{\text{right}}$$

>> ... and take the **posterior/prior density ratio** at 0.5

>> this is the **Bayes factor**

testing split symmetry



building a graph

$$P_{post} = p_h \frac{BF}{(p_h \cdot BF + 1 - p_h)}$$

- >> using the Bayes factor from each pair of predictors, we calculate the **posterior probability of symmetry**
- >> i.e. that the true proportion is 0.5
- >> we use a high prior probability of the hypothesis (e.g. $p_h = 0.999999$)

building a graph

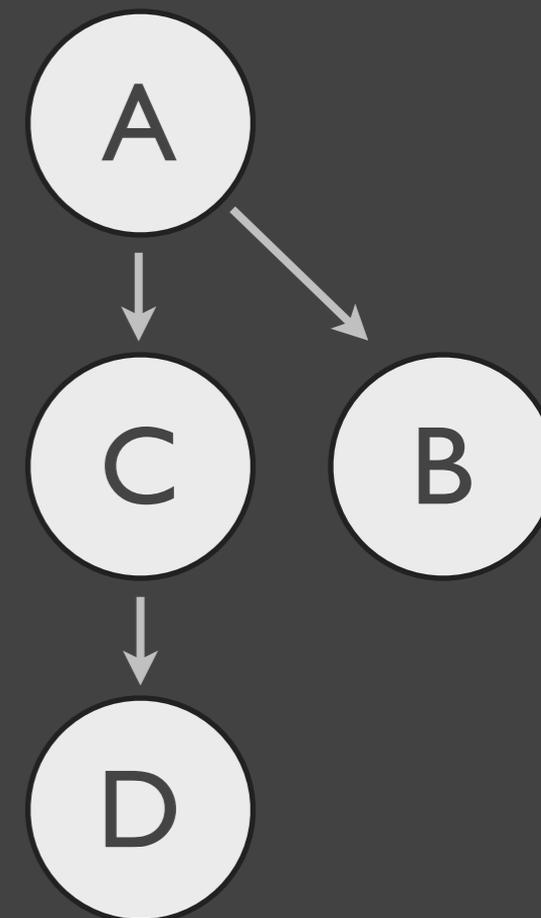
posterior probabilities

	A	B	C	D
A	1	0.001	0.001	0.3
B	0.8	1	0.99	0.2
C	0.99	0.3	1	0.003
D	1	0.89	0.99	1

adjacency matrix

	A	B	C	D
A	0	1	1	0
B	0	0	0	0
C	0	0	0	1
D	0	0	0	0

graph



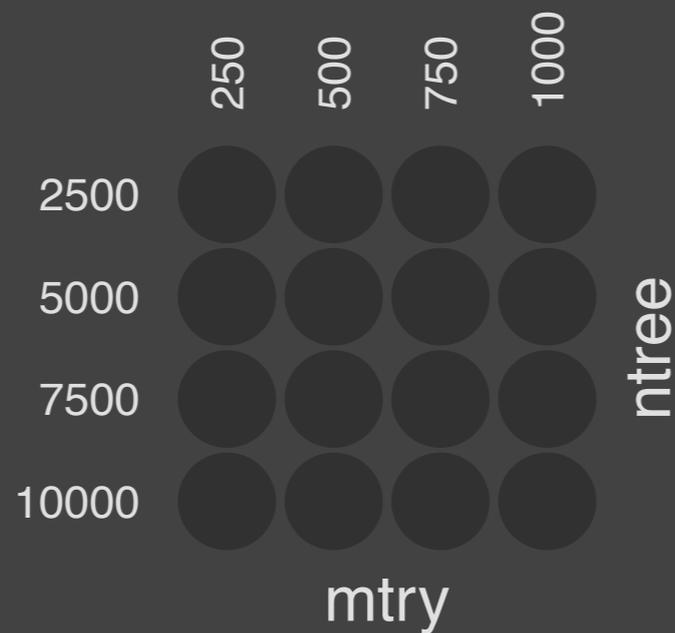
simulations

- >> 1000 binary predictor variables, 200 observations
- >> 3 - 4 predictors participate in true model
- >> tested ability of the method to recover the true topology of the simulated model
- >> recorded TP, FP while varying mtry and ntree

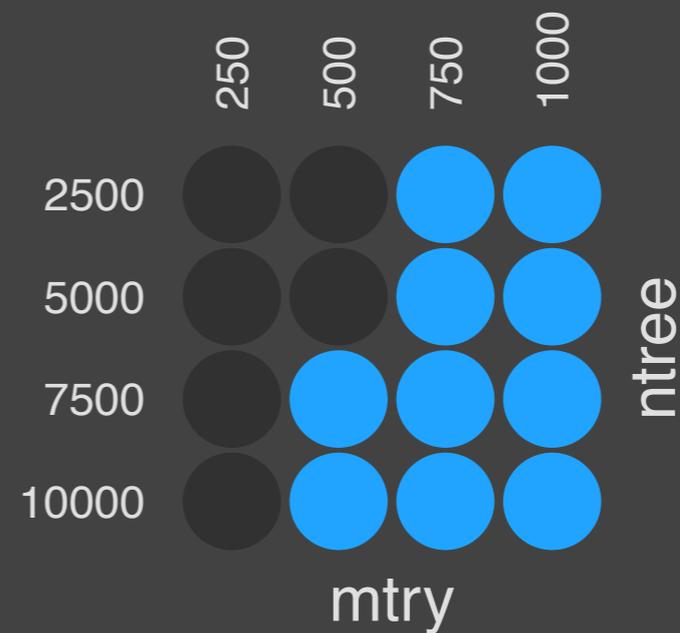
test models



3 independent effects
(i.e. no edges)

