

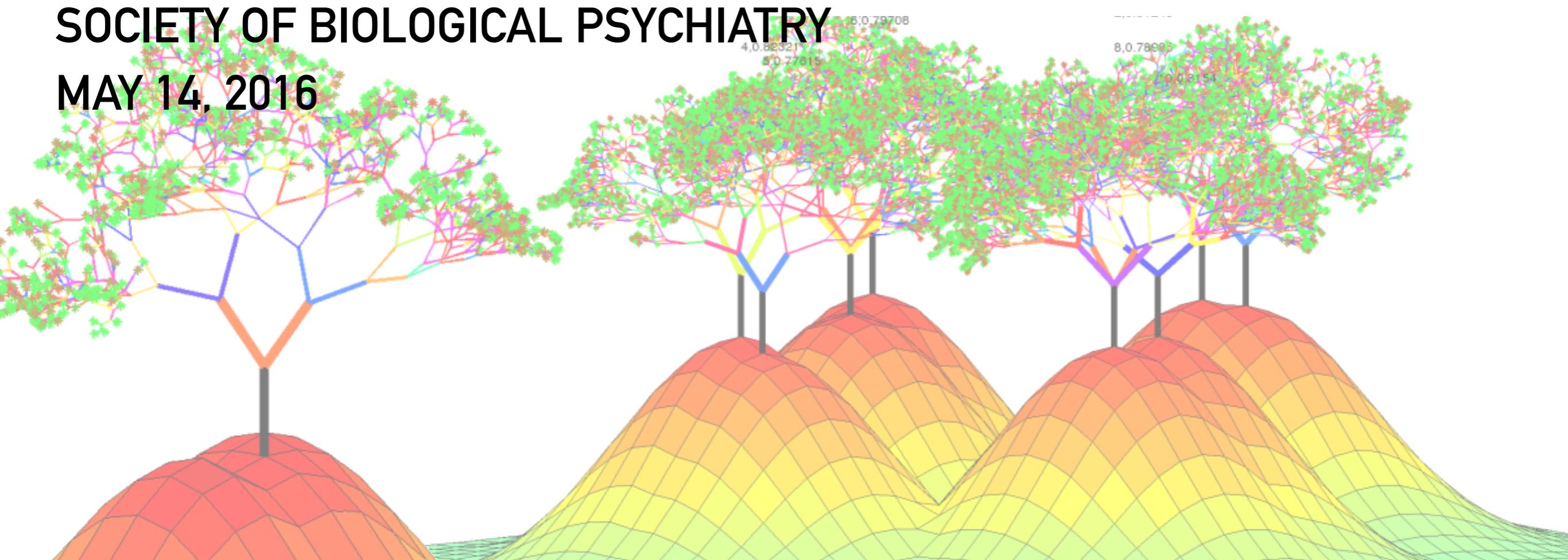
MULTIVARIATE PATTERN ANALYSIS OF GENOTYPE-PHENOTYPE RELATIONSHIPS IN SCHIZOPHRENIA

AMANDA ZHEUTLIN

YALE UNIVERSITY

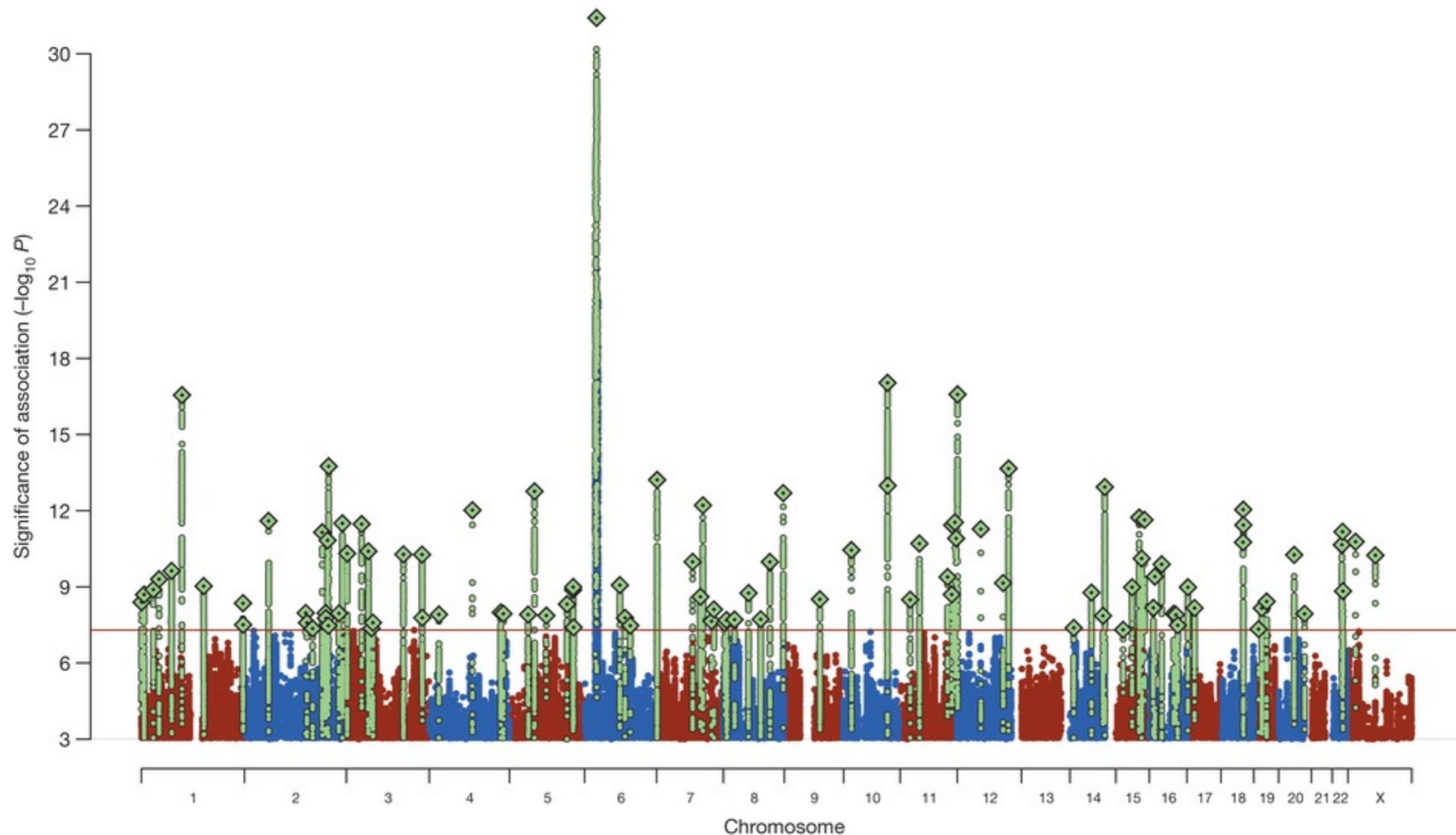
SOCIETY OF BIOLOGICAL PSYCHIATRY

MAY 14, 2016



SCHIZOPHRENIA GENETICS

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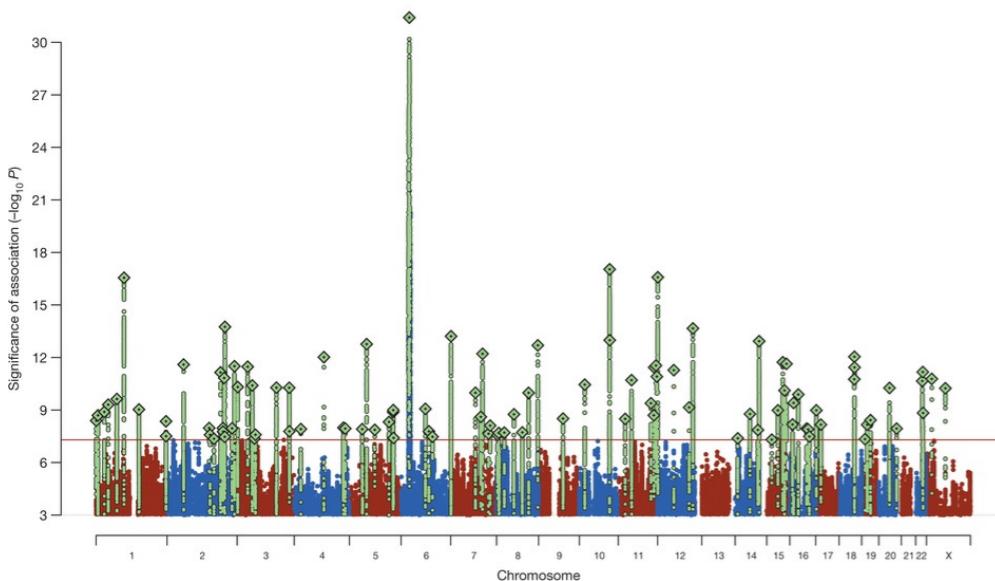


BACKGROUND

HOW DO GENES CONFER RISK?

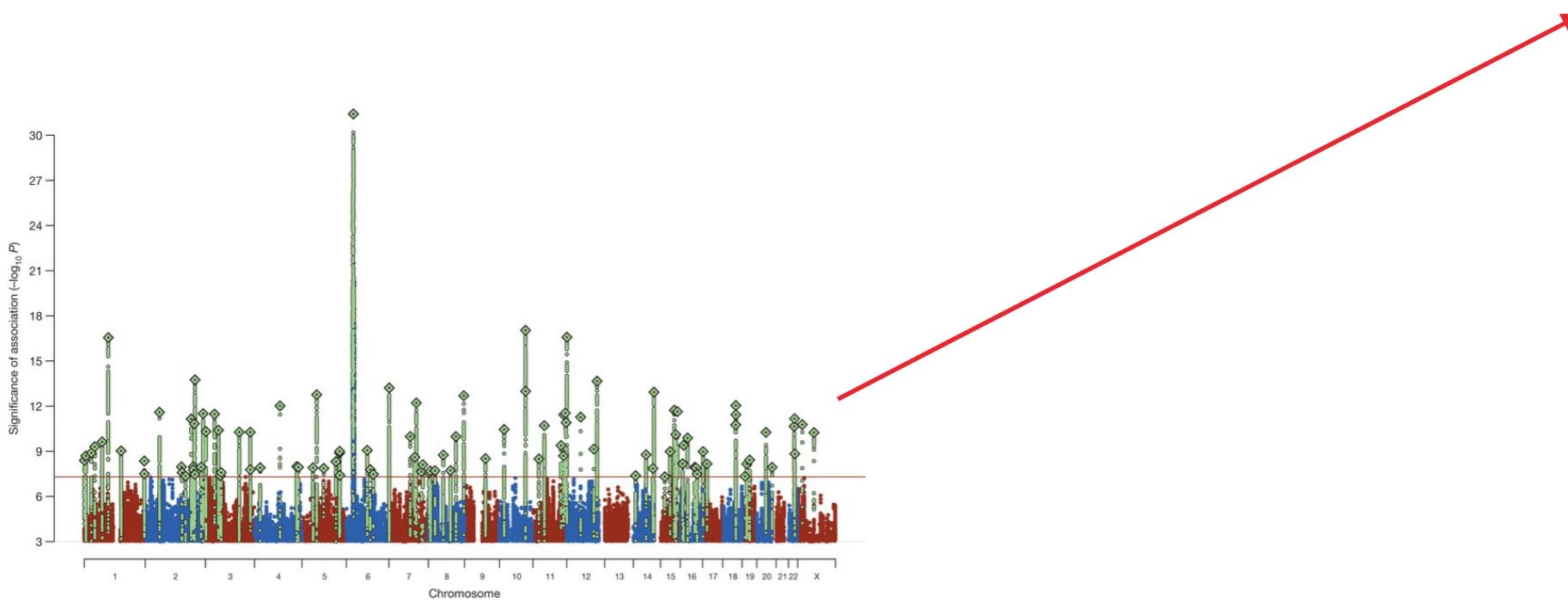
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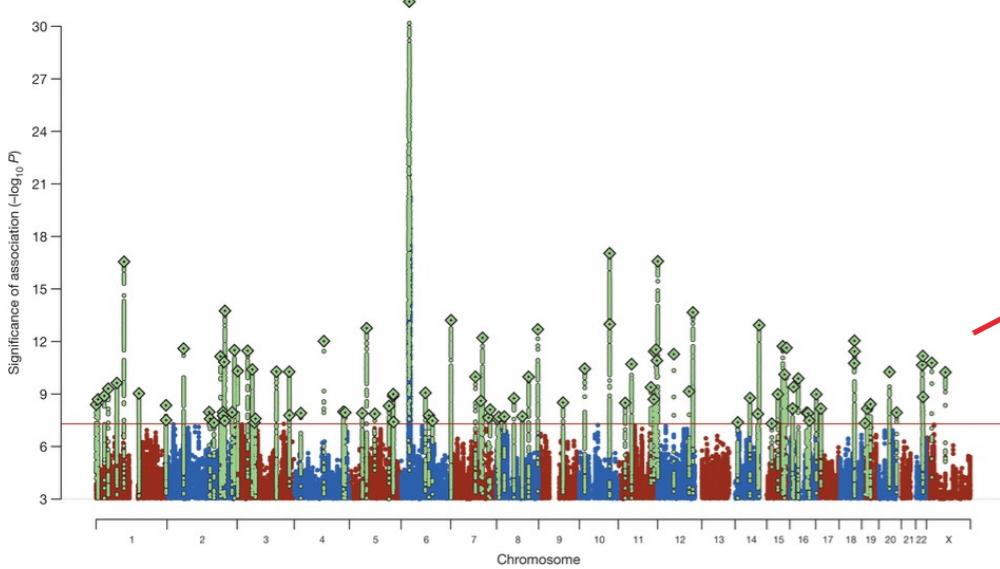
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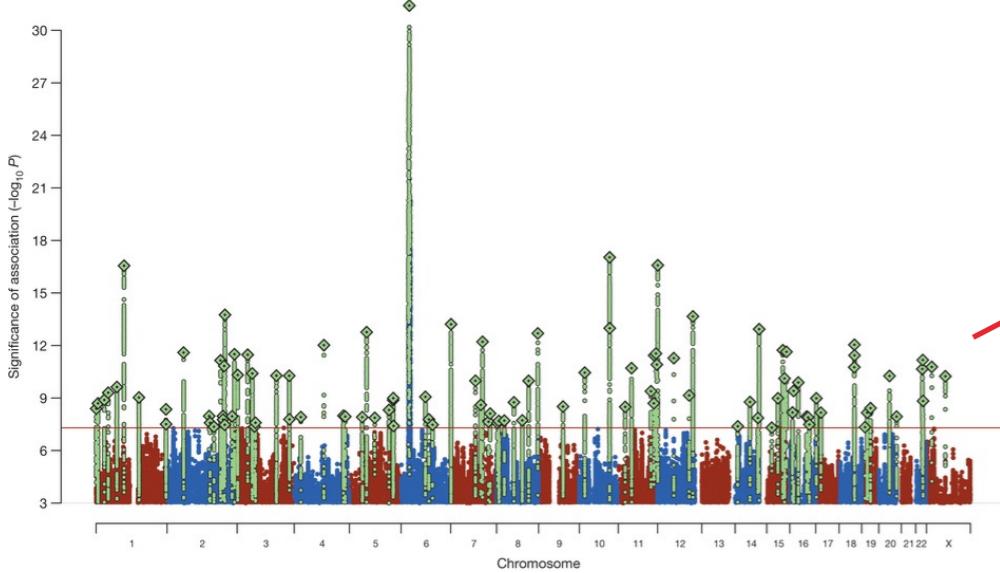
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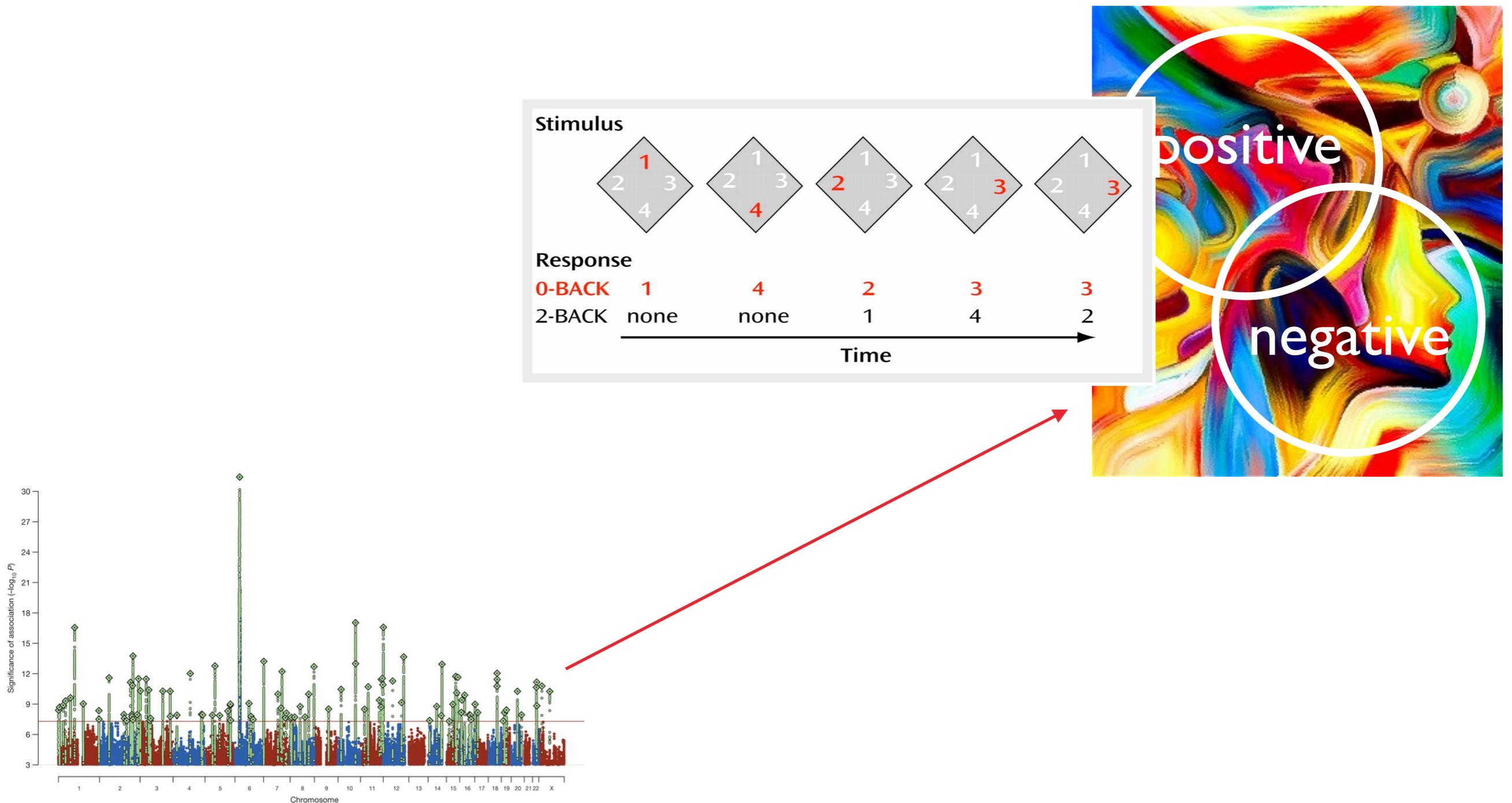
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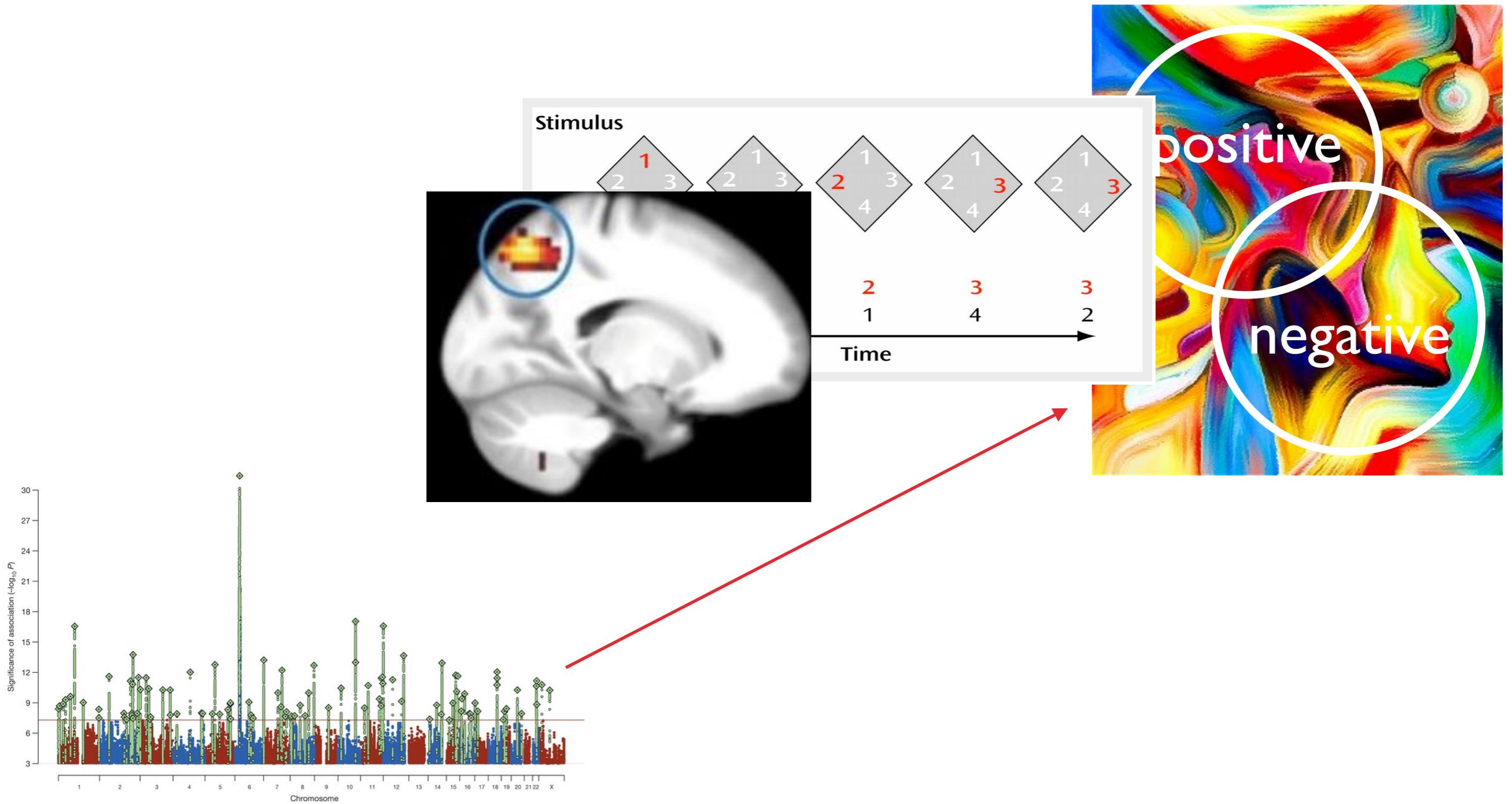
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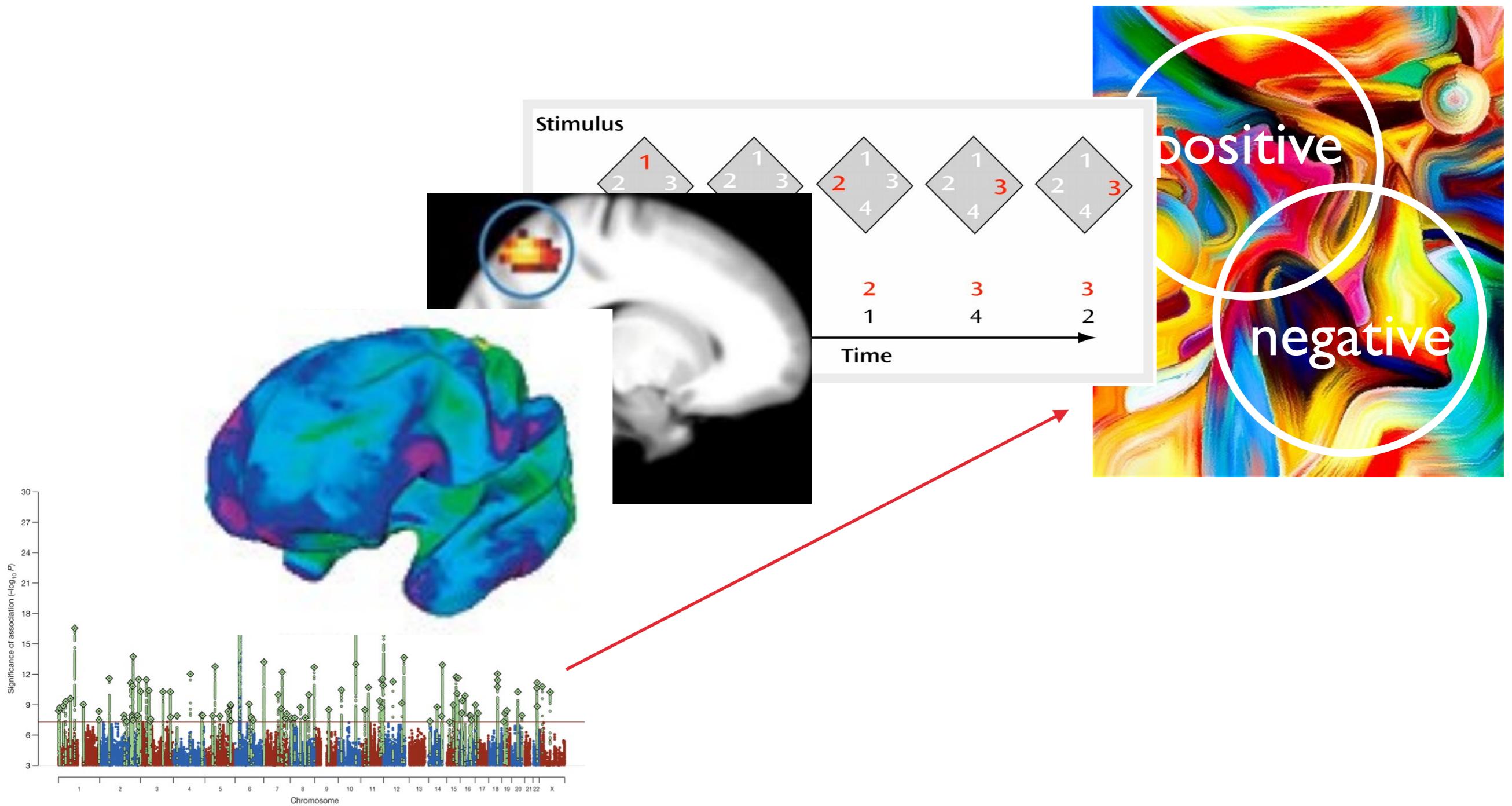
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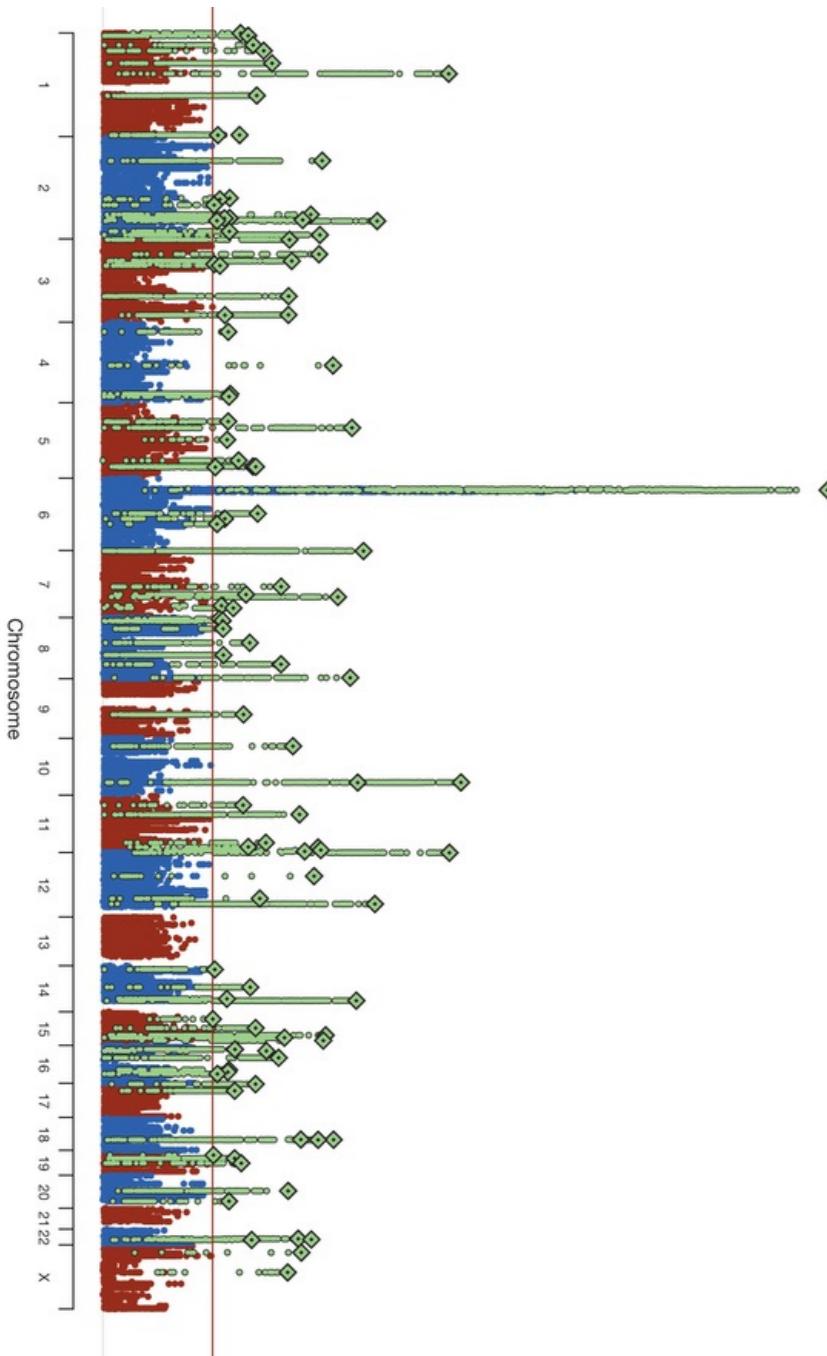
- ▶ Are there differential genotypic effects by phenotype?