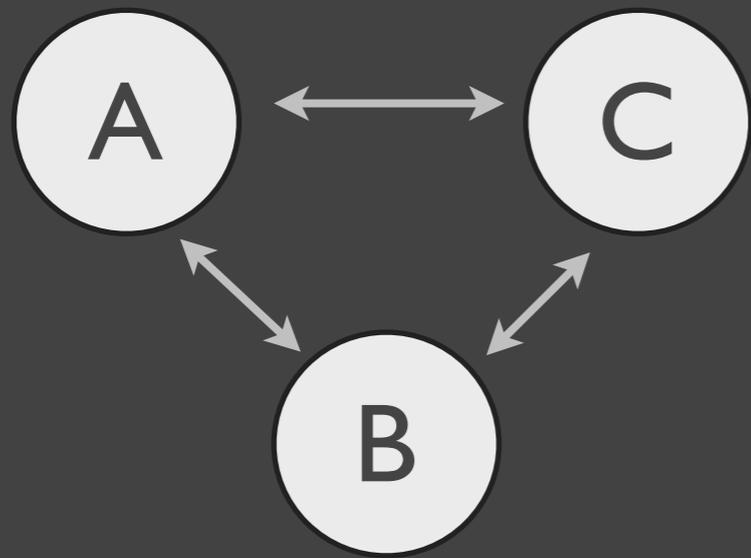


TP

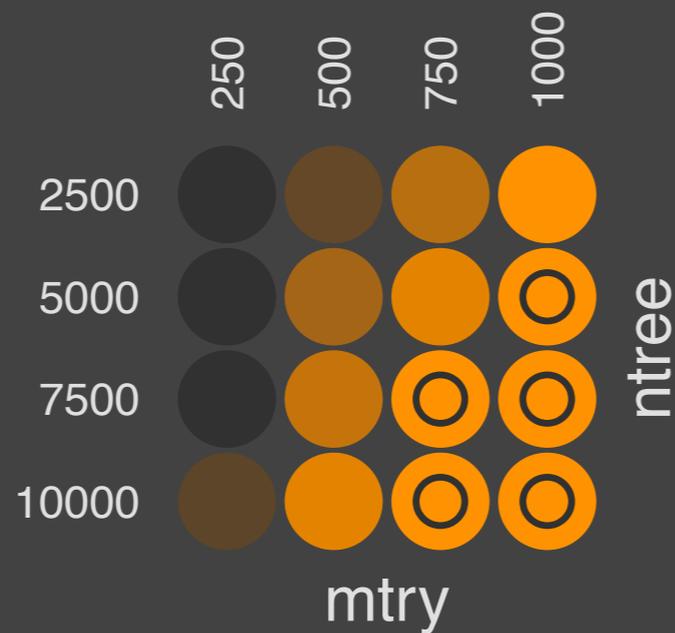


FP

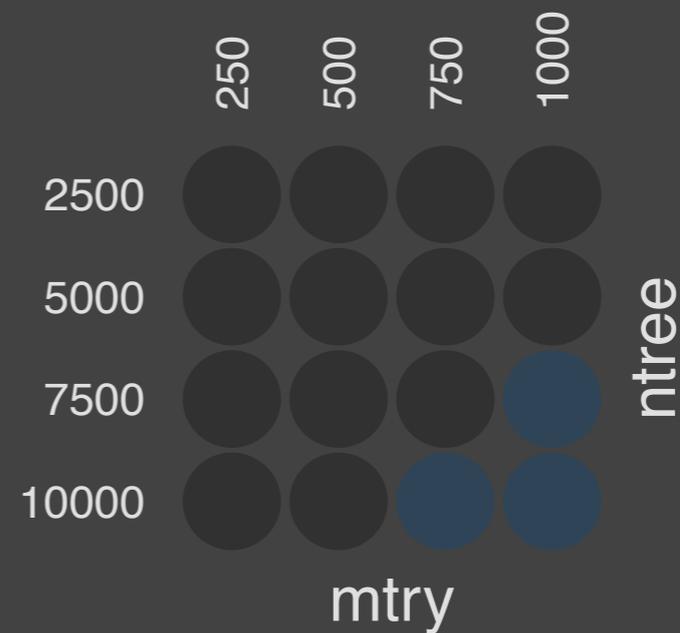
test models



3-way unordered
interaction

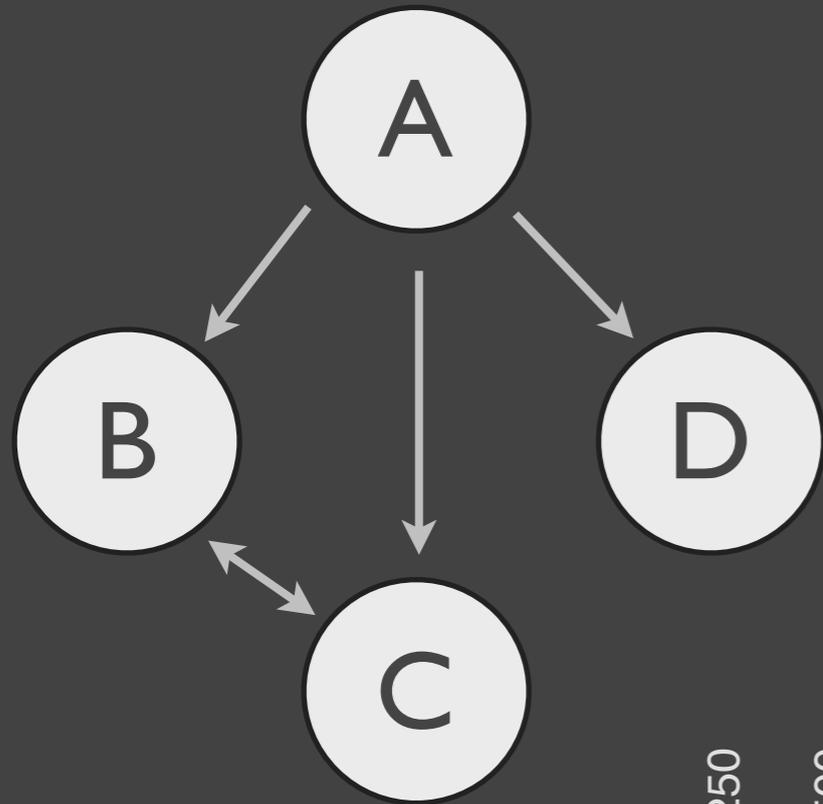


TP

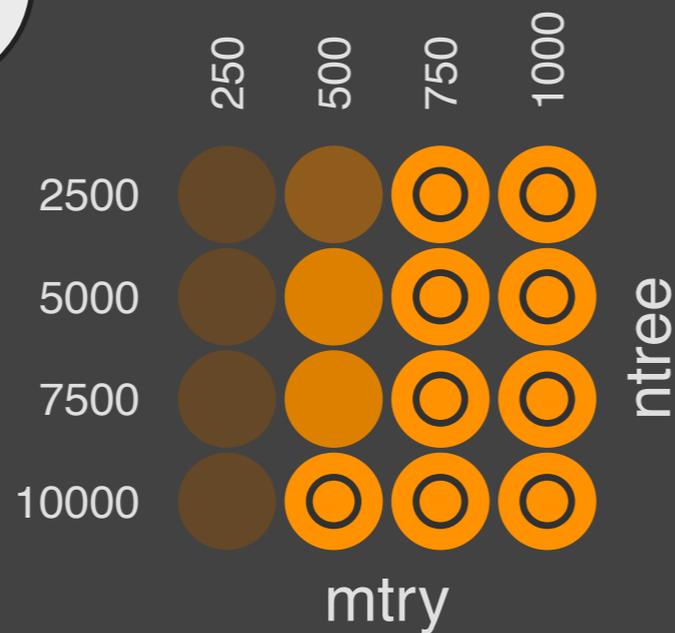


FP

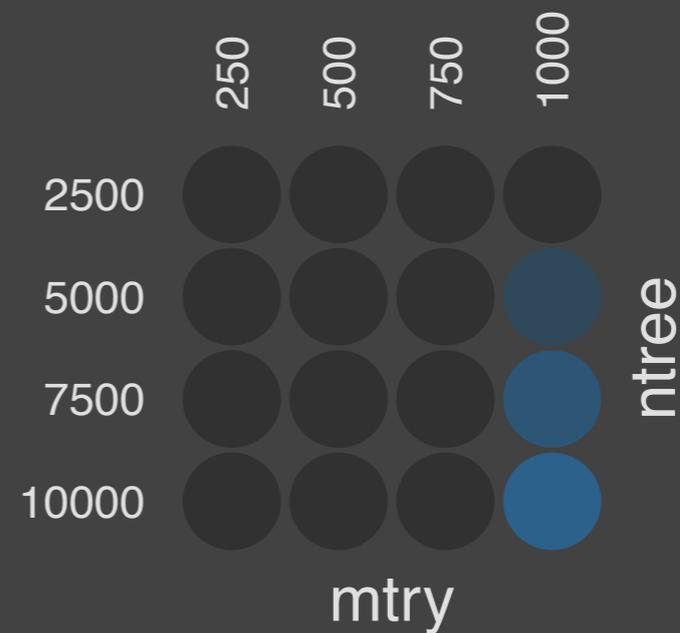
test models



one main effect,
one ordered 3-way interaction,