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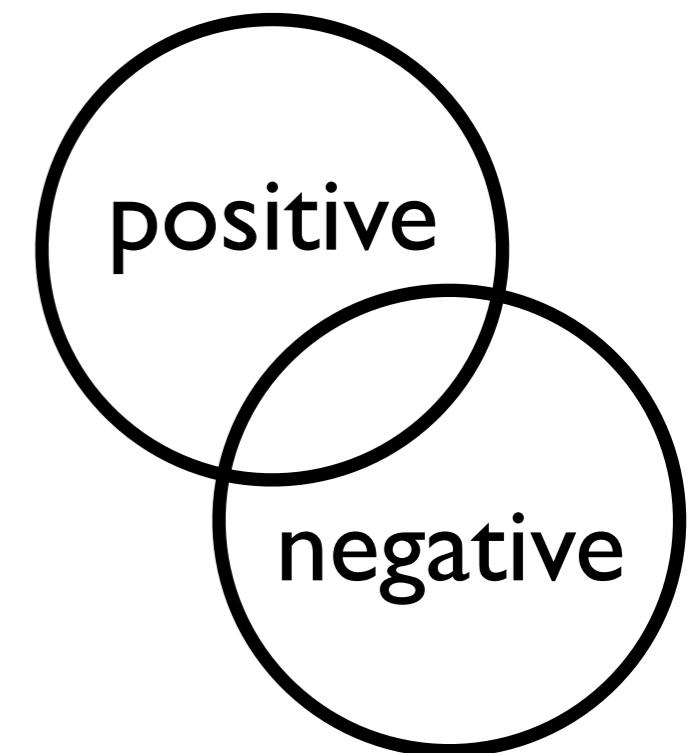
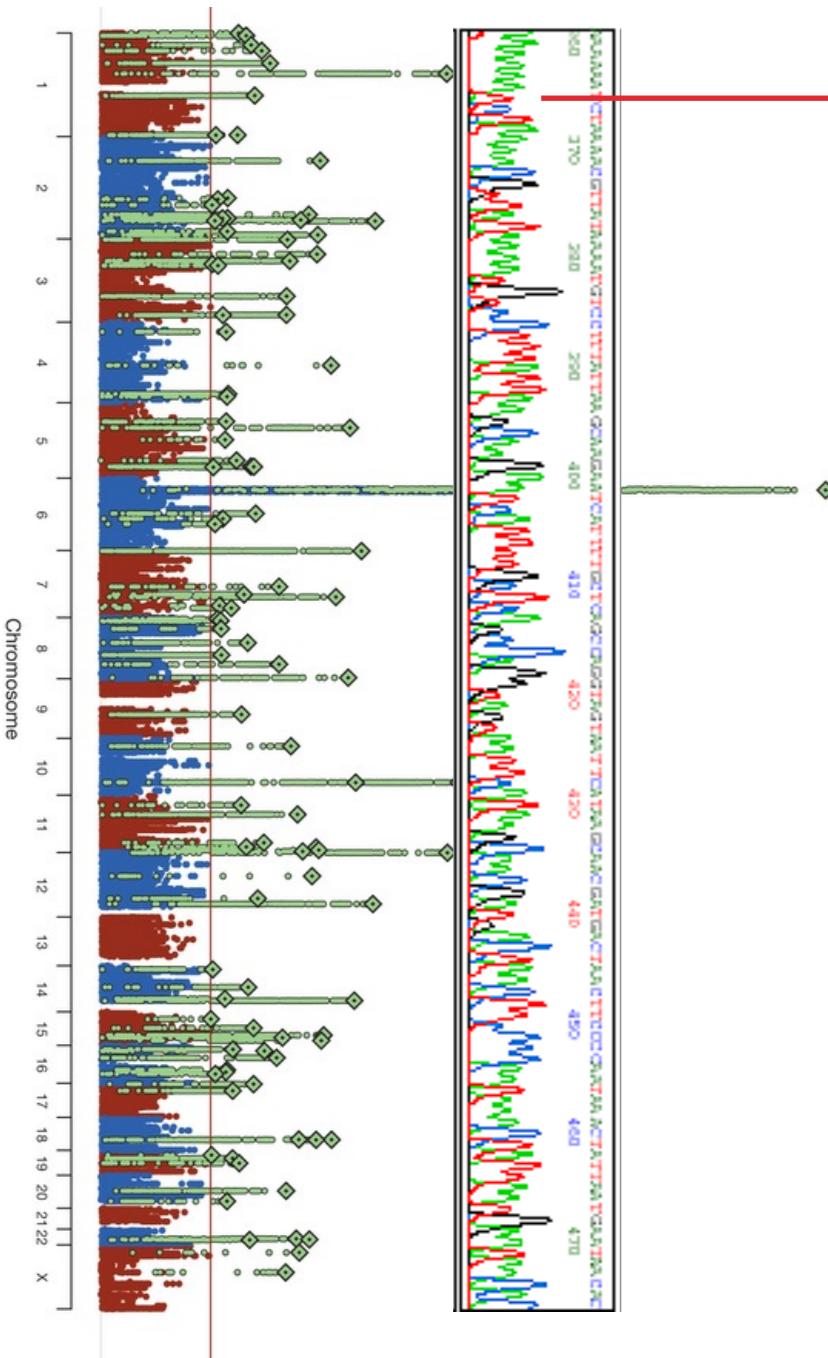
- ▶ Are there differential genotypic effects by phenotype?
- ▶ Are there non-linear effects?