one ordered 2-way interaction

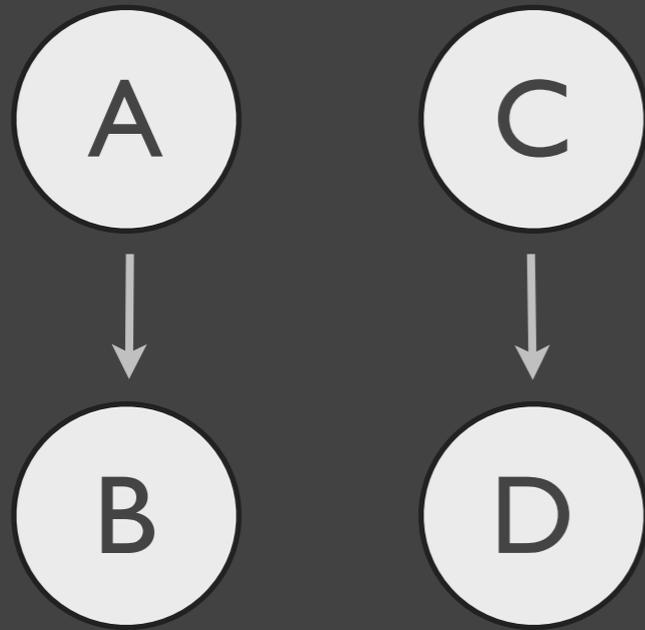


TP

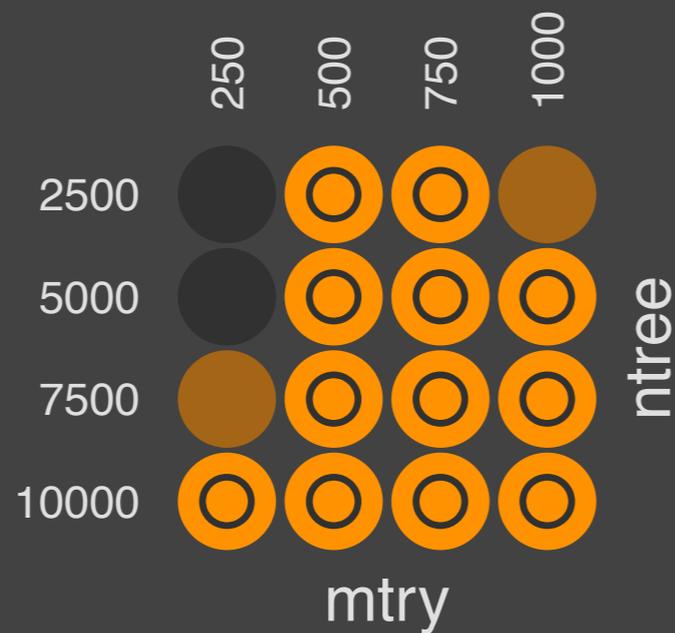


FP

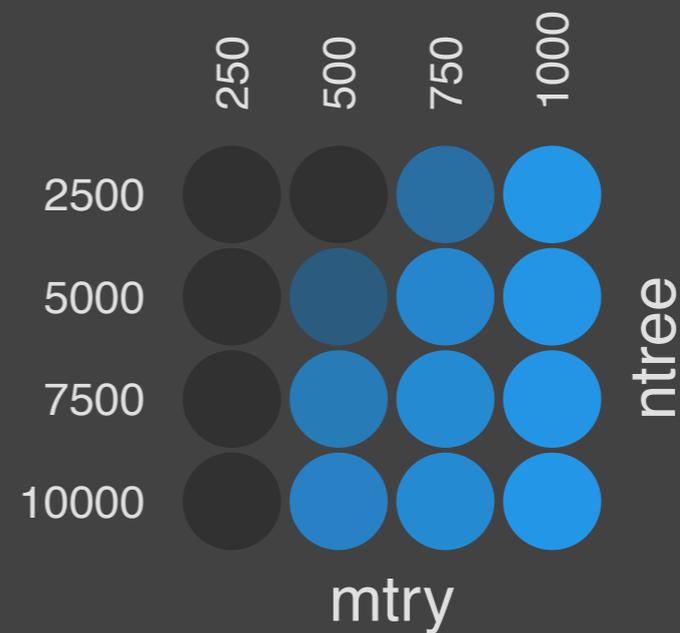
test models



two independent, ordered
two-way interactions



TP



FP

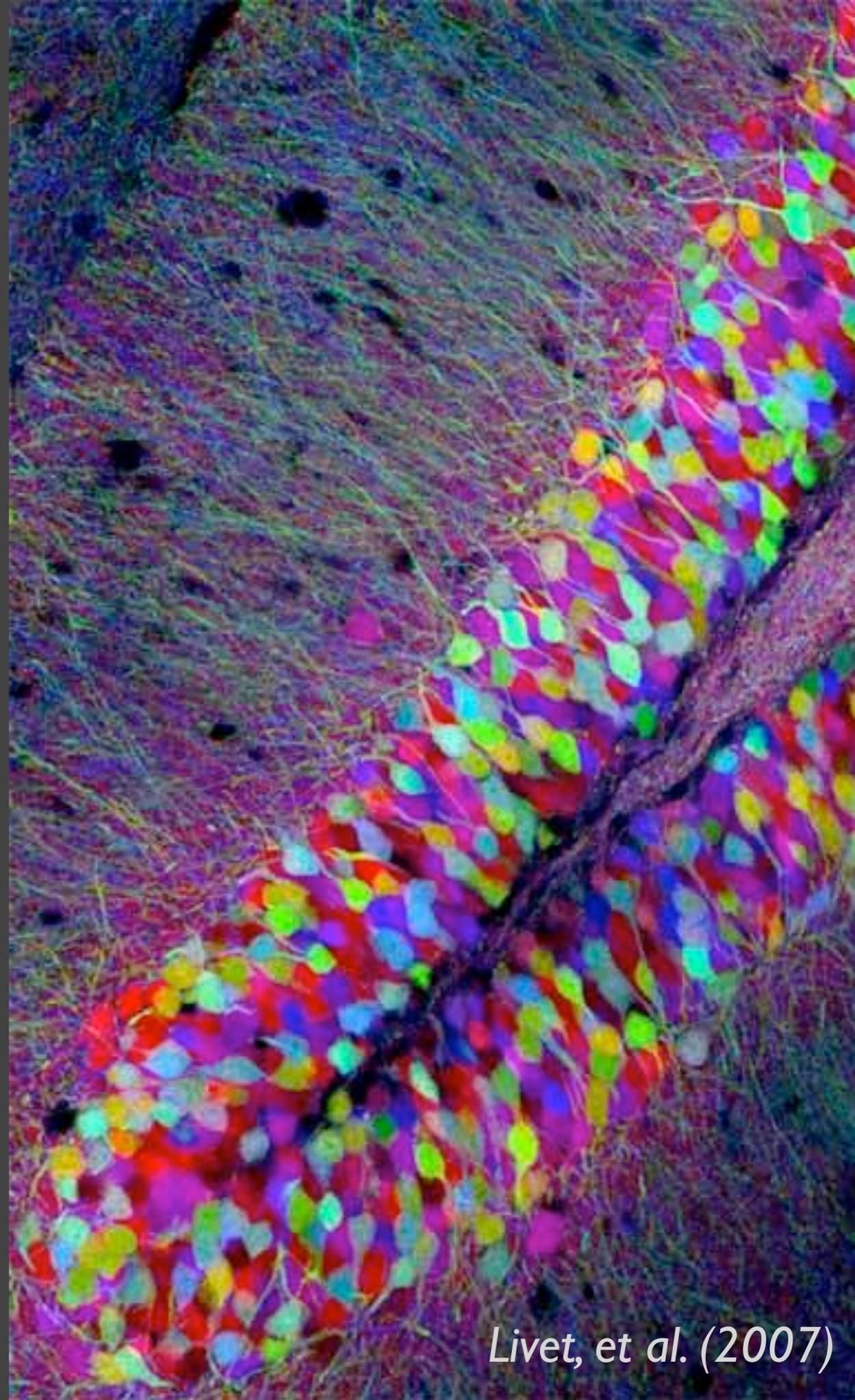
real world

>> Gabrb3

>> neurotransmitter
receptor subunit