GENOTYPIC PATTERNS

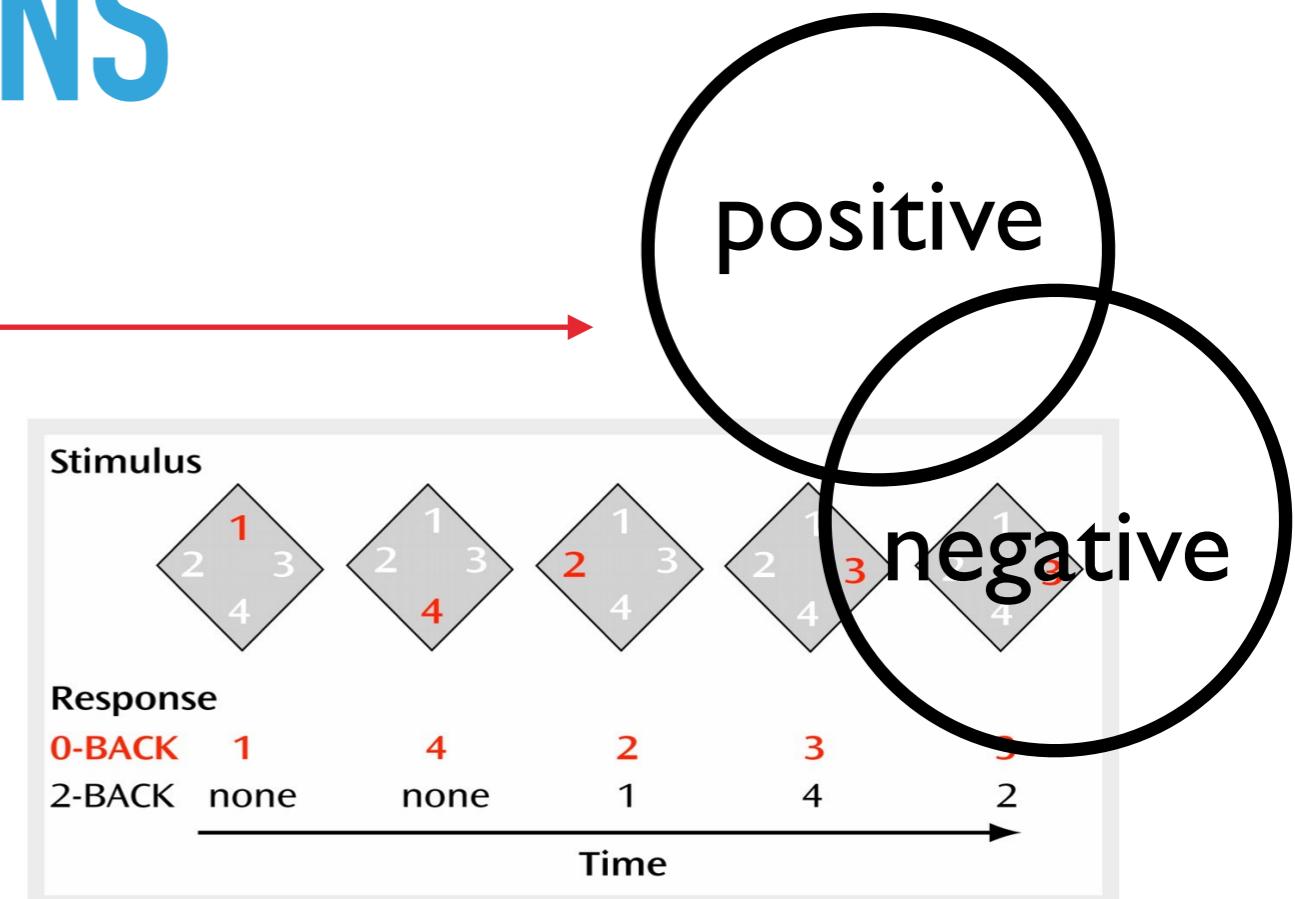
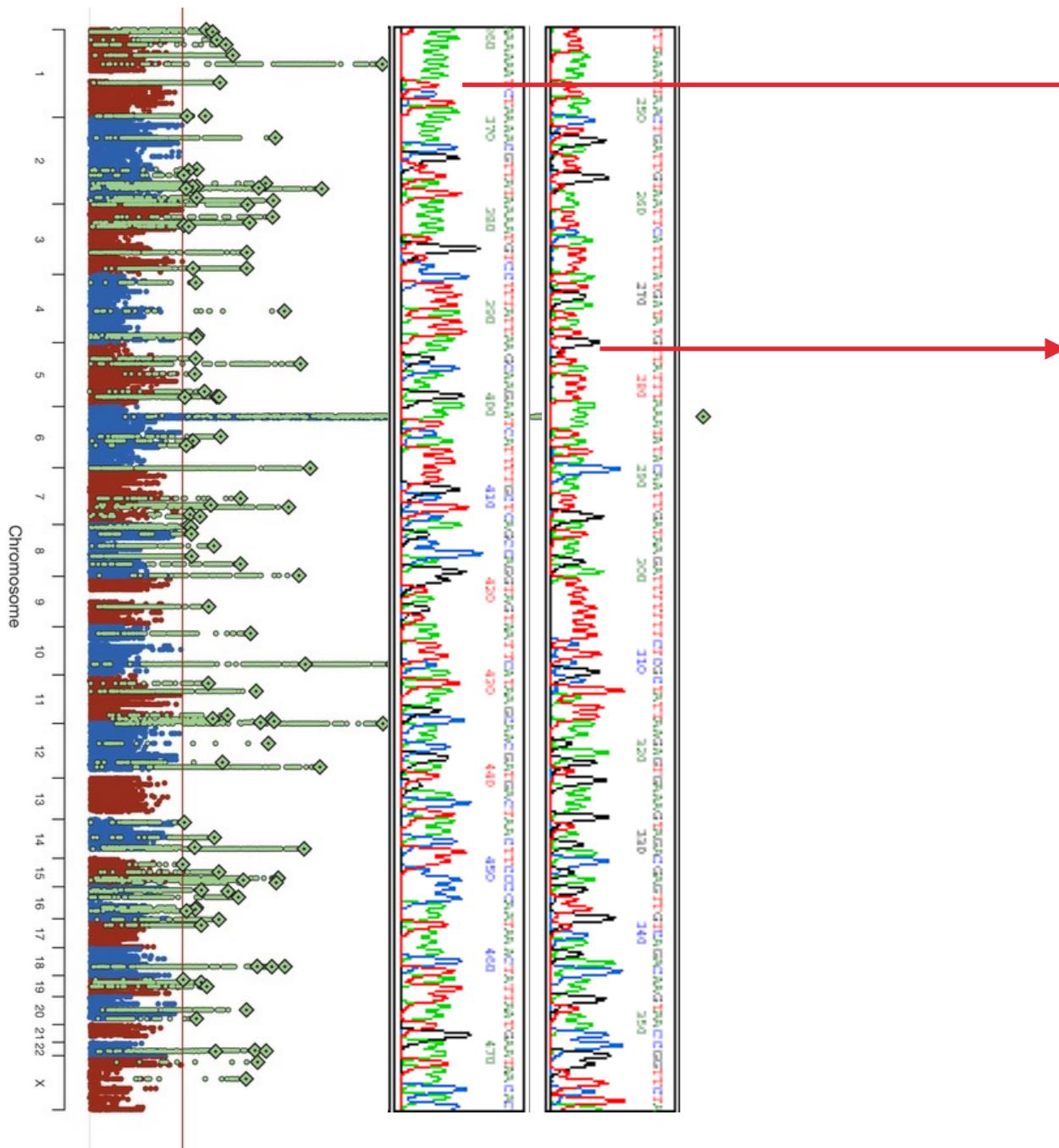
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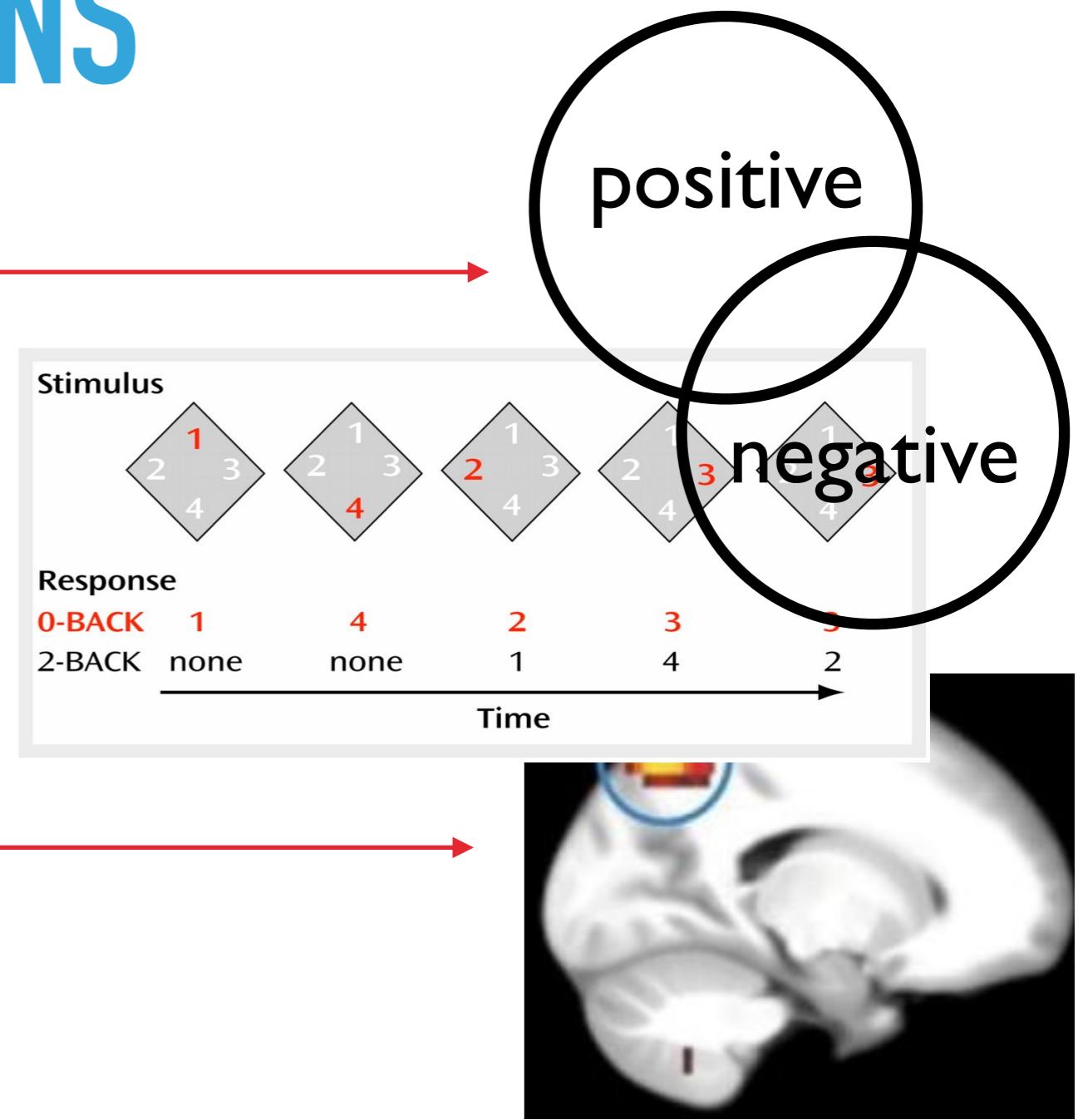
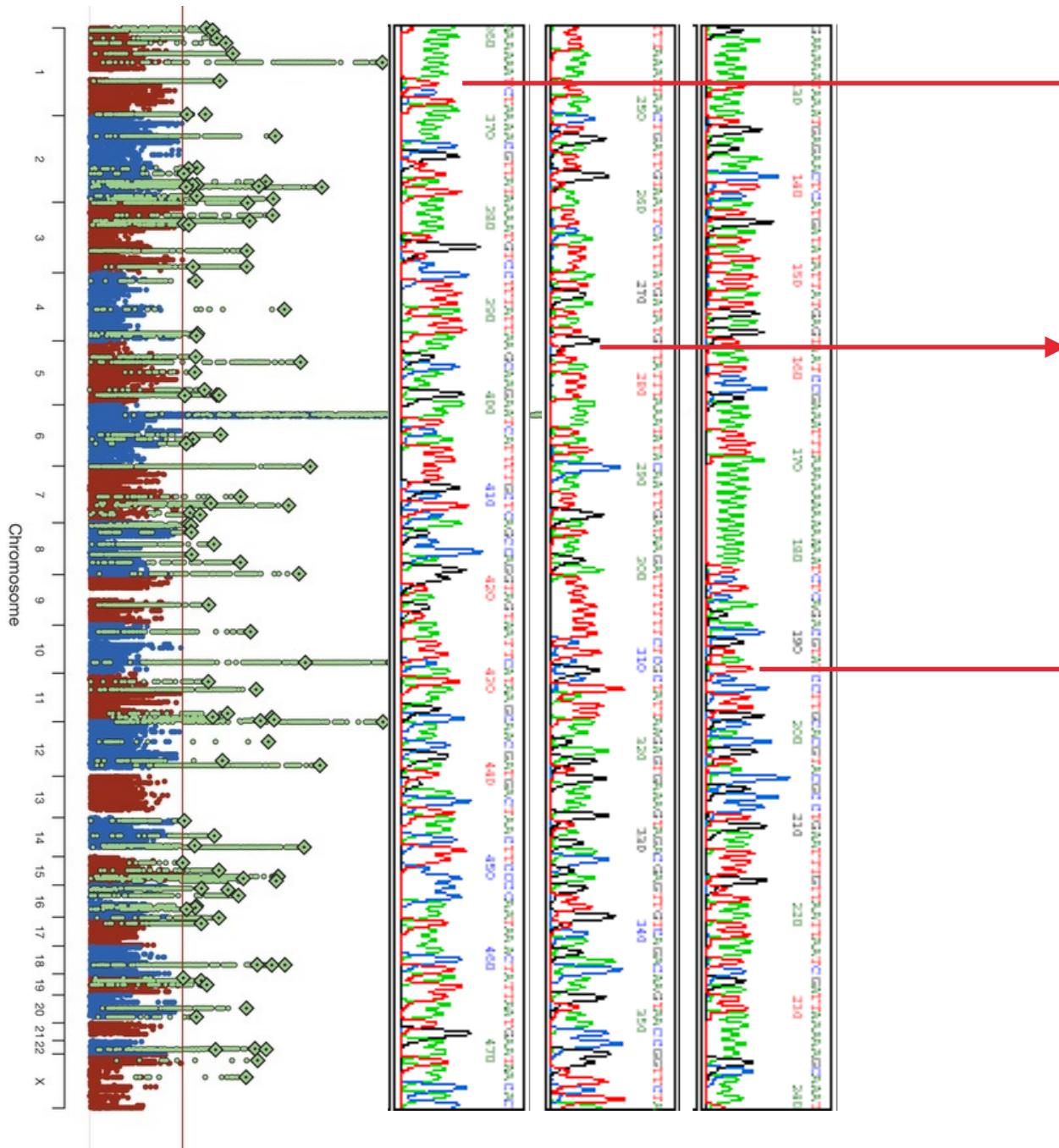
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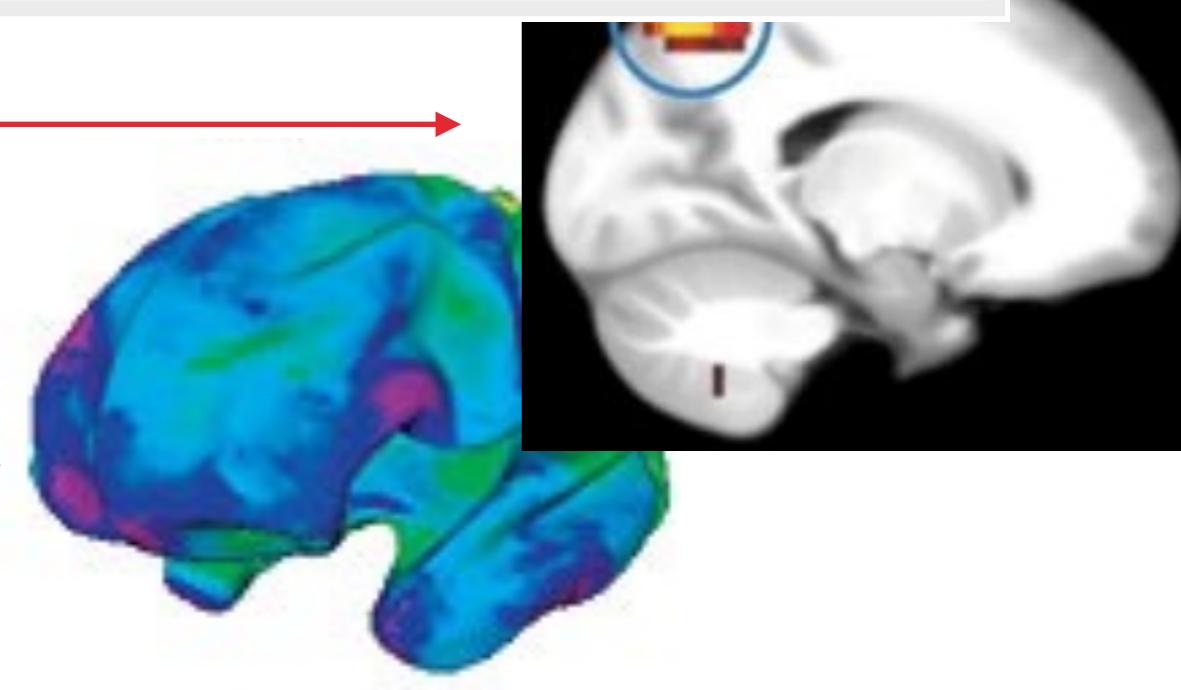
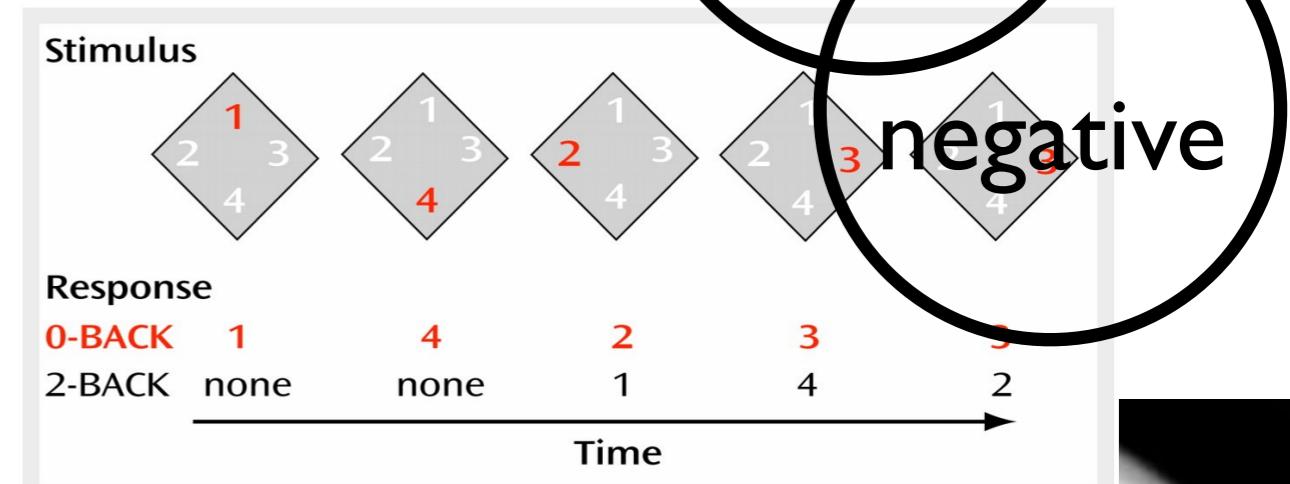
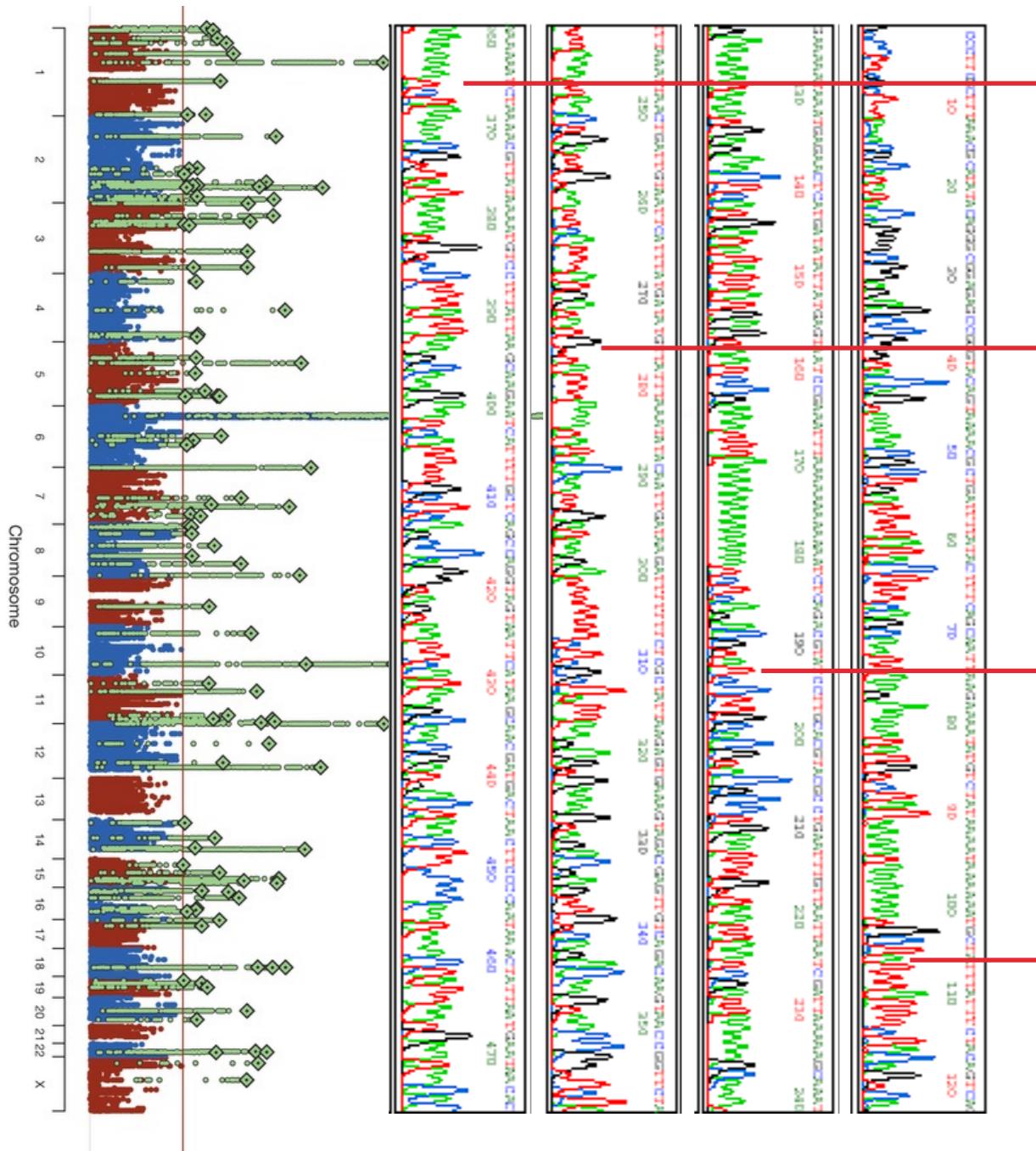


GENOTYPIC PATTERNS



BACKGROUND

GENOTYPIC PATTERNS



AIMS

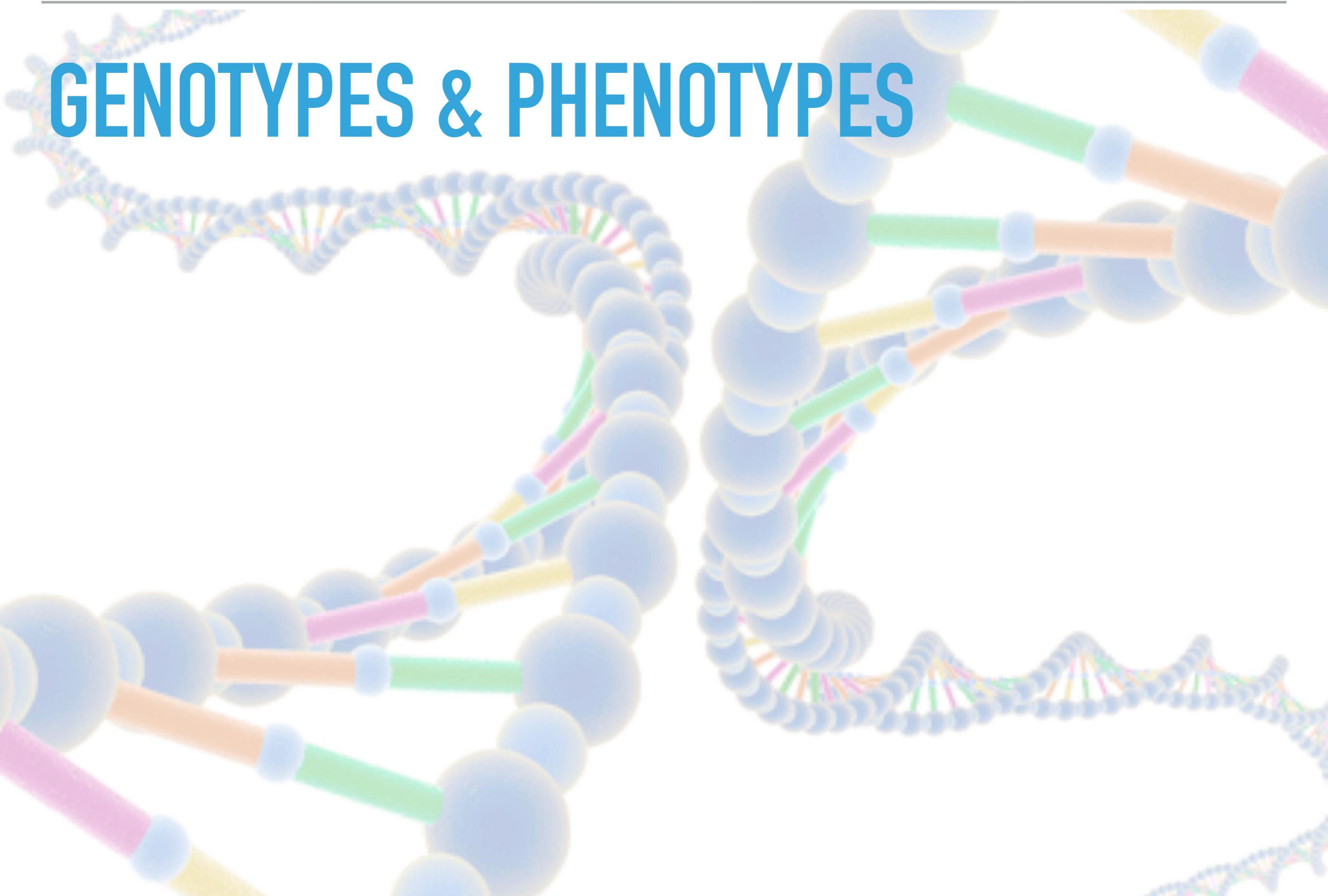
AIMS

- ▶ Proof of principle application of machine learning to genotype-phenotype mapping
 - ▶ Schizophrenia-associated variants
 - ▶ Cognitive endophenotypes

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- ▶ Proof of principle application of machine learning to genotype-phenotype mapping
 - ▶ Schizophrenia-associated variants
 - ▶ Cognitive endophenotypes
- ▶ Compare this approach to more widely used methods (GLM, polygenic scores) using the same loci and outcomes

GENOTYPES & PHENOTYPES



GENOTYPES & PHENOTYPES

- ▶ Samples
 - ▶ Training: American sample – SZ, BP, ADHD, controls ($N = 739$)
 - ▶ Validation: Swedish twin sample – SZ, BP, controls ($N = 364$)

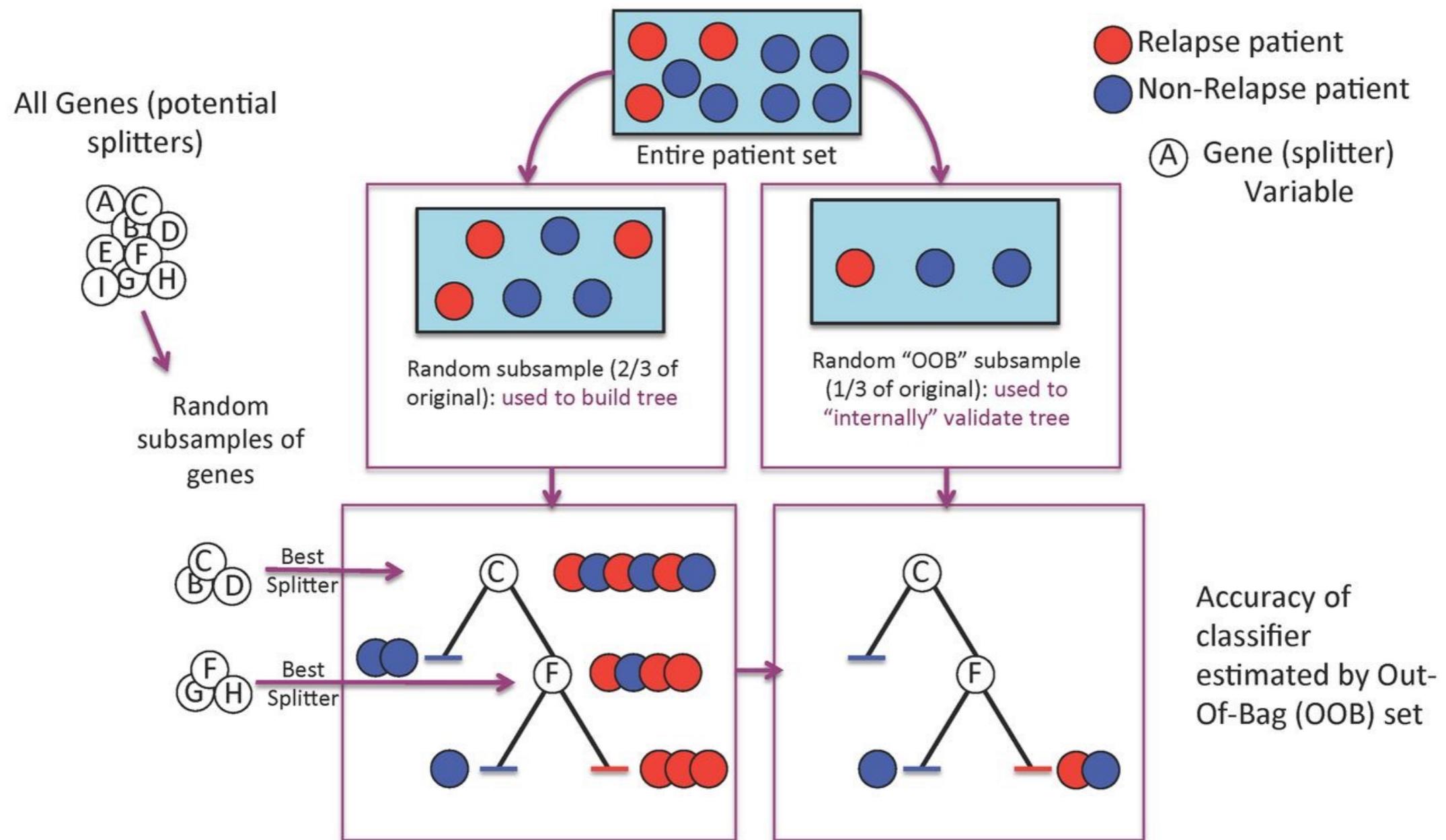
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- ▶ Samples
 - ▶ Training: American sample – SZ, BP, ADHD, controls ($N = 739$)
 - ▶ Validation: Swedish twin sample – SZ, BP, controls ($N = 364$)
- ▶ Measures
 - ▶ Predictors: 77 of 108 PGC SNPs
 - ▶ Outcomes: 6 cognitive measures
 - ▶ CVLT, VR I & II, Digit Span, Trail Making Test A, Vocabulary

METHODS

RANDOM FOREST

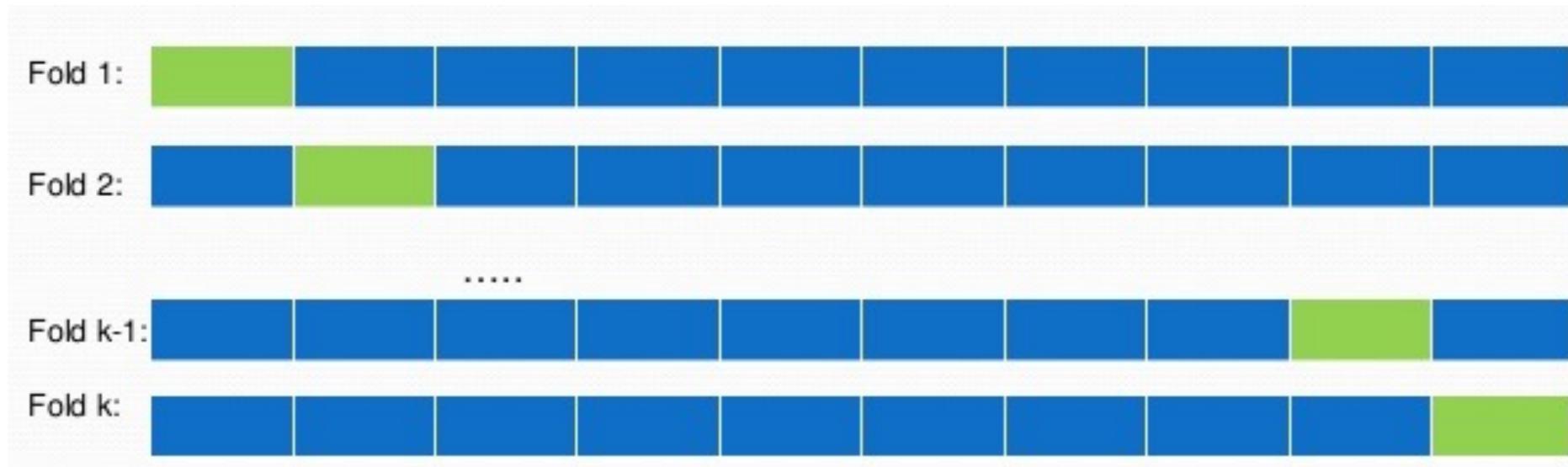
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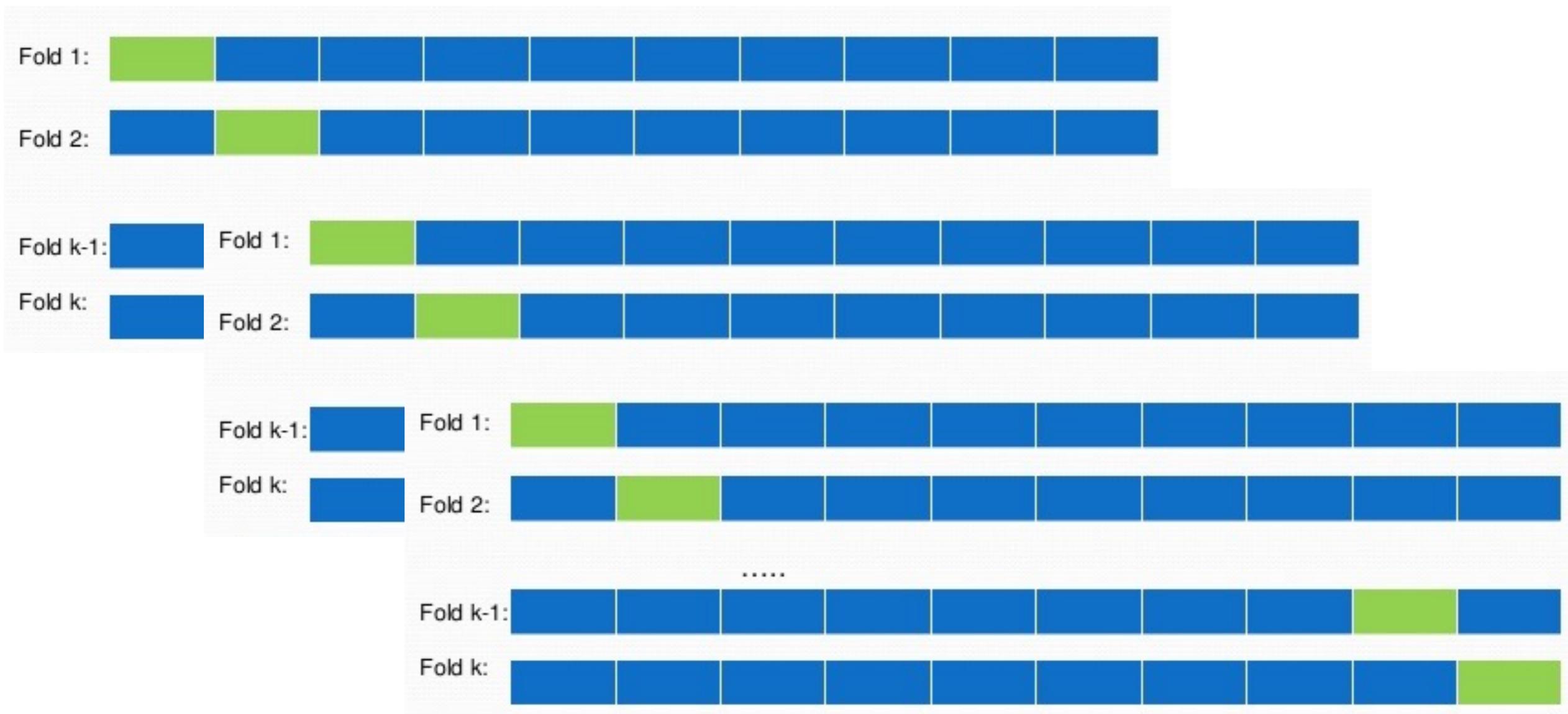
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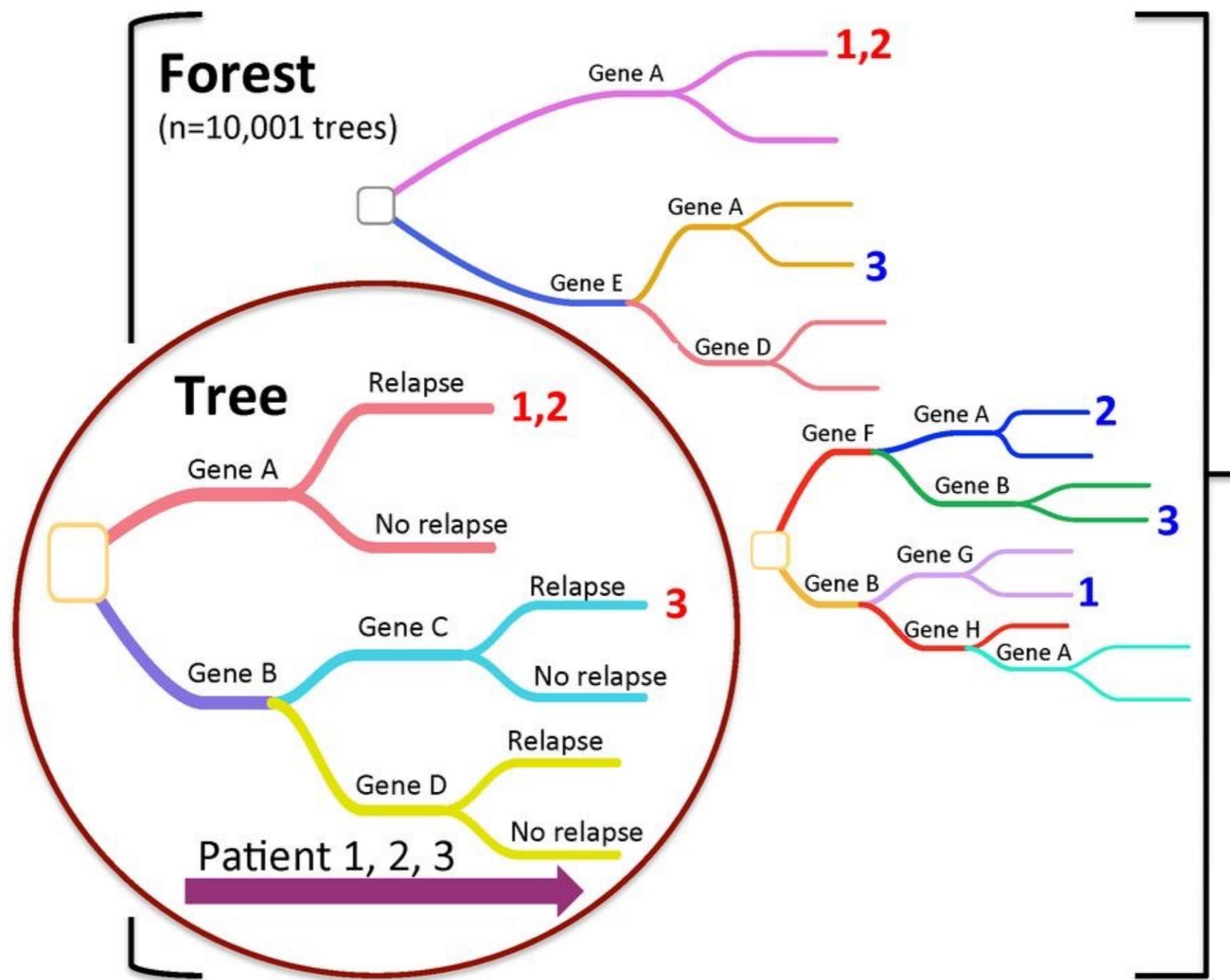
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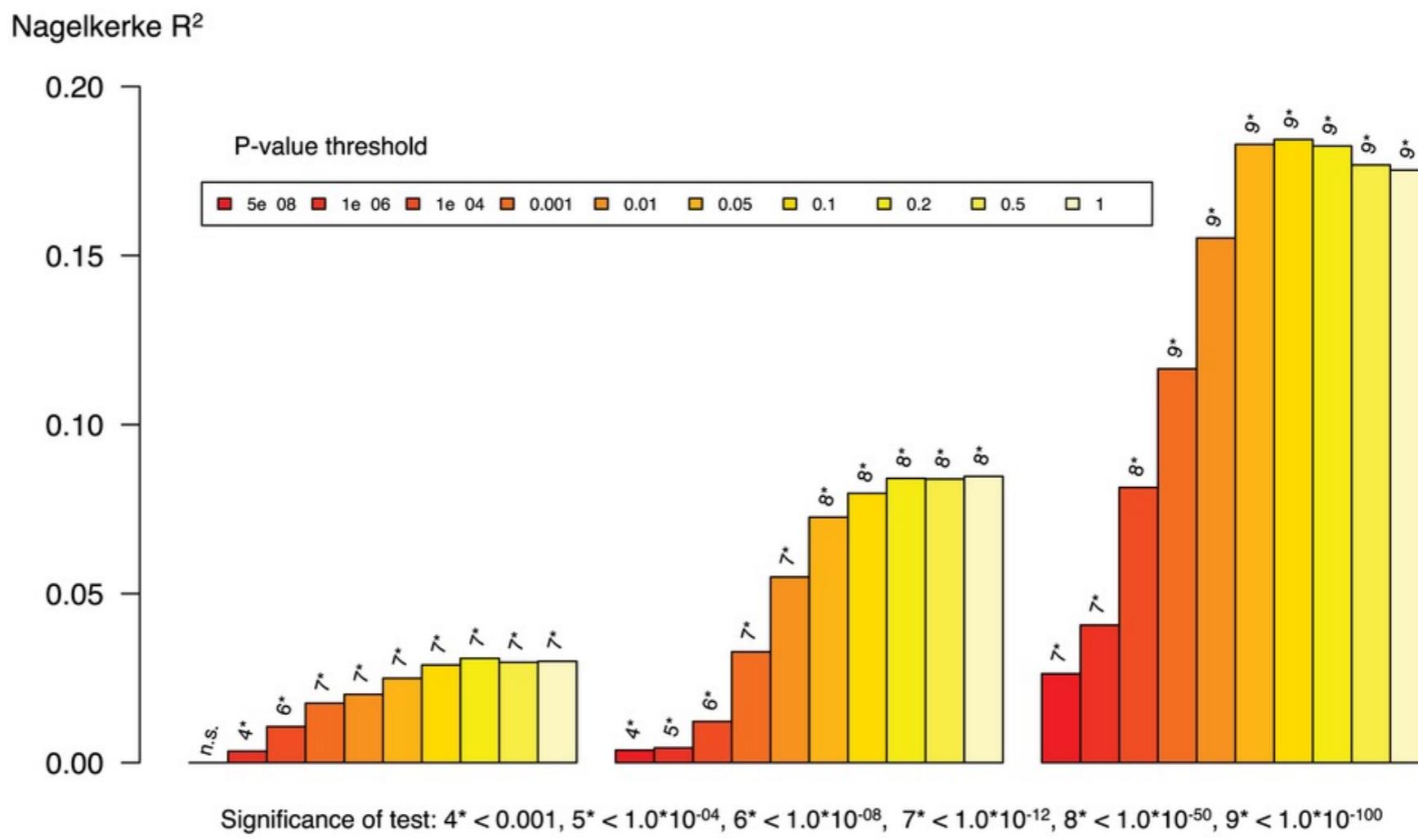


RANDOM FOREST



COMPARISON MODELS

- ▶ General linear models (GLM)
- ▶ Polygenic risk scores (PRS)