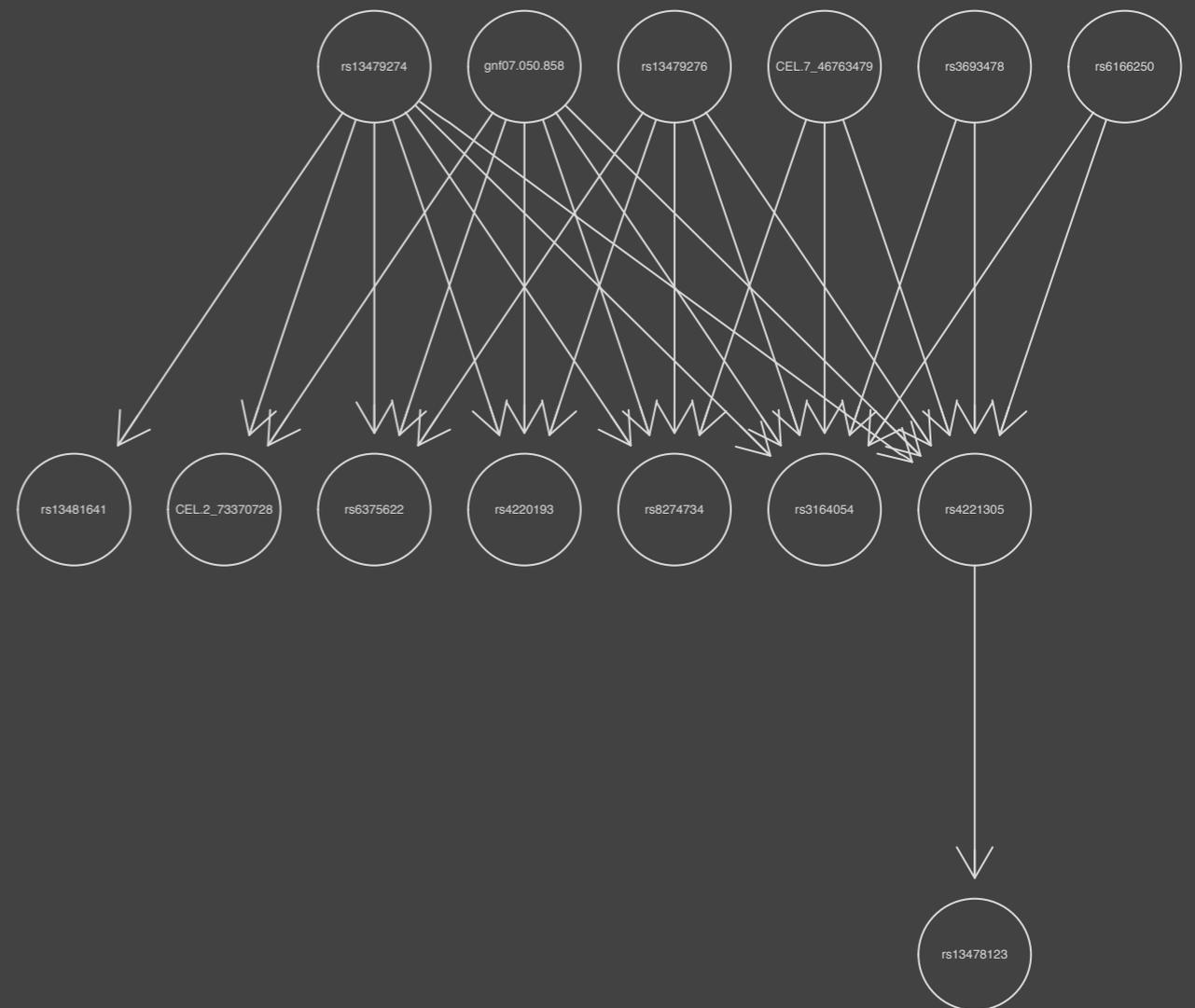
>> absence (or
misexpression) yields
autism-like behavior

>> what mechanisms
influence Gabrb3
expression?



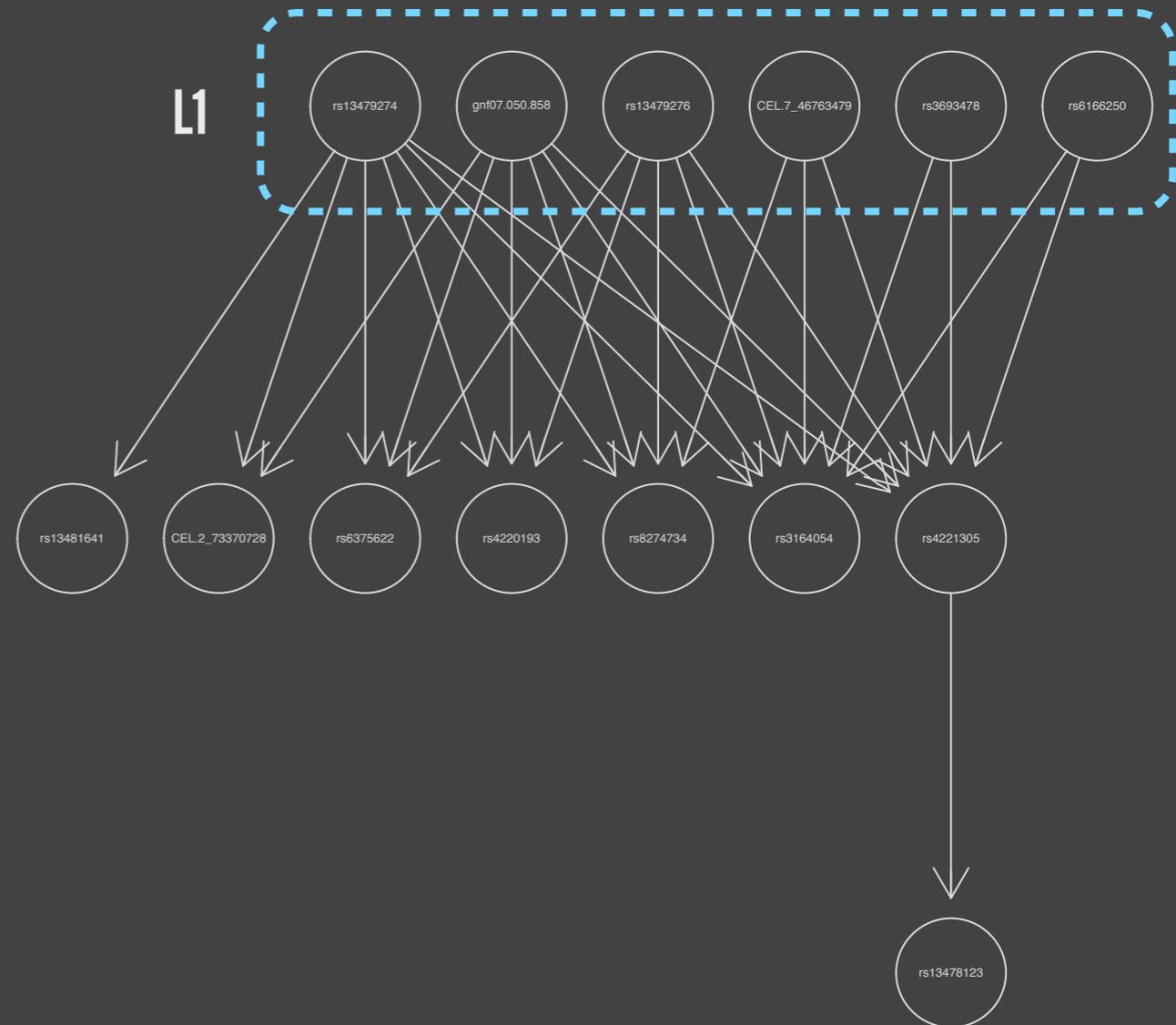
regulation of Gabrb3

grow an RF that **regresses** hippocampal Gabrb3 **expression** on the **genotypes** ($m = 3,794$) of the same population of mice, then **extract the interaction graph**