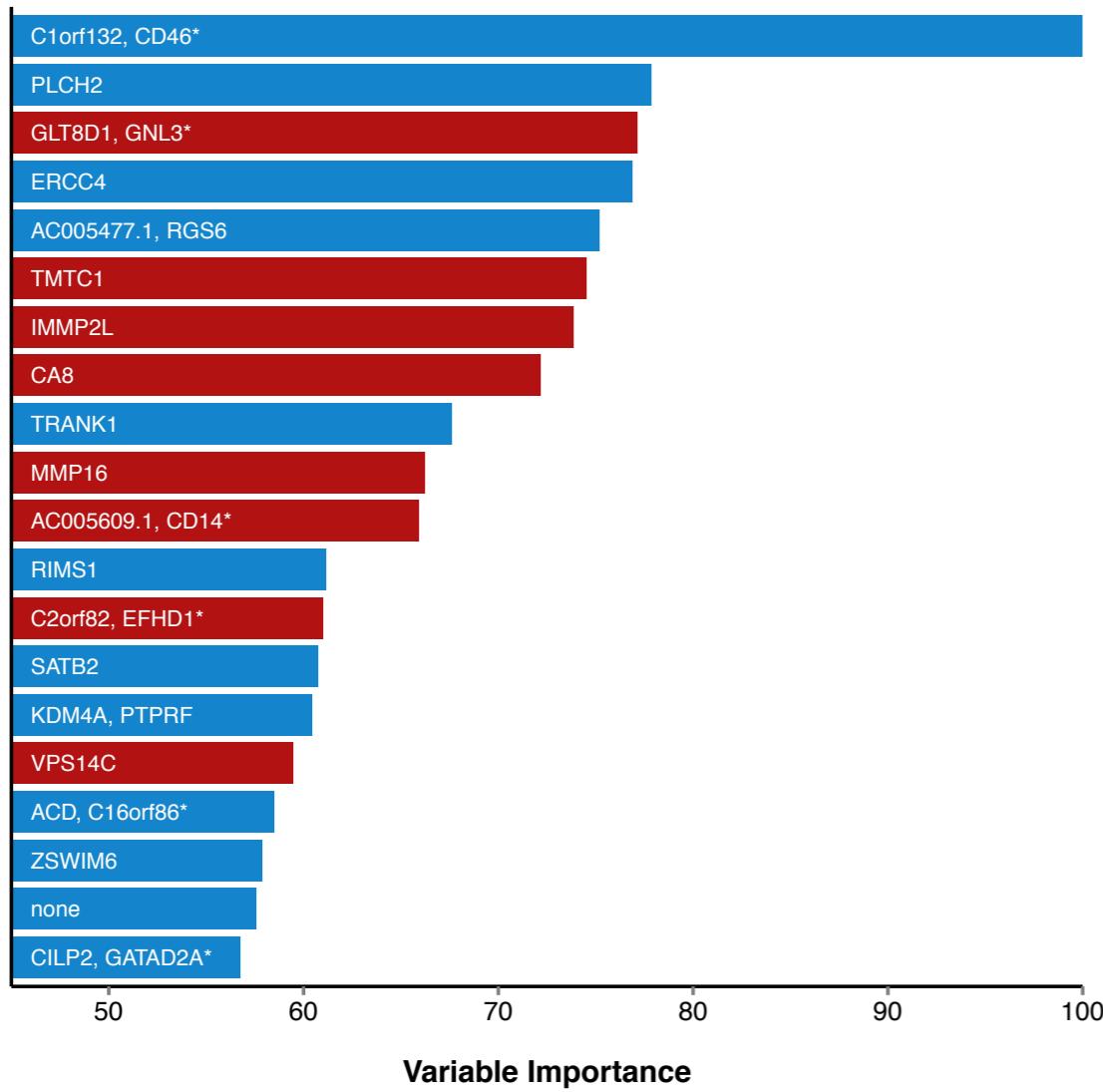
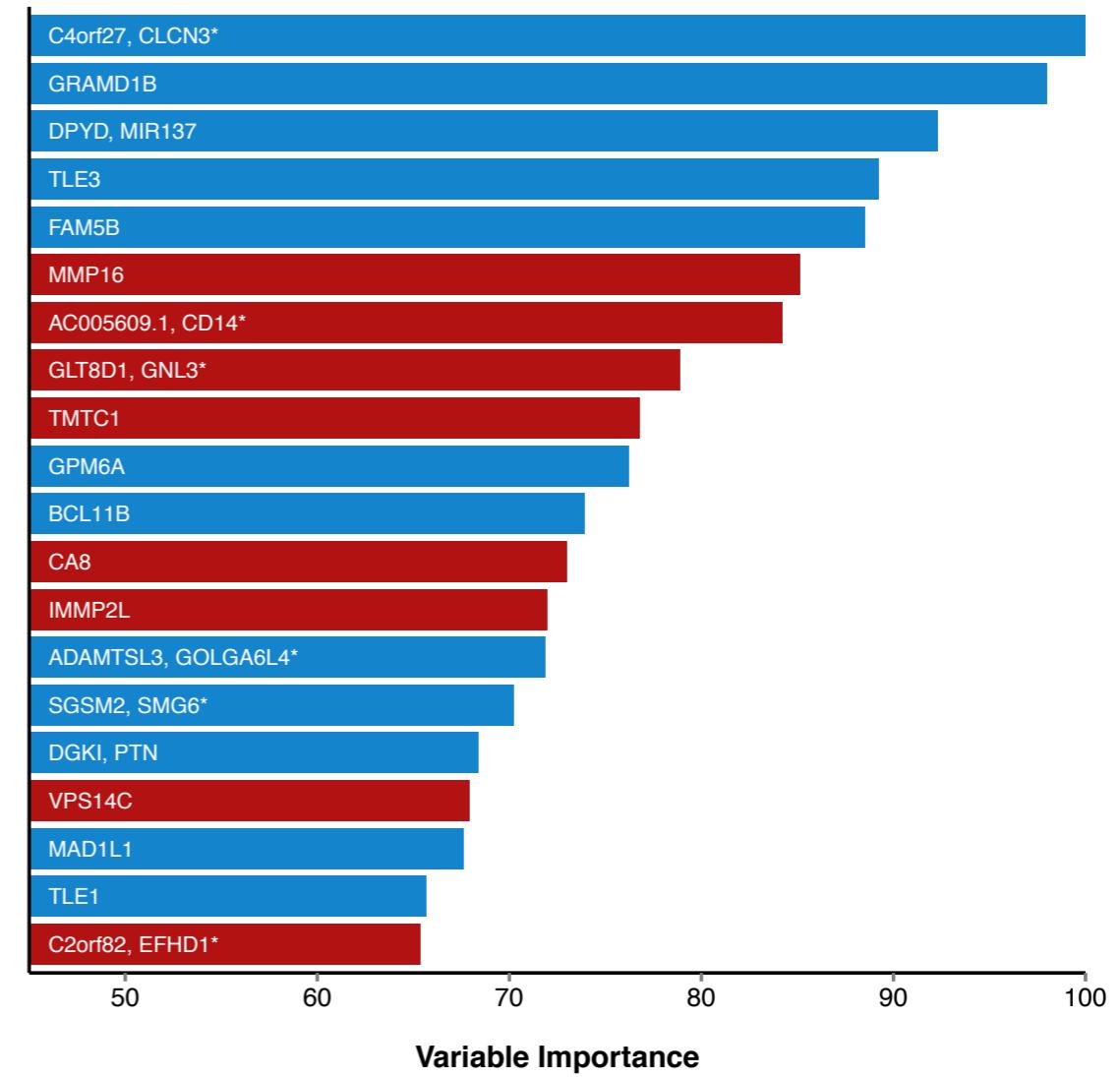


MODEL PERFORMANCE

	American Sample					
	<u>RF</u>		<u>GLM</u>		<u>PRS</u>	
	<i>R</i> ²	<i>p</i>	<i>R</i> ²	<i>p</i>	<i>t</i>	<i>p</i>
CVLT	0.015	< .001	0.013	.002	-2.32	.126
Vocabulary	0.010	.005	0.017	< .001	-0.75	.683
Trails 1	0.010	.006	0.015	.001	-0.16	.871
Digit Span	0.018	.001	0.014	.001	-1.45	.444
VR I	0.012	.003	0.010	.006	0.98	.654
VR II	0.013	.001	0.012	.002	-0.54	.706

	Swedish Sample					
	<u>RF</u>		<u>GLM</u>		<u>PRS</u>	
	<i>t</i>	<i>p</i>	<i>t</i>	<i>p</i>	<i>t</i>	<i>p</i>
CVLT	-0.81	.209	-0.44	.332	-	-
Vocabulary	-0.06	.478	-0.24	.407	-	-
Trails A	2.86	.003	1.05	.147	-	-
Digit Span	0.15	.440	-0.05	.482	-	-
VR I	-0.55	.291	-0.20	.421	-	-
VR II	1.76	.040	0.31	.377	-	-

VALIDATED MODELS

A) Trails 1/A**B) Visual Reproduction II**

CONCLUSIONS

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- ▶ **Statistical validation:** Random forest outperformed GLM and polygenic risk scores in an independent sample

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- ▶ **Statistical validation:** Random forest outperformed GLM and polygenic risk scores in an independent sample
- ▶ **Biological validation:** Random forest models identified calcium ion binding and cell adhesion genes, which have previously been mapped to cognitive impairment in schizophrenia
- ▶ **Relevance:** Pattern analysis may be able to identify more specific and generalizable genotype-phenotype associations than standard linear methods

LIMITATIONS

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- ▶ PRS typically include 100s - 1000s of variants

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- ▶ Relatively small samples

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- ▶ Relatively small samples
- ▶ Limited by current knowledge of genetic risk variants for schizophrenia

ACKNOWLEDGEMENTS

THANK YOU!



Yale University

- ▶ Adam Chekroud, MSc
- ▶ Ty Cannon, PhD

New Haven VA

- ▶ Renato Polimanti, PhD
- ▶ Joel Gelernter, MD

UCLA

- ▶ Fred Sabb, PhD
- ▶ Robert Bilder, PhD
- ▶ Nelson Friemer, MD
- ▶ Edythe London, PhD

Karolinska Institutet

- ▶ Christina Hultman, PhD

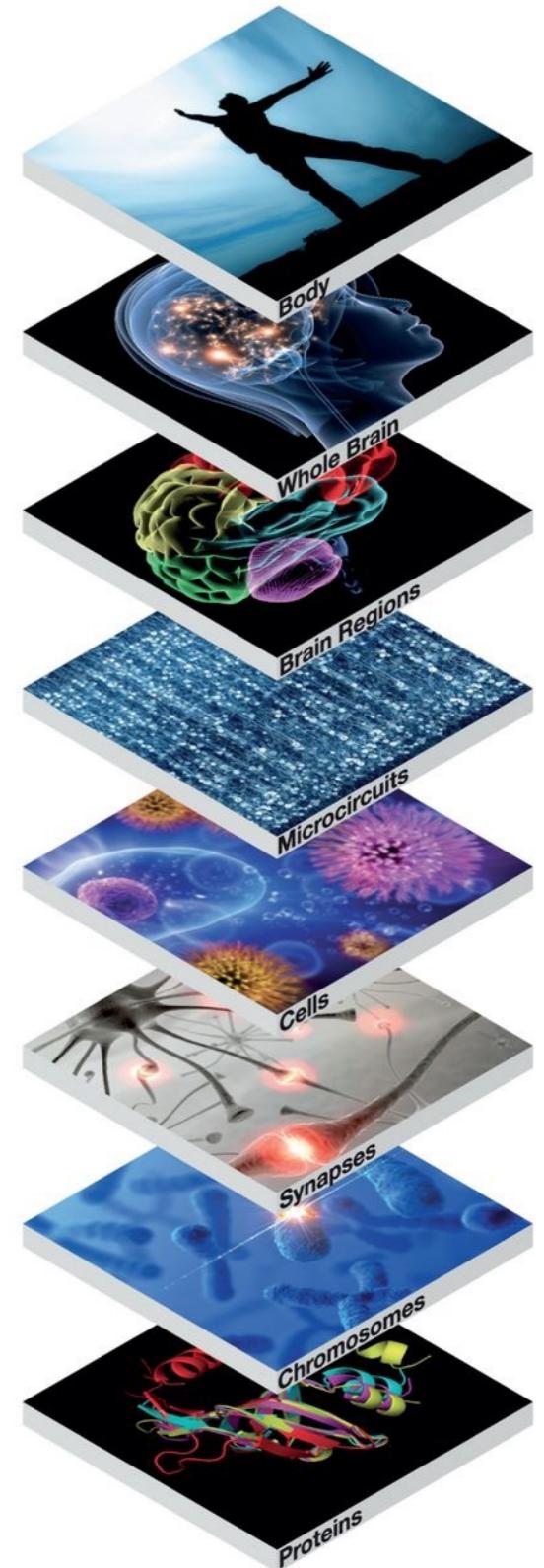


CLINICAL NEUROSCIENCE LAB

TEXT

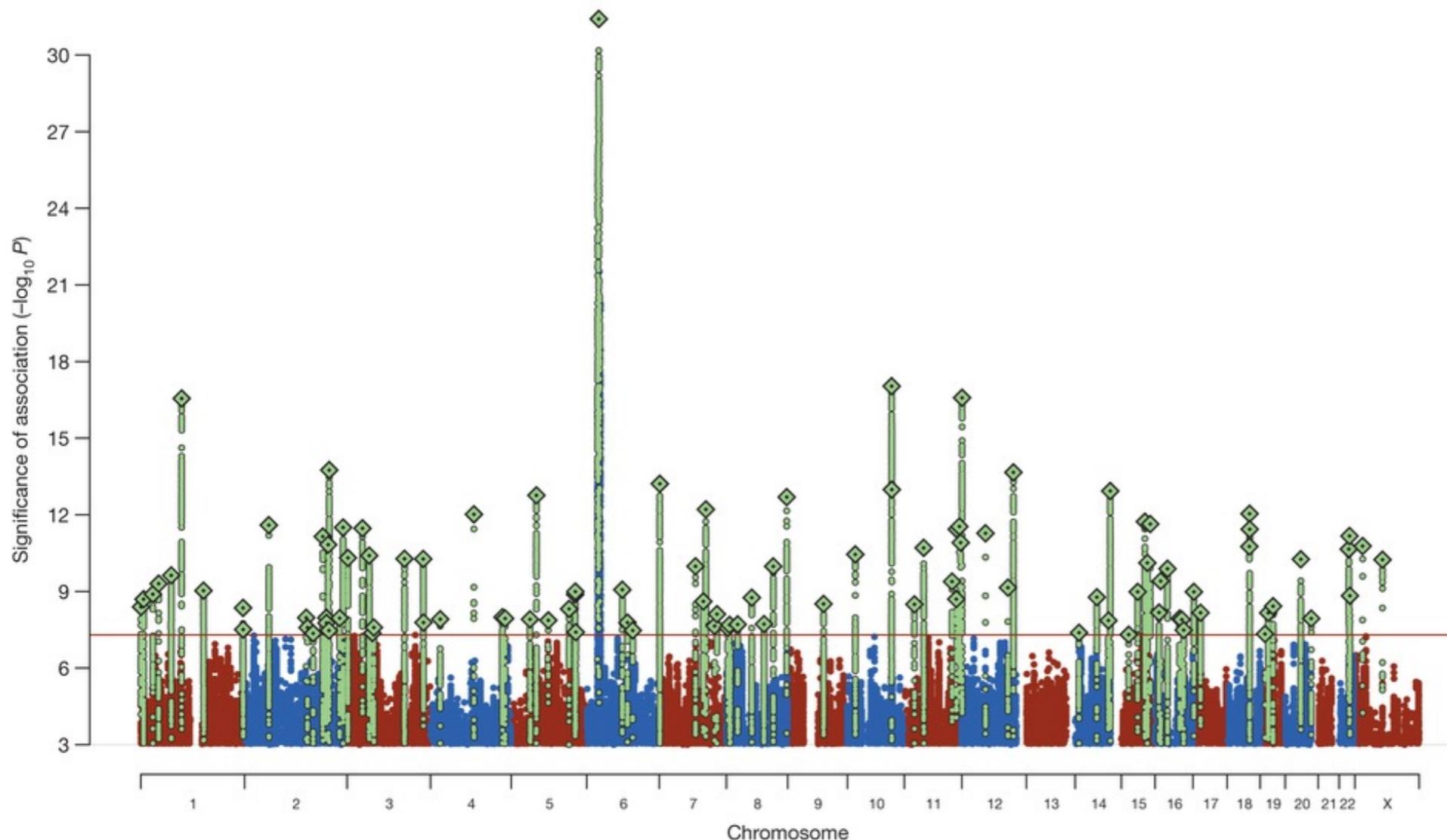
SCHIZOPHRENIA

- ▶ 1% of global disease burden
- ▶ 21 million affected
- ▶ \$6.8 billion per year

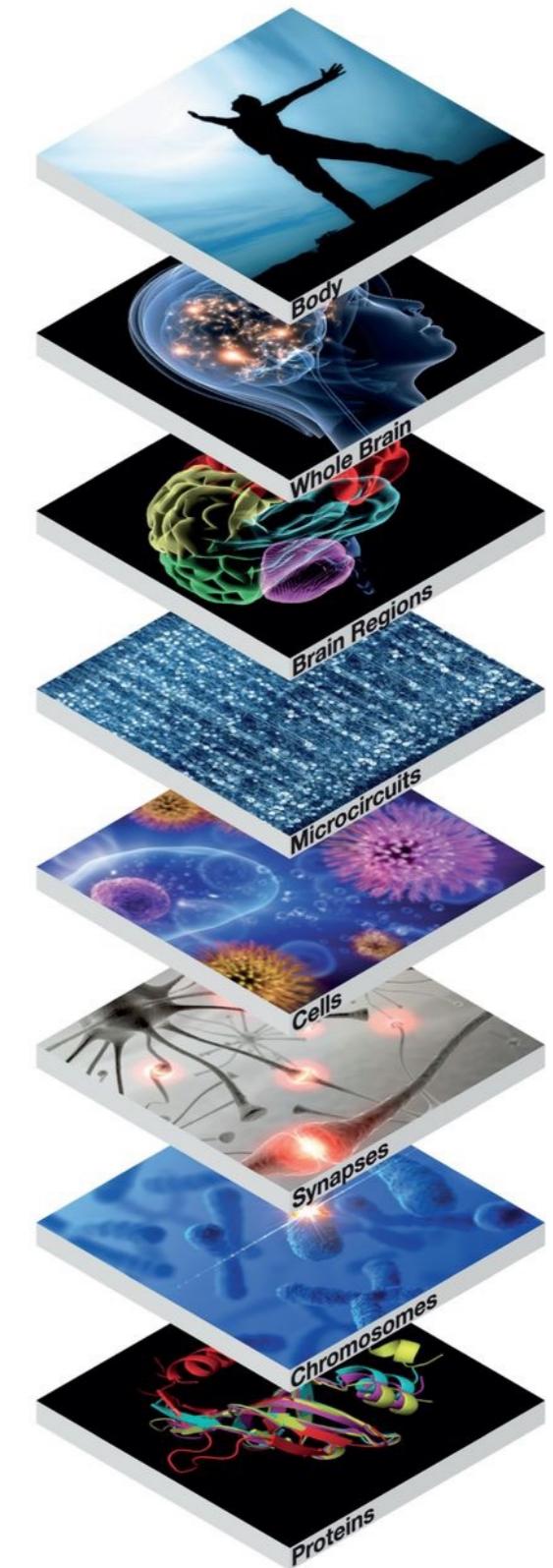
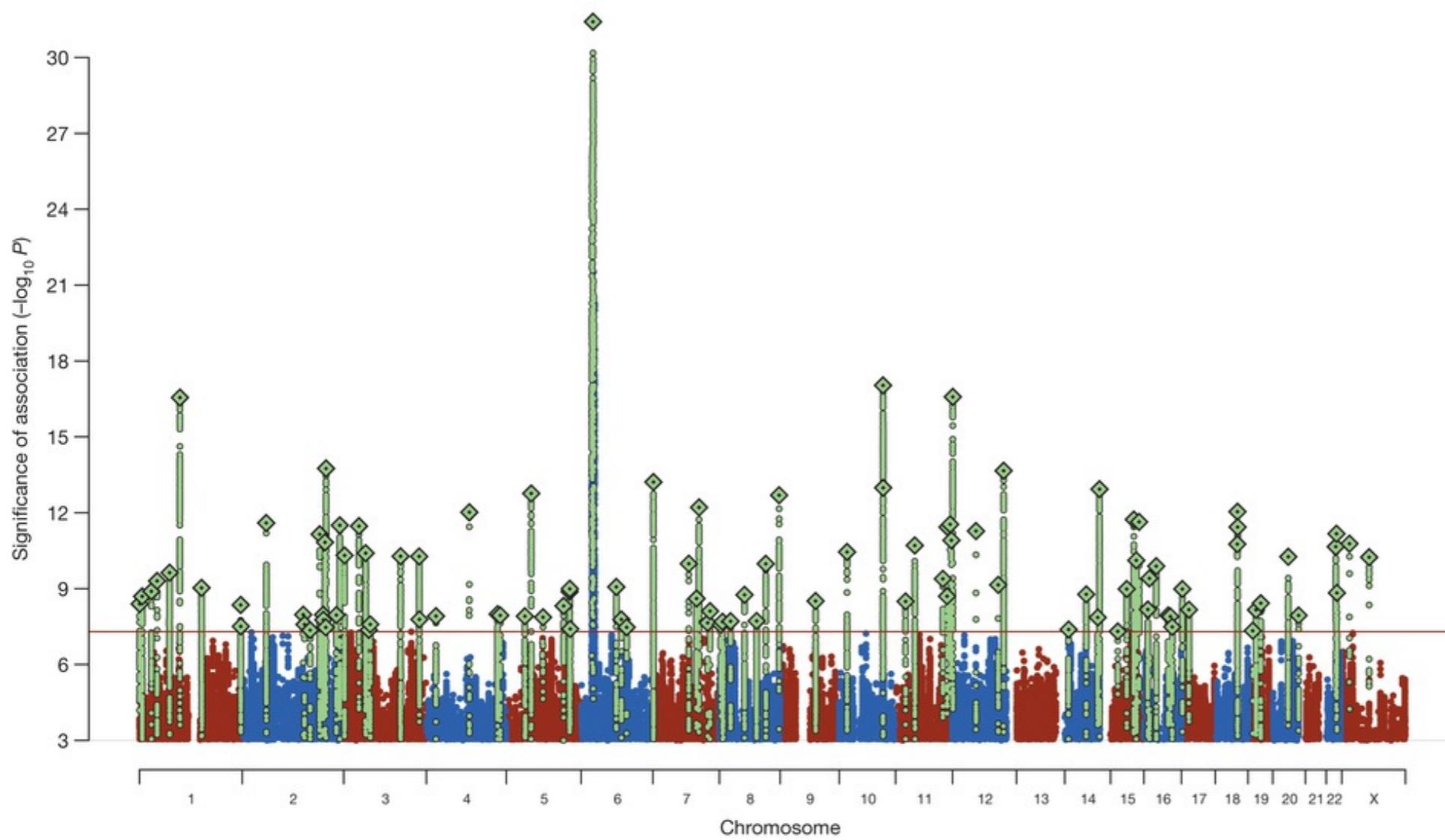


SCHIZOPHRENIA GENETICS

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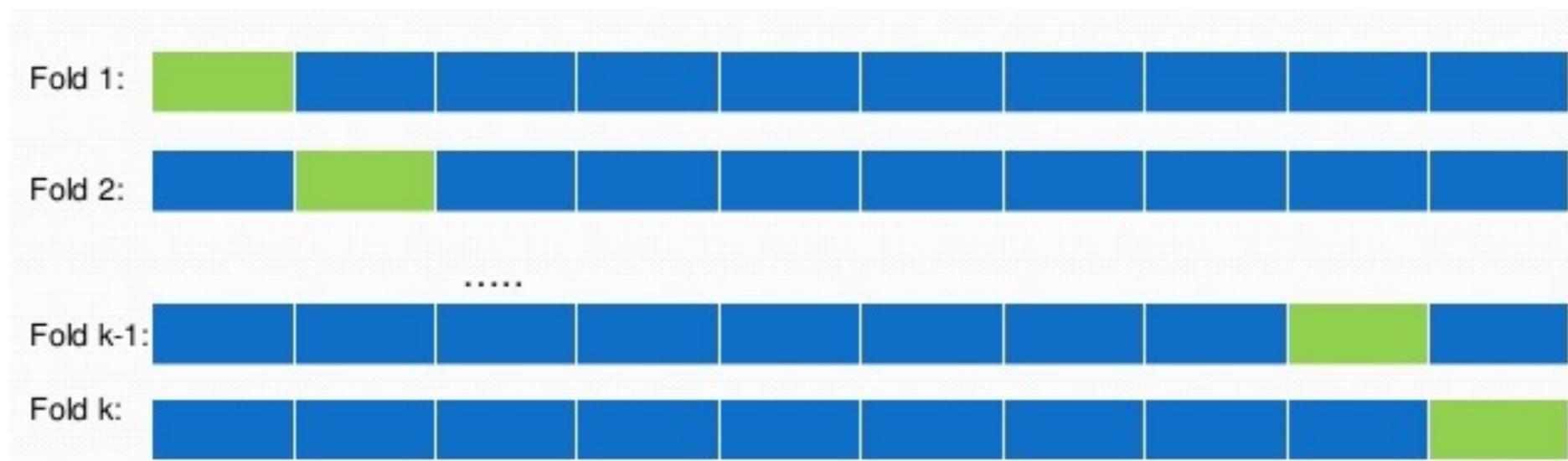
STATISTICAL ANALYSES

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- ▶ Training and validation

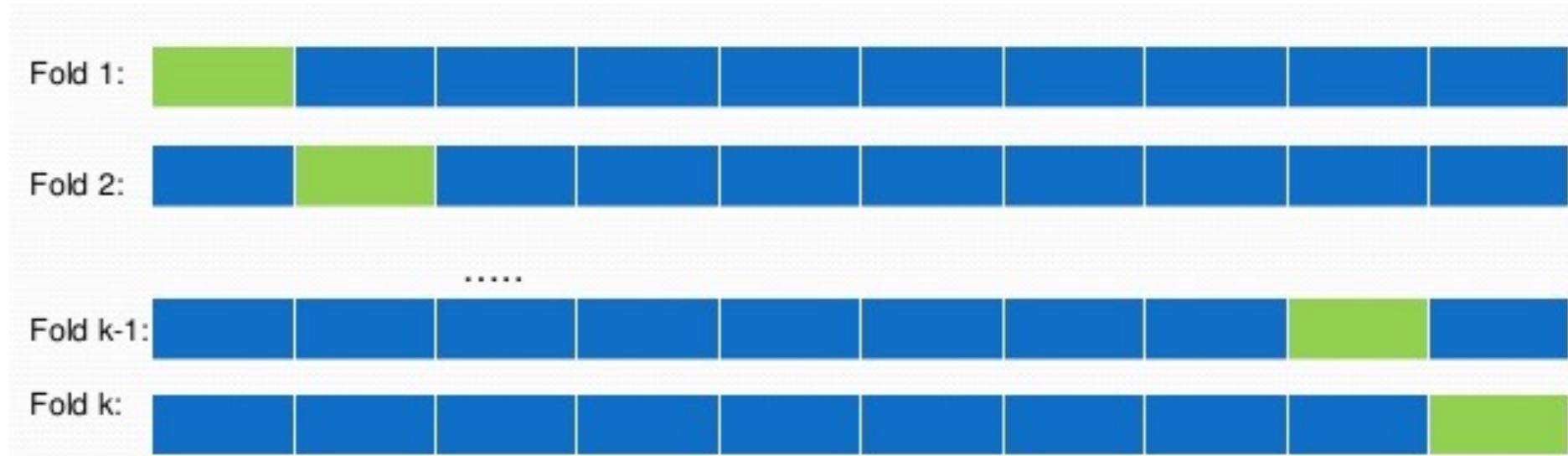
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- ▶ Training and validation
 - ▶ 10-fold CV // 3 sets in training sample



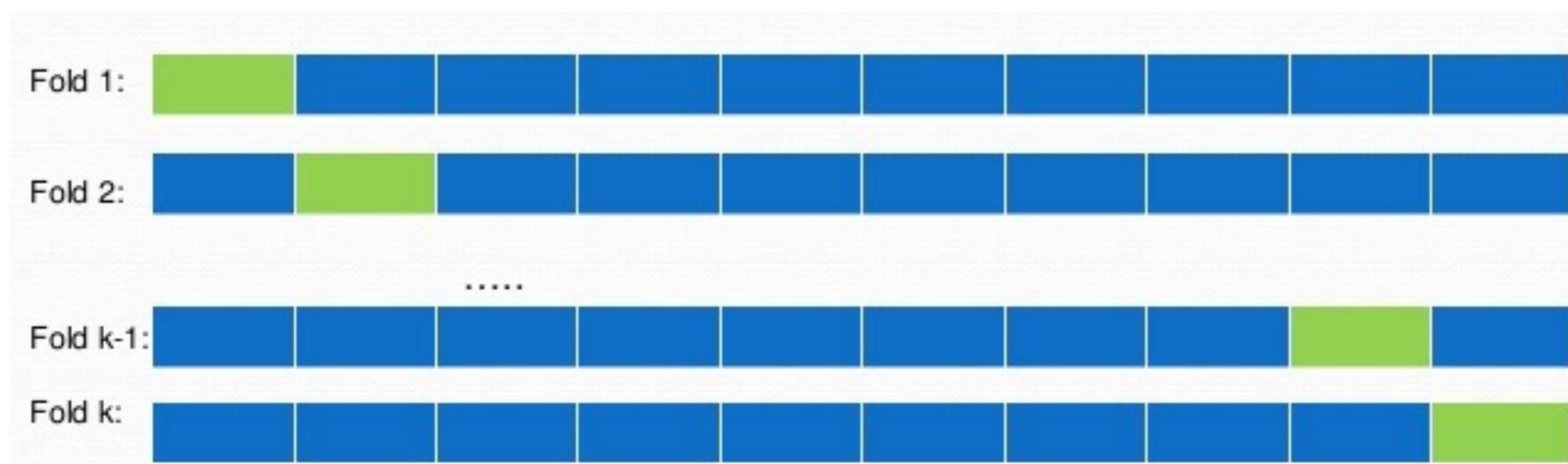
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 - ▶ 10-fold CV // 3 sets in training sample
 - ▶ Performance metric = R^2



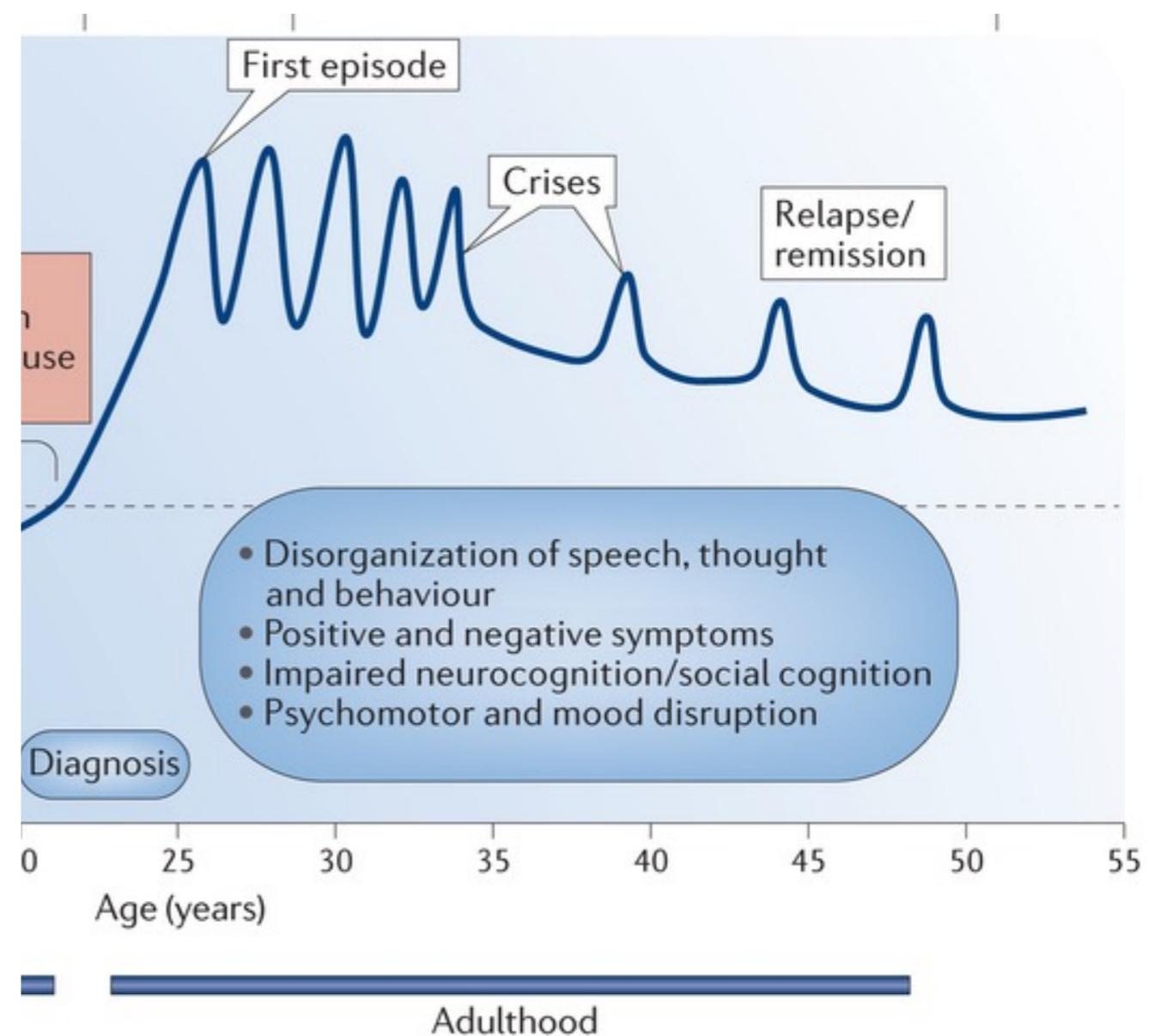
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- ▶ Training and validation
 - ▶ 10-fold CV // 3 sets in training sample
 - ▶ Performance metric = R^2
 - ▶ Training model applied without modification to validation sample

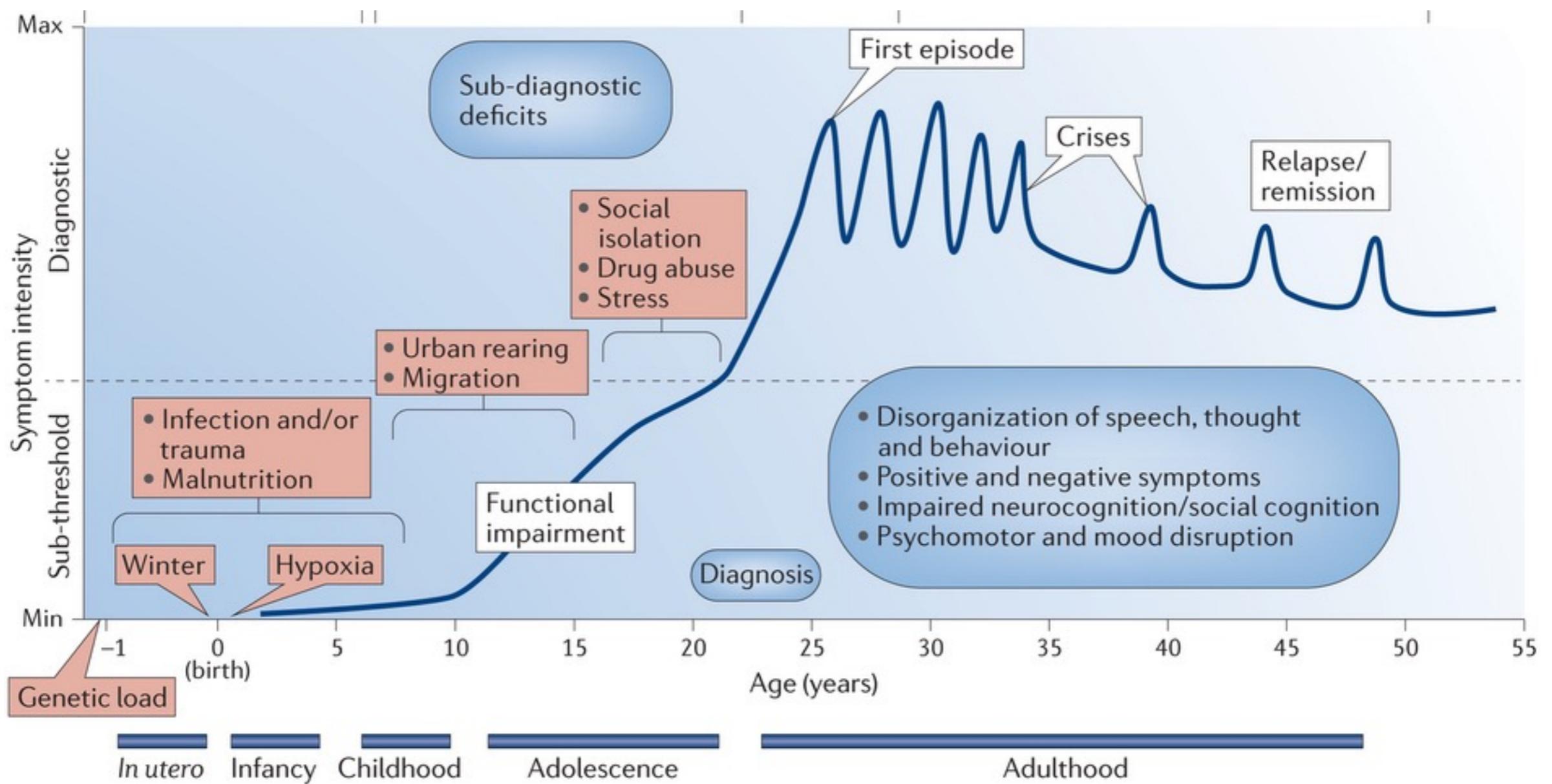


DEVELOPMENT OF SCHIZOPHRENIA

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FROM GENES TO BEHAVIOR

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statistical
association

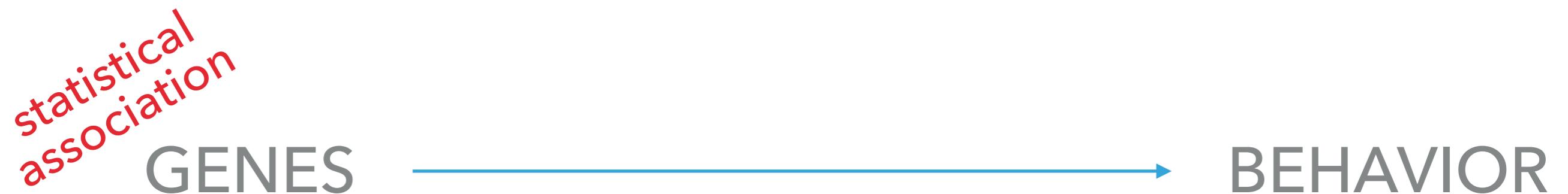
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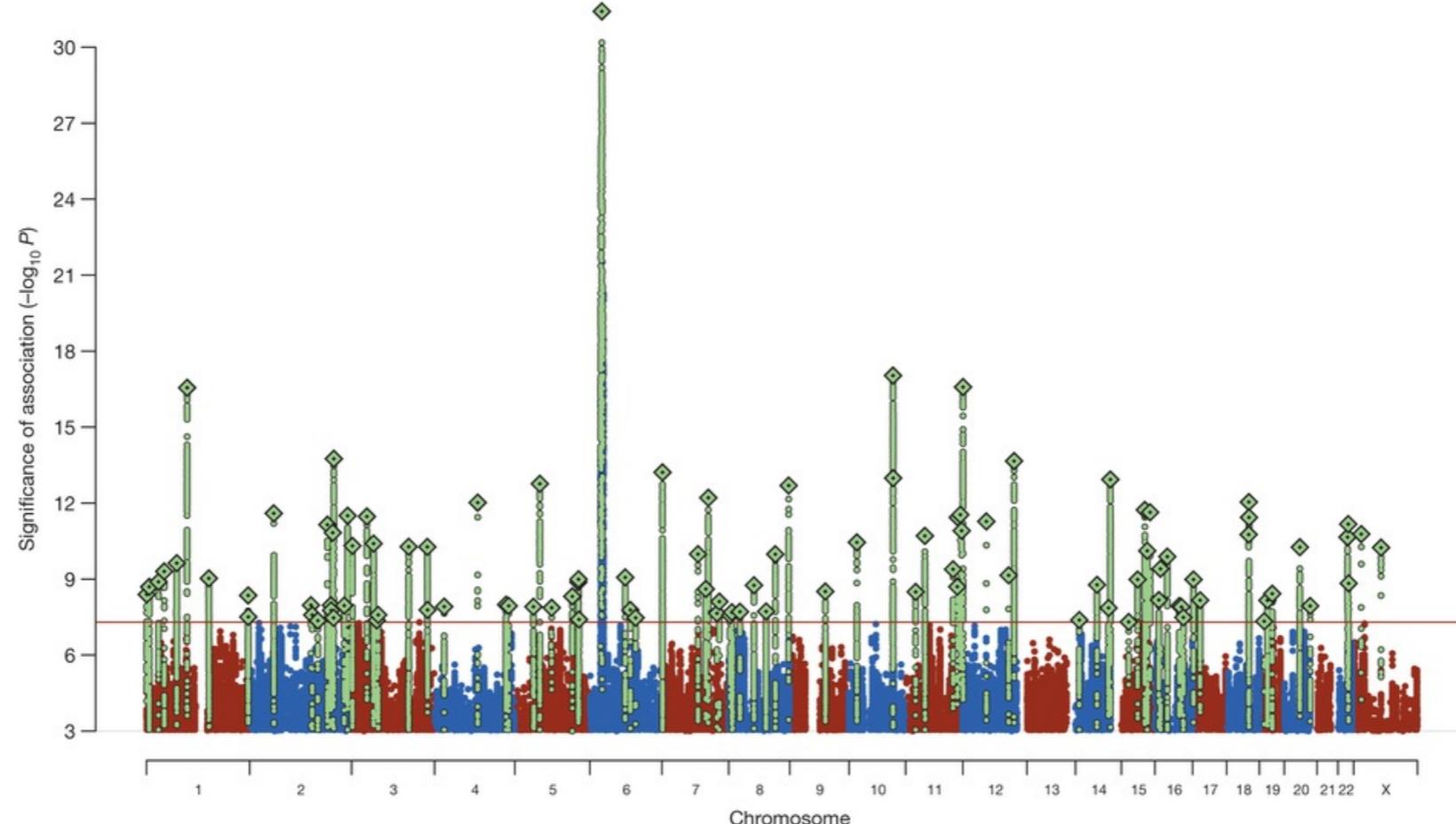