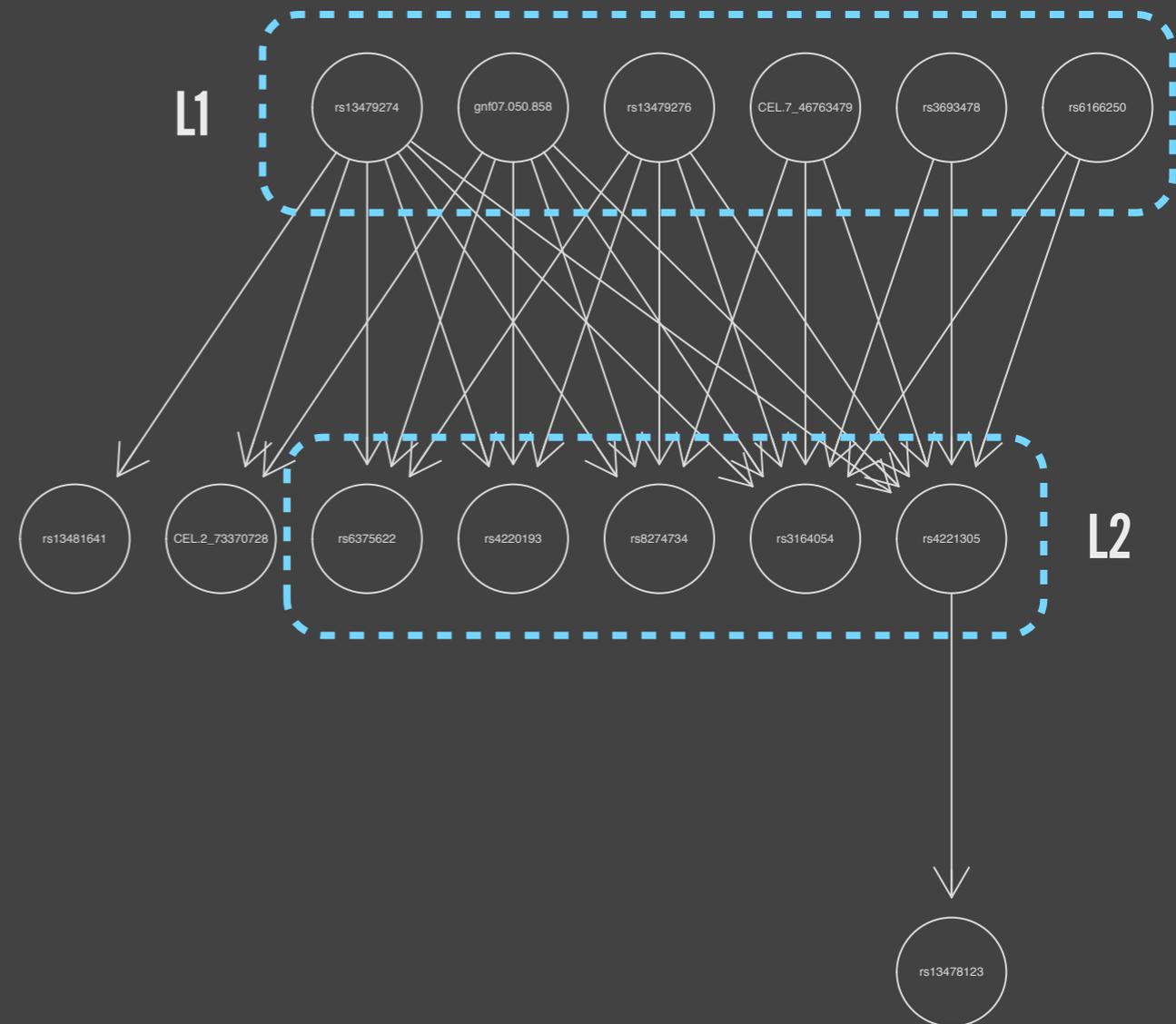
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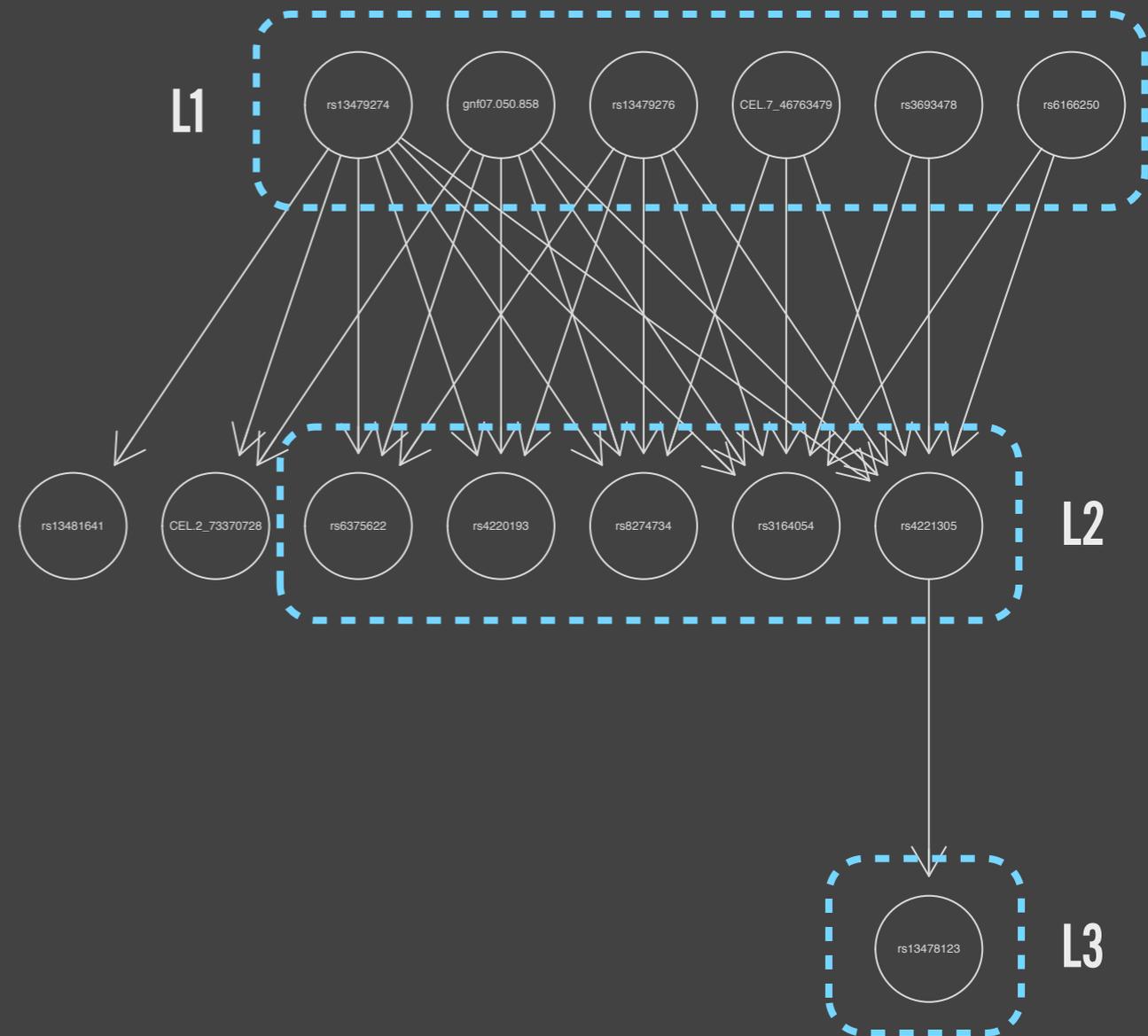
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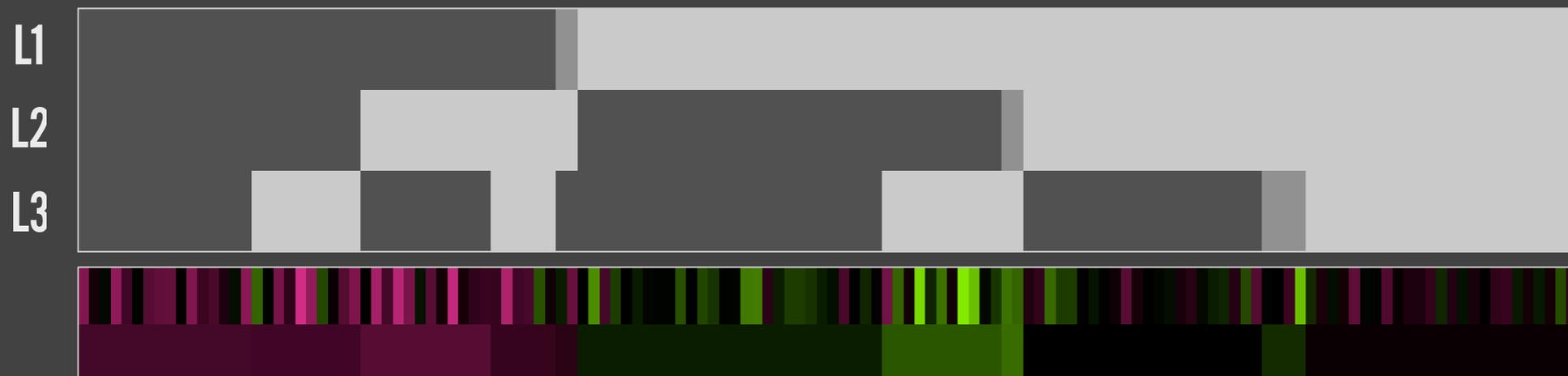