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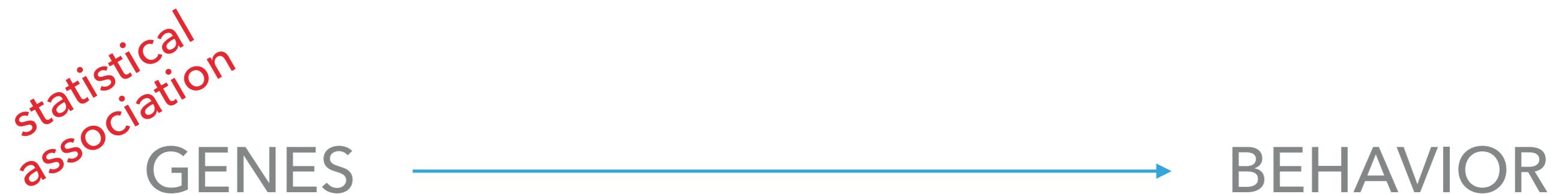
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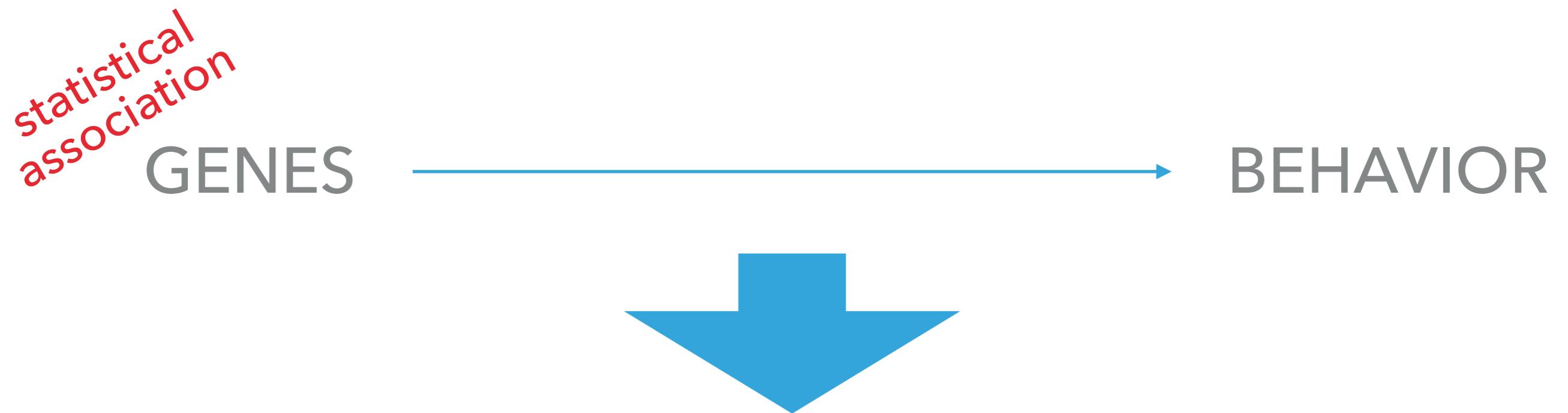
BEHAVIOR