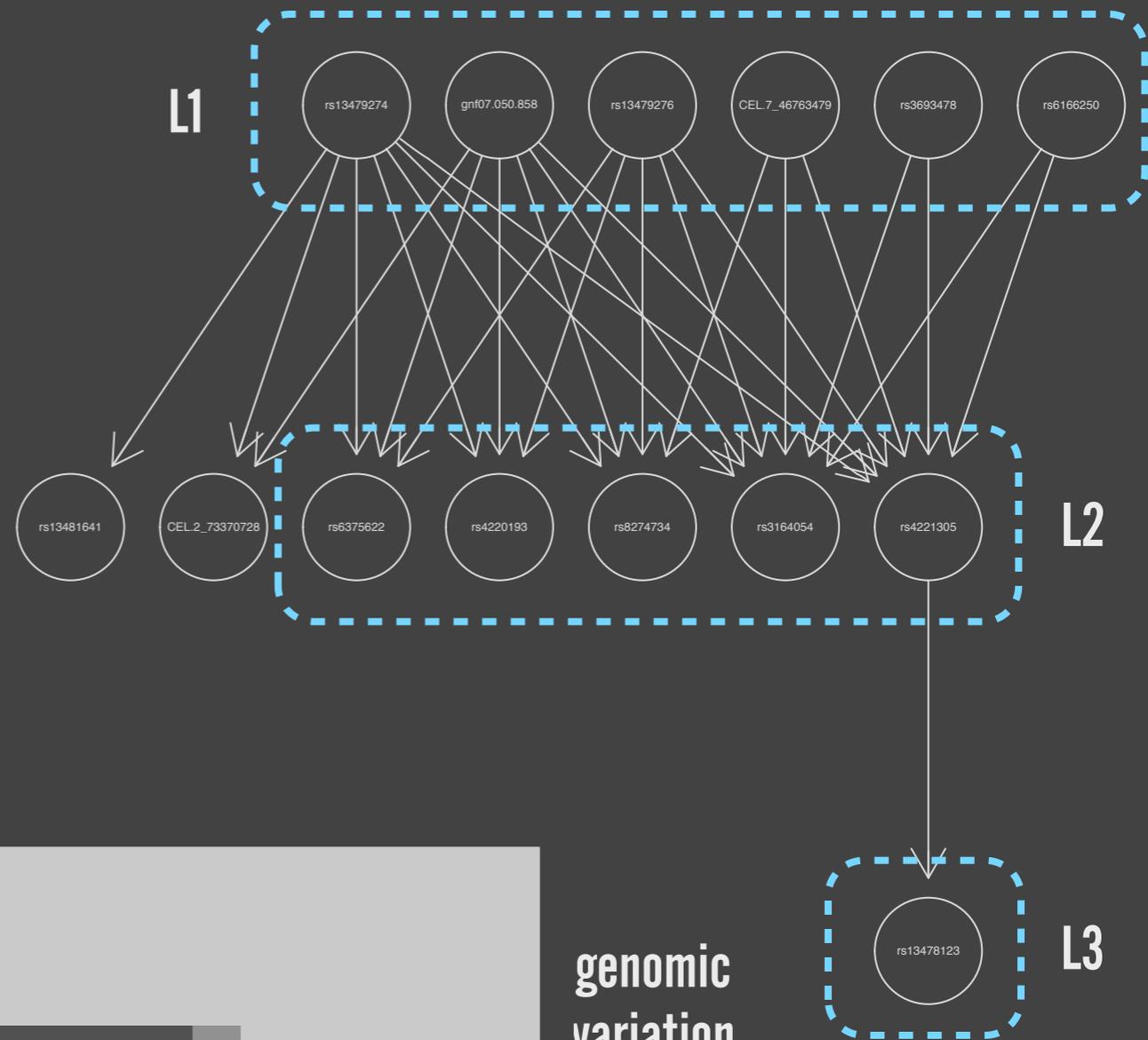
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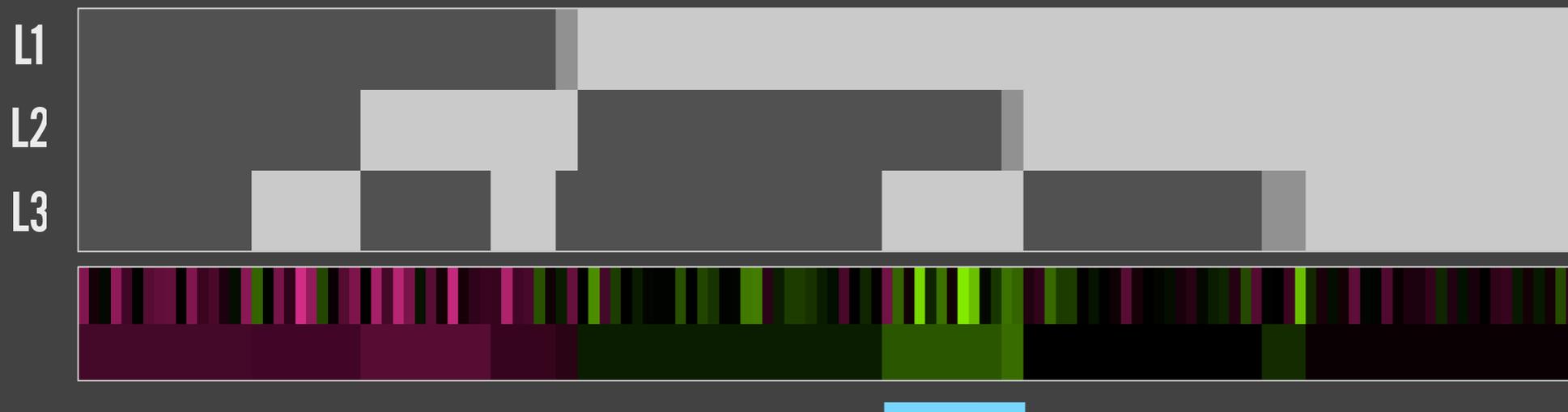
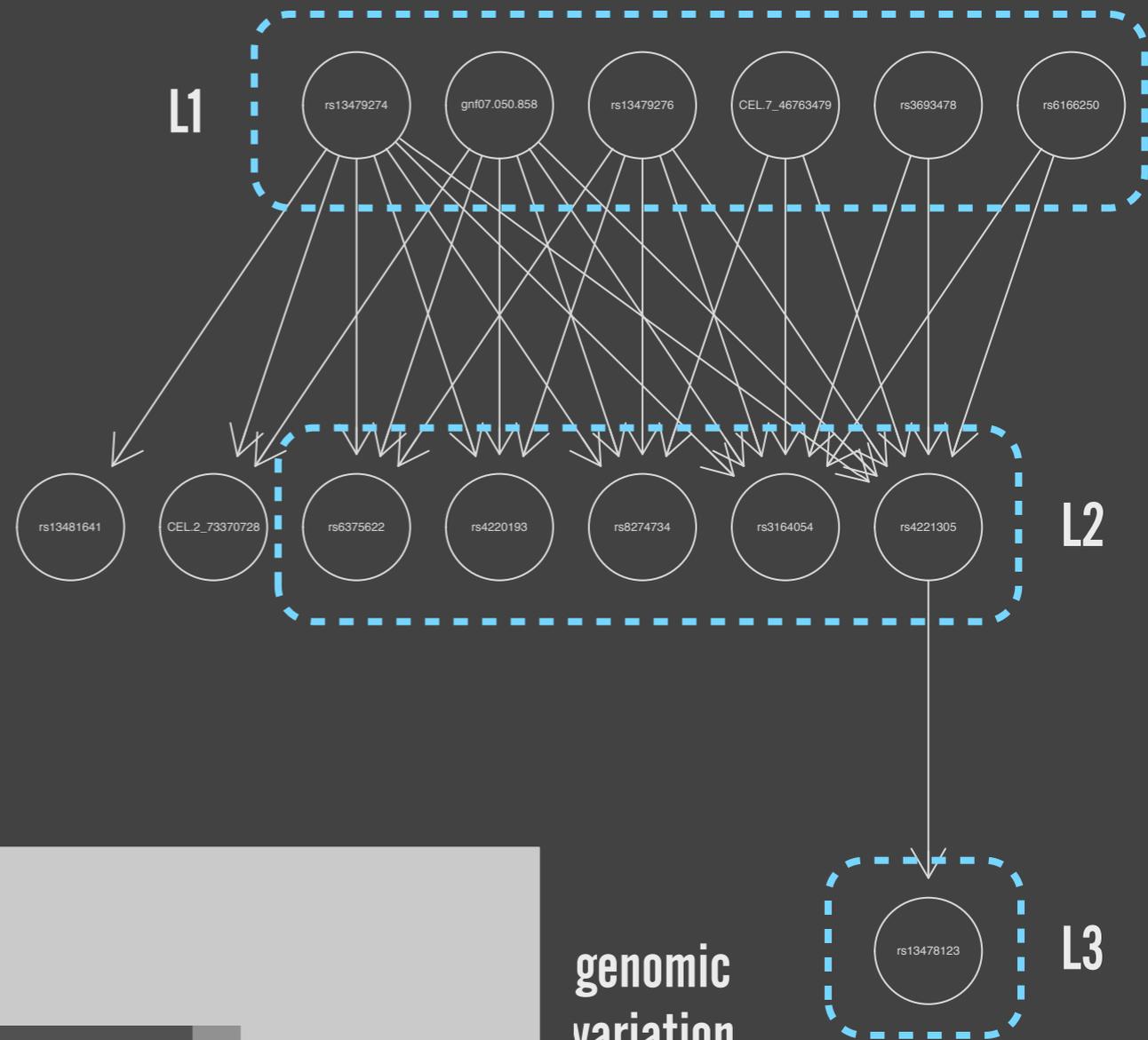


genomic variation

Gabrb3 expression

regulation of Gabrb3

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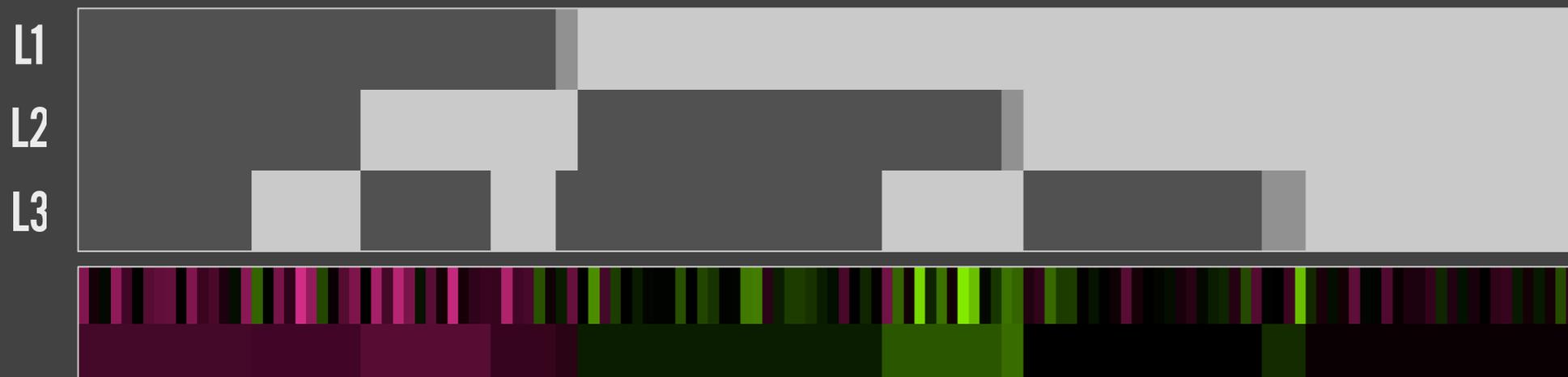
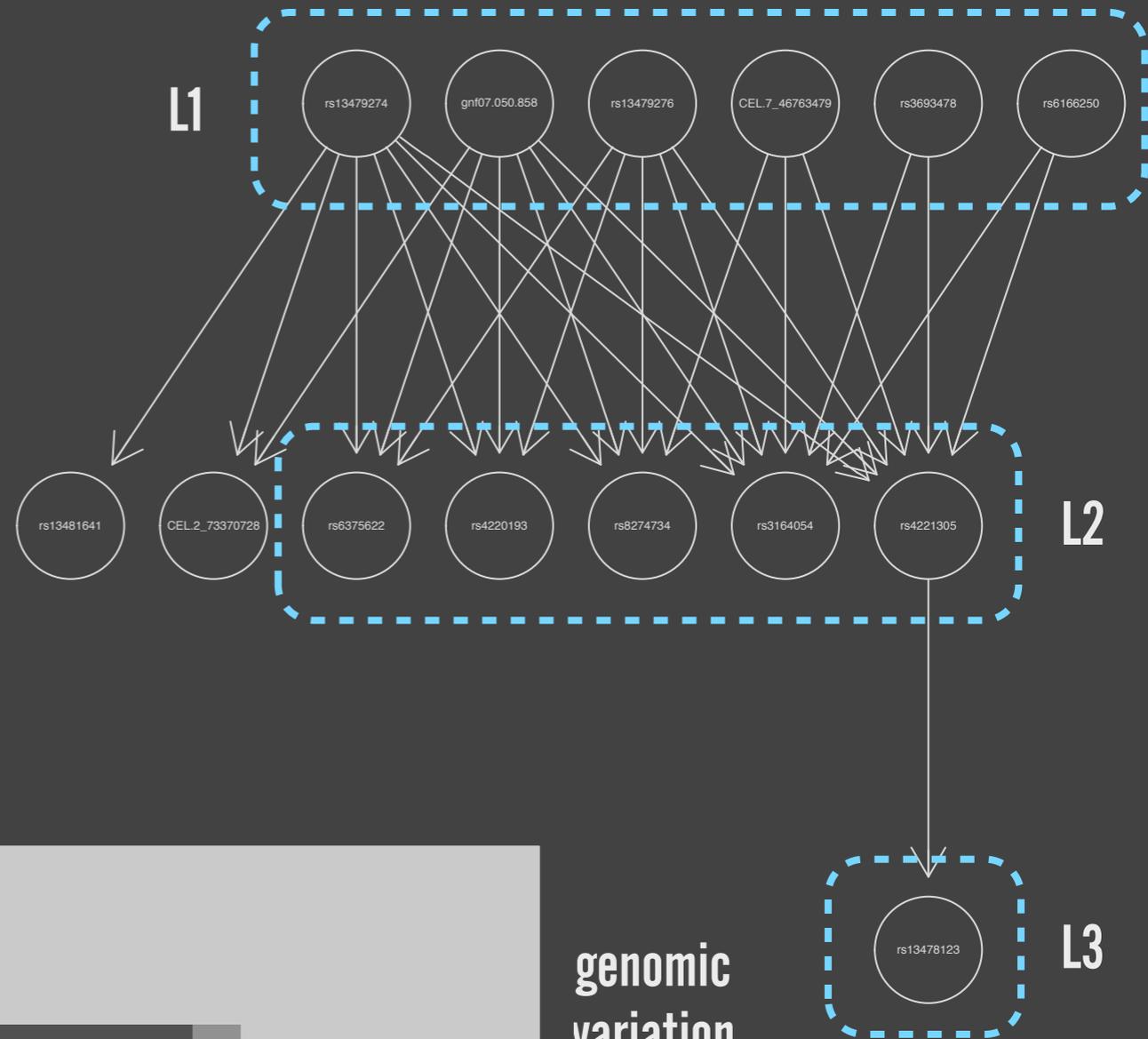


genomic variation

Gabrb3 expression

regulation of Gabrb3

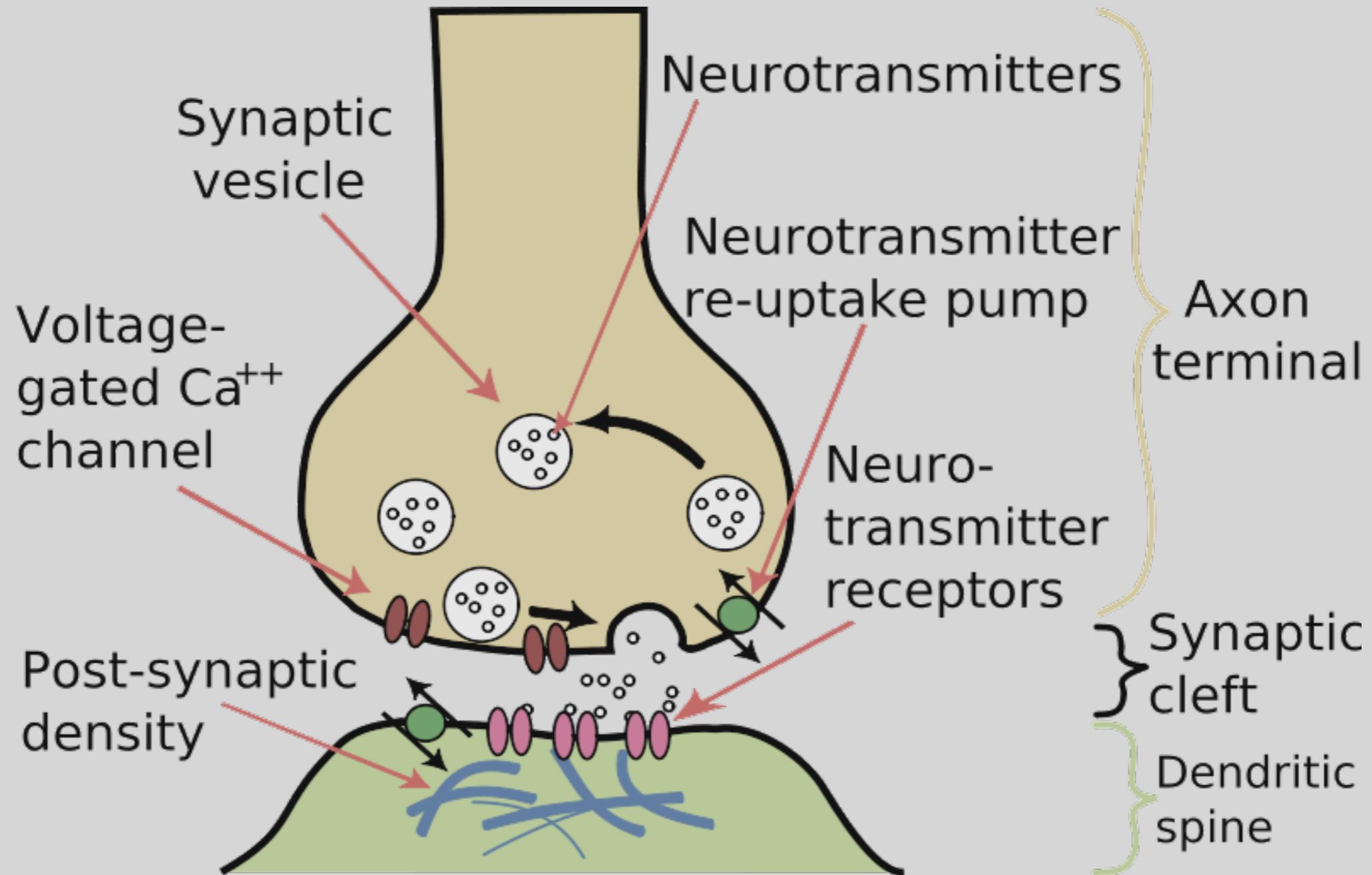
- L1 - **Gabrb3** (cis effect)
- L2 - **Dscam** (axon guidance)
- L3 - **Magi2** (synaptic scaffolding)



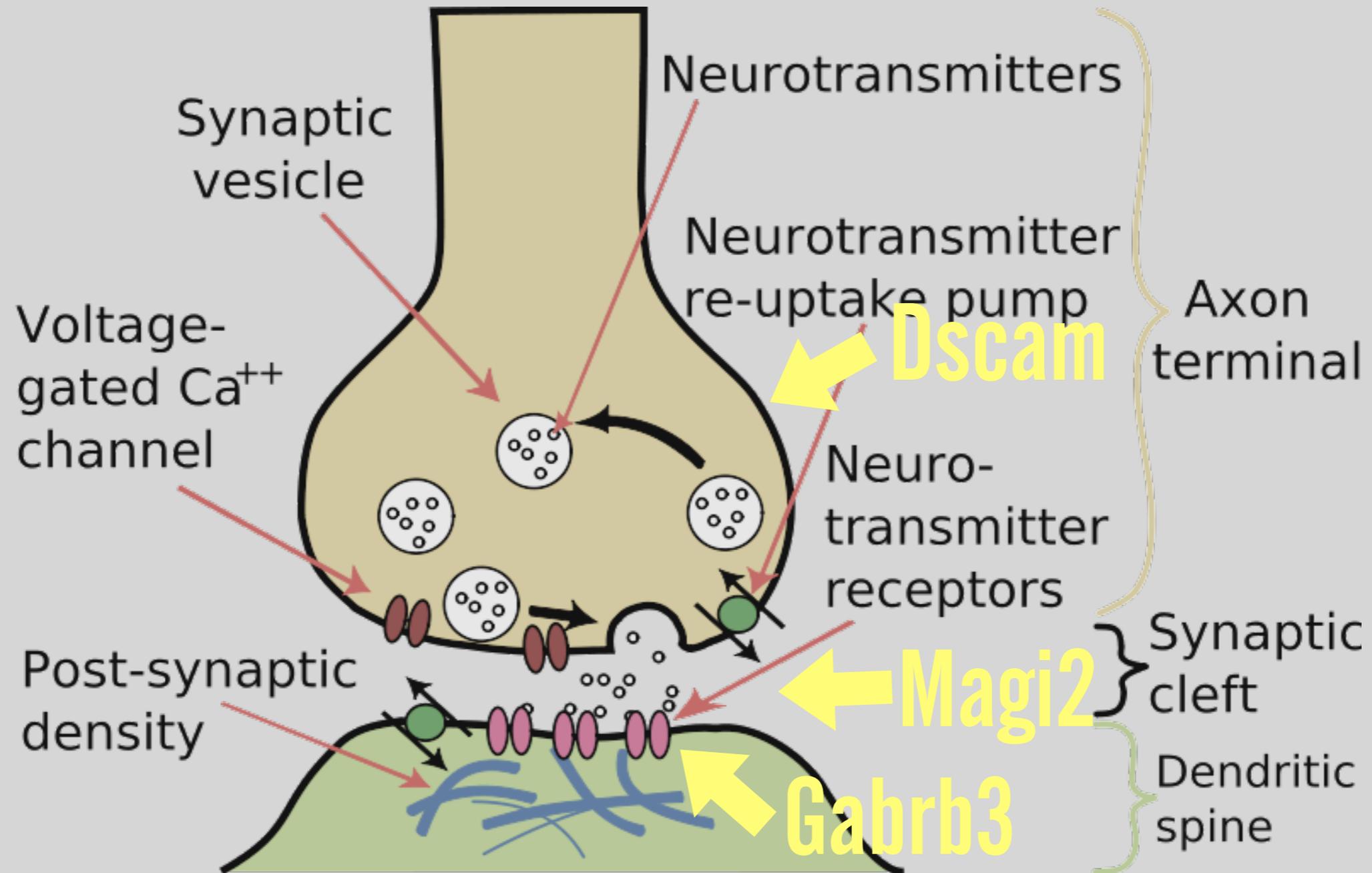
genomic
variation

Gabrb3 expression

the context



the context



conclusion

- >> (a) **symmetry of transitions** between subsequently selected variables can give us clues about the **degree of dependence** between them
- >> constructing a graph of these dependencies can illustrate the **emergent dependency structure** of the predictors in light of the response

forthcoming...

- >> does this work for continuous and categorical predictors?
- >> what about correlated predictors?
- >> strategy for choosing optimal m_{try} and n_{tree} ?

RF is an example of a tool that is useful in doing analyses of scientific data.

But the cleverest algorithms are **no substitute for human intelligence and knowledge of the data** in the problem.

Take the output of random forests not as absolute truth, but as smart computer generated guesses that may be **helpful in leading to a deeper understanding of the problem.**

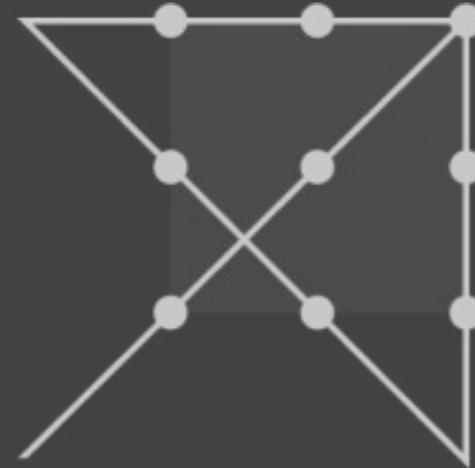
- Breiman & Cutler

Thanks!



HELMHOLTZ
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Alliance on Systems Biology



KTF

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FOUNDATION GMBH

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