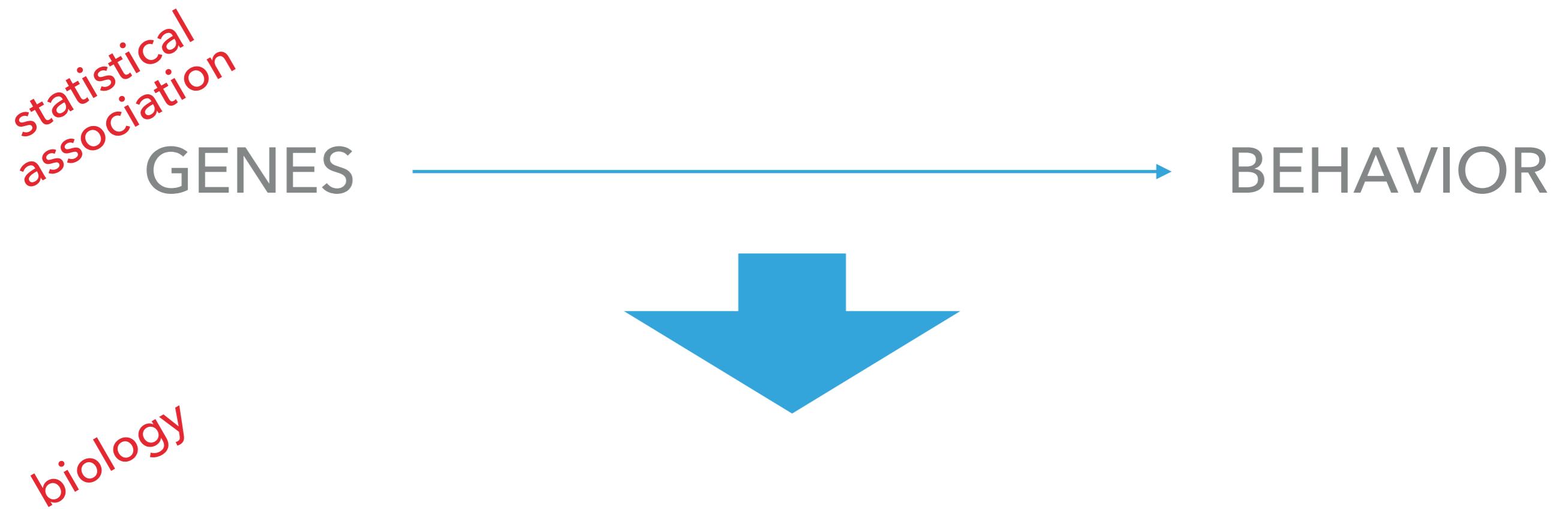
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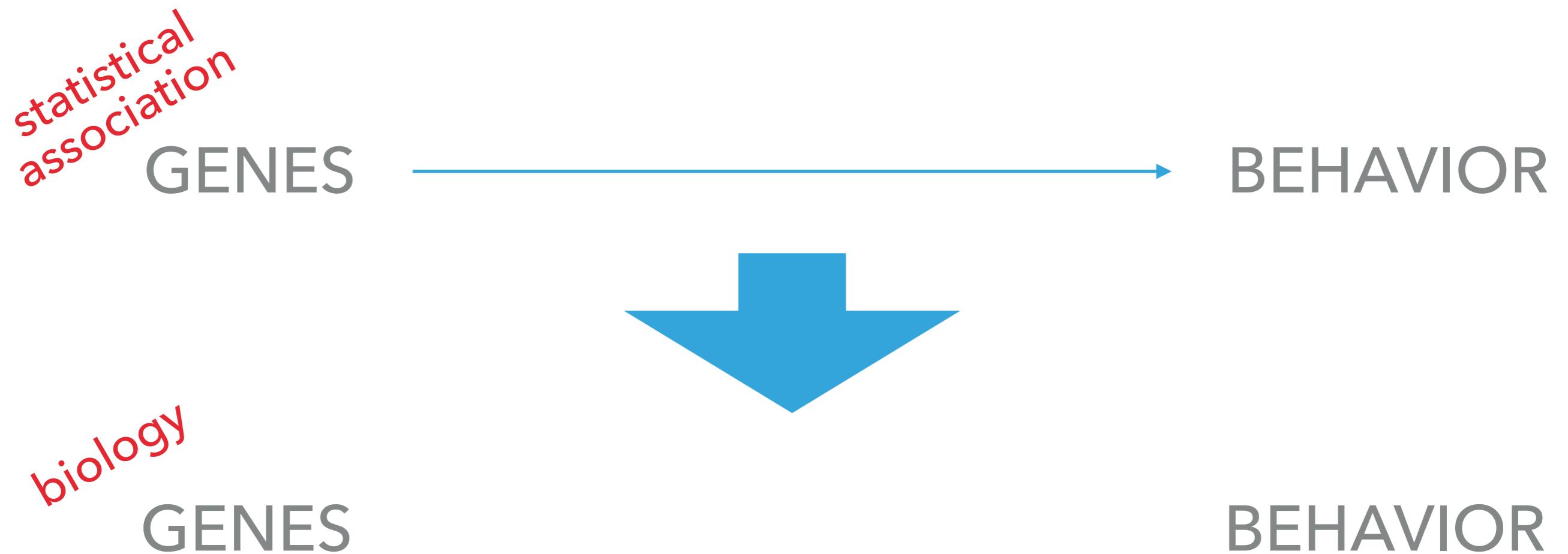
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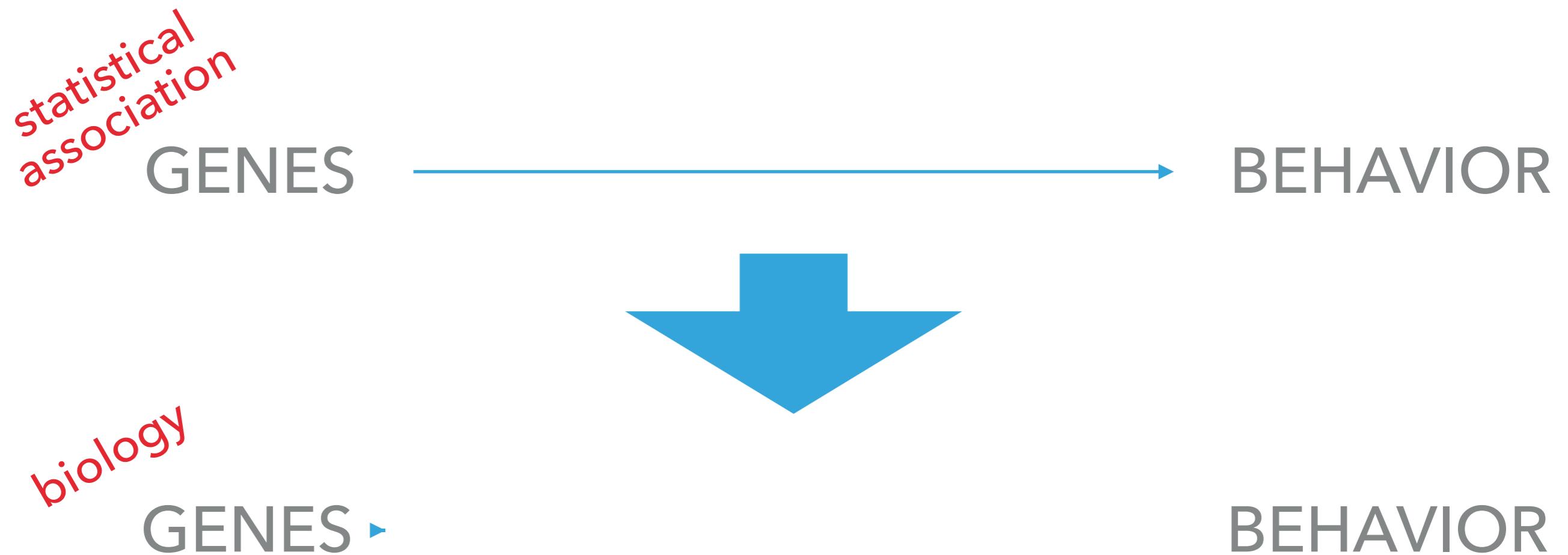
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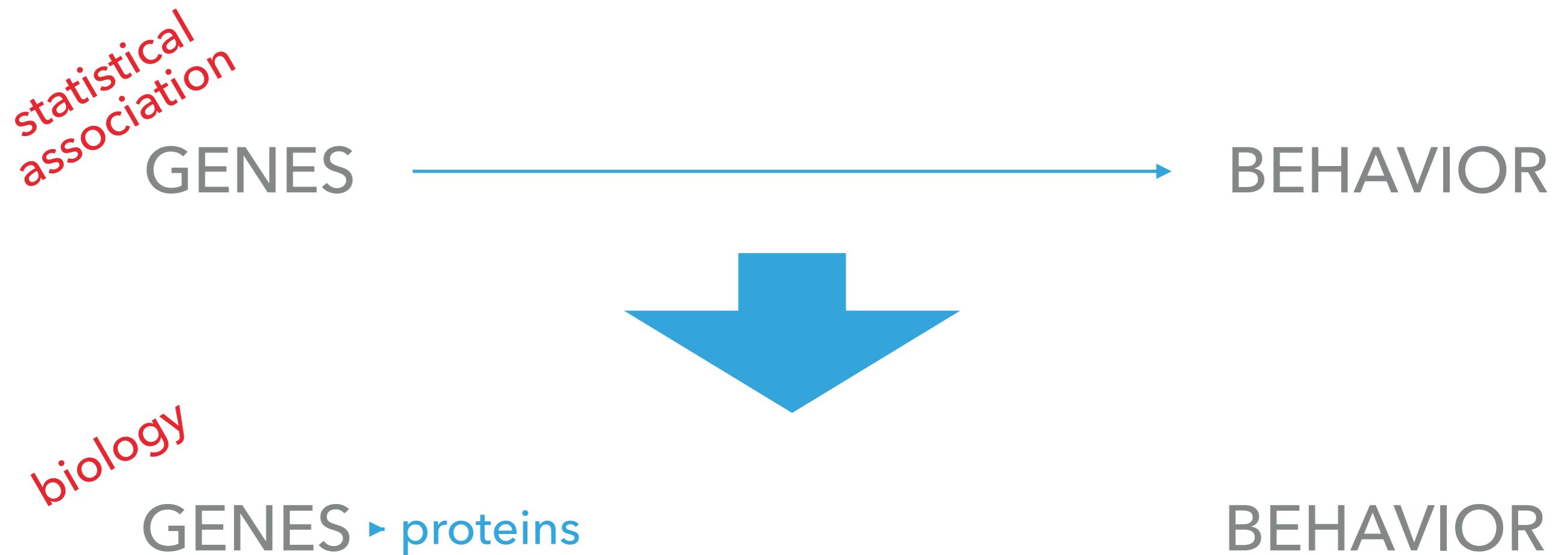
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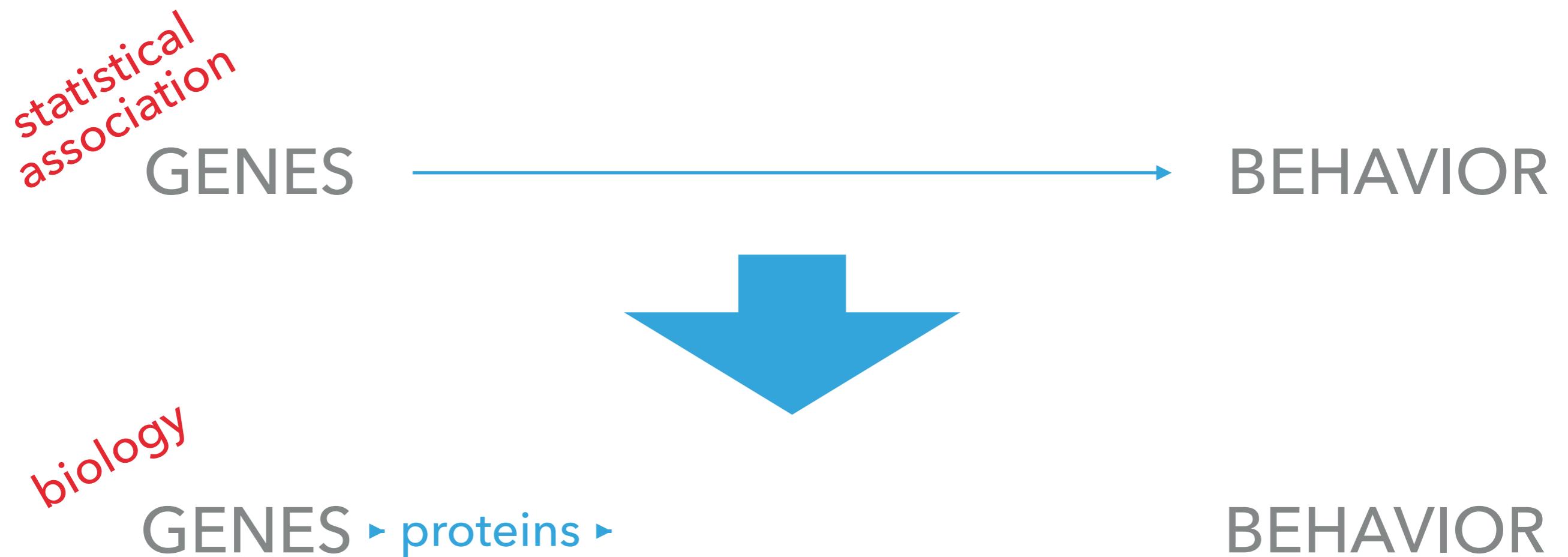
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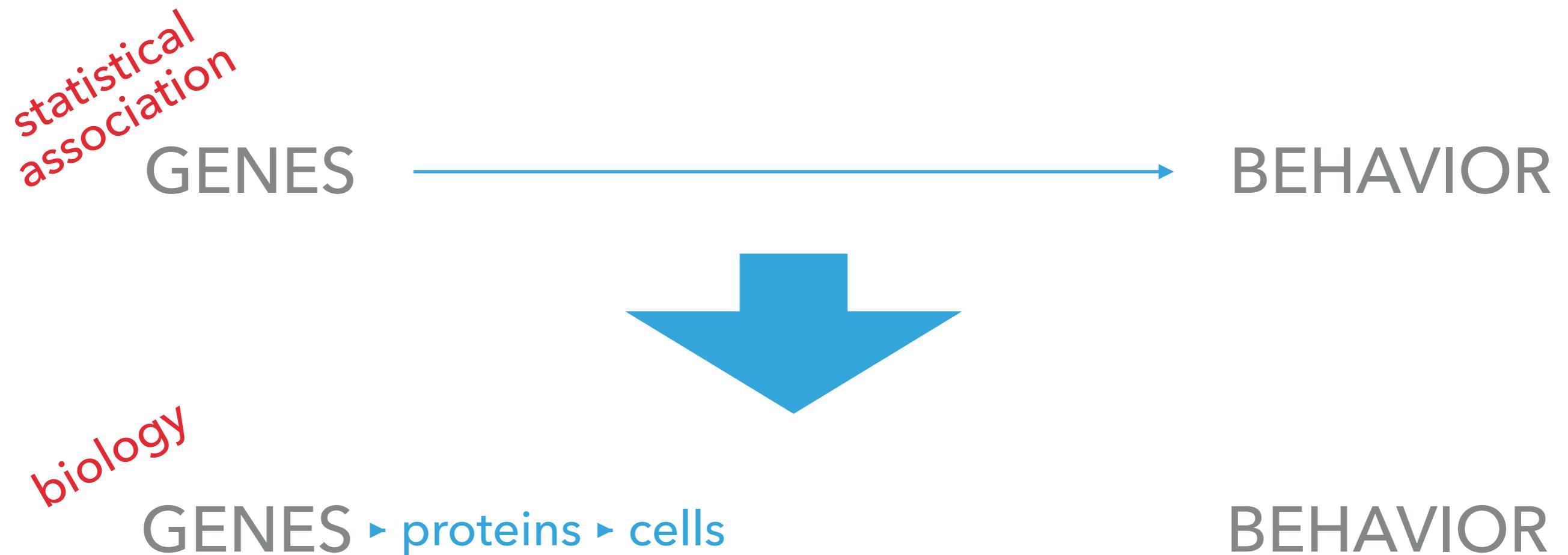
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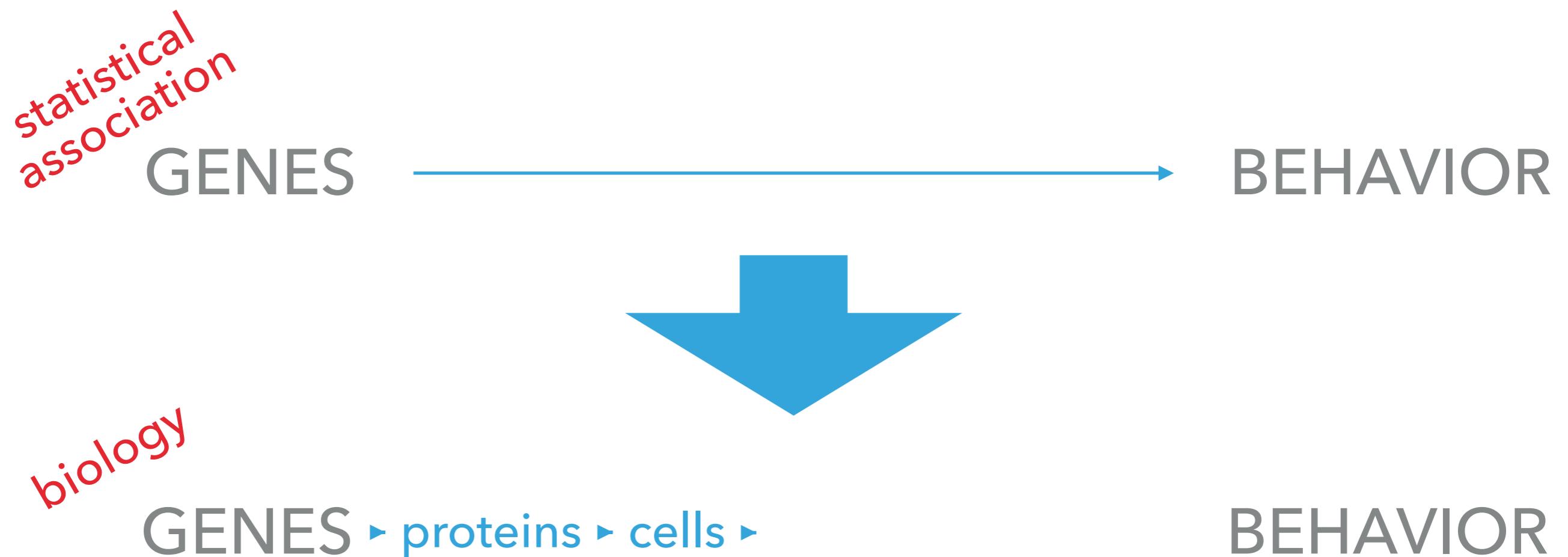
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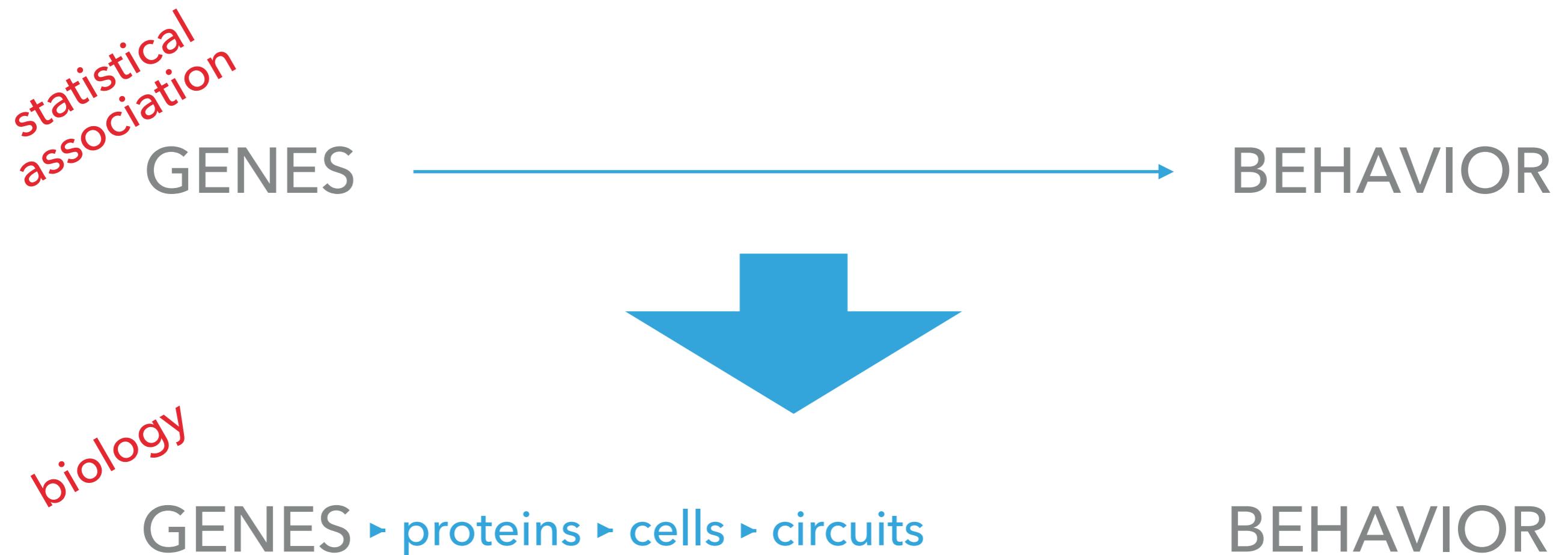
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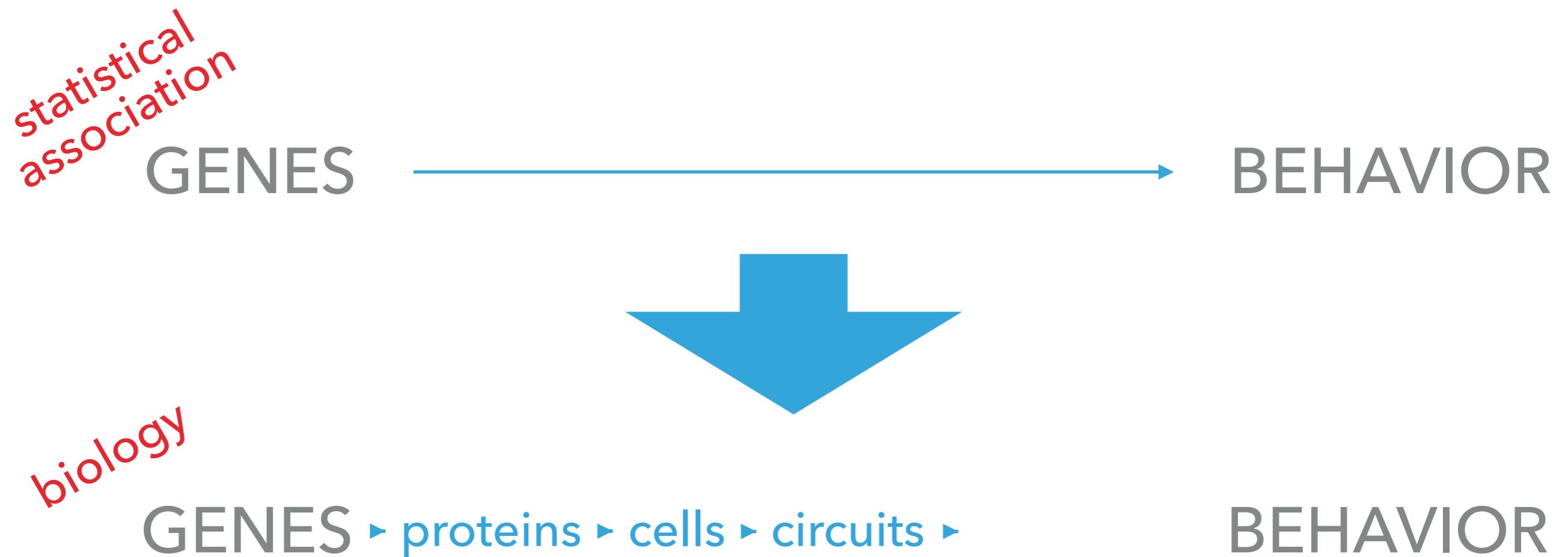
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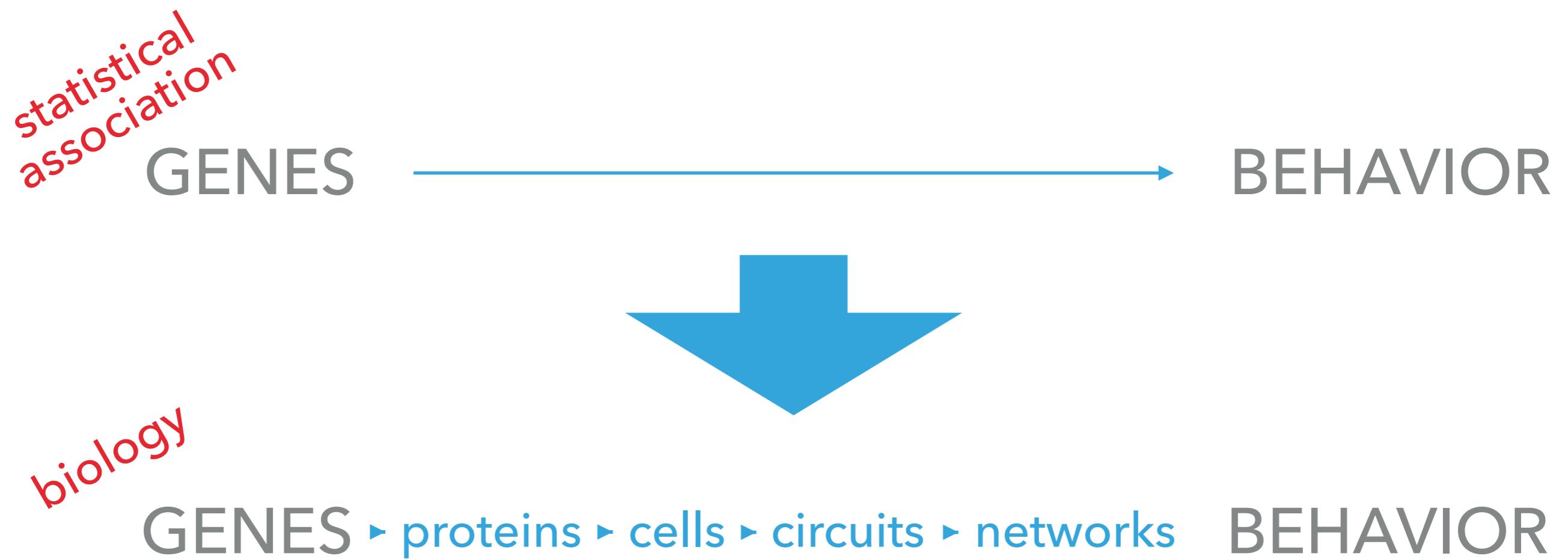
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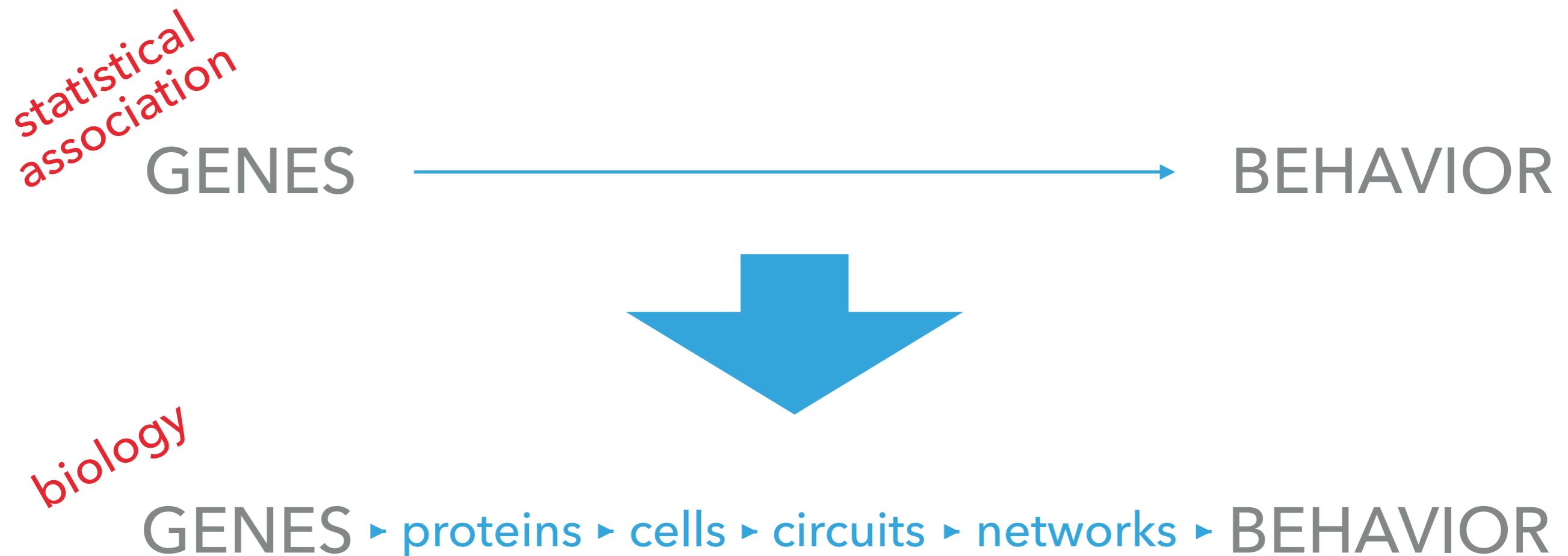
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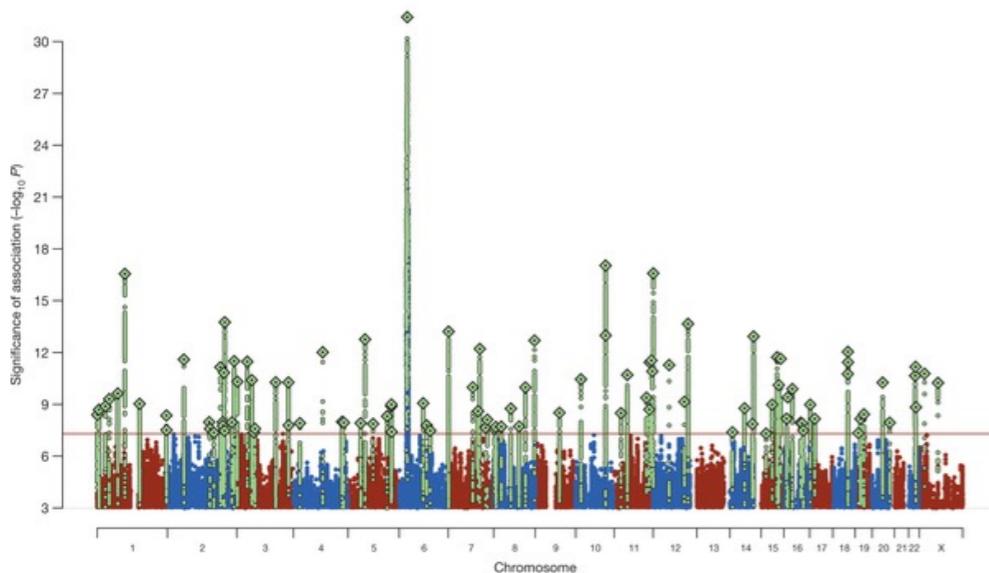
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GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

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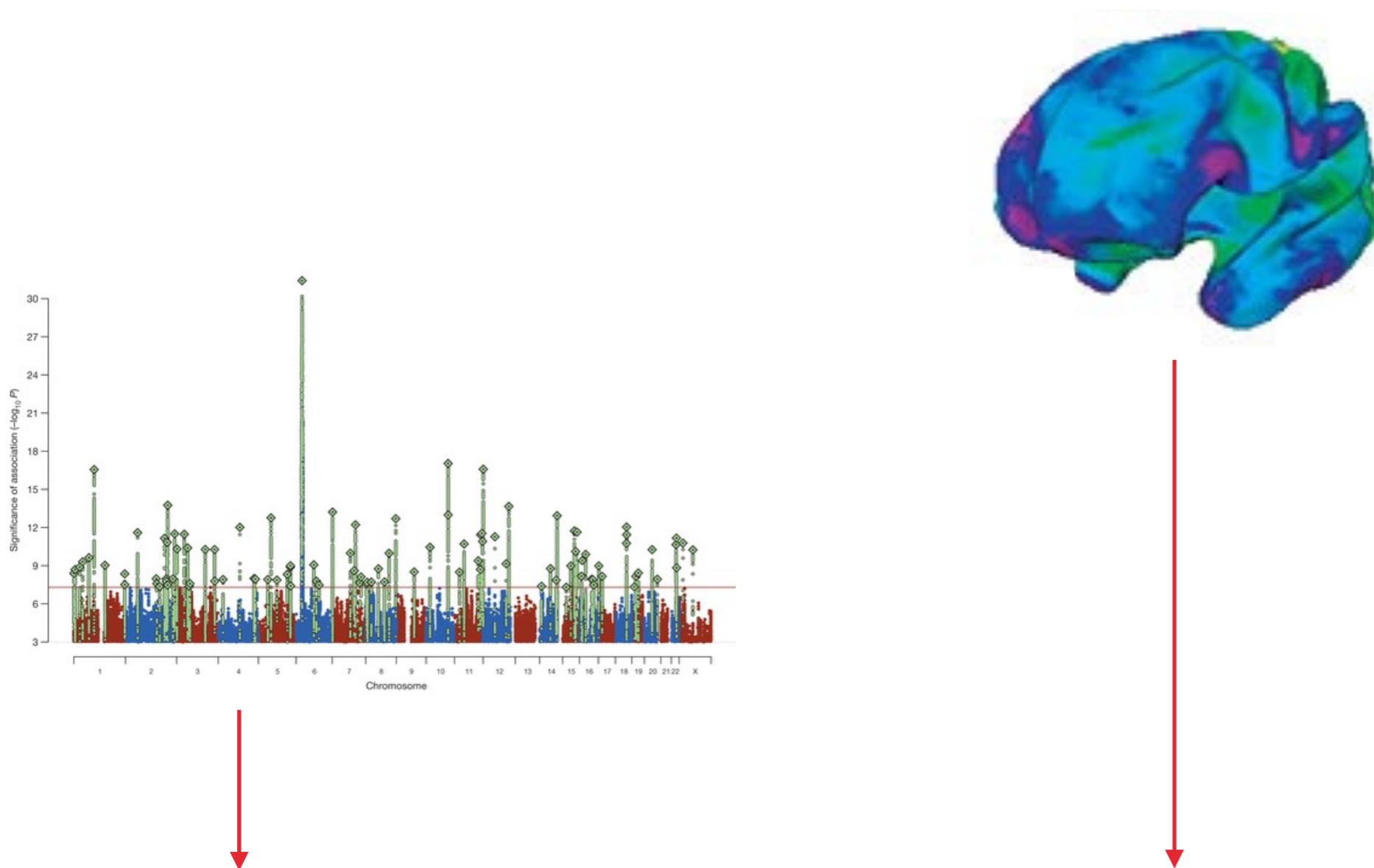
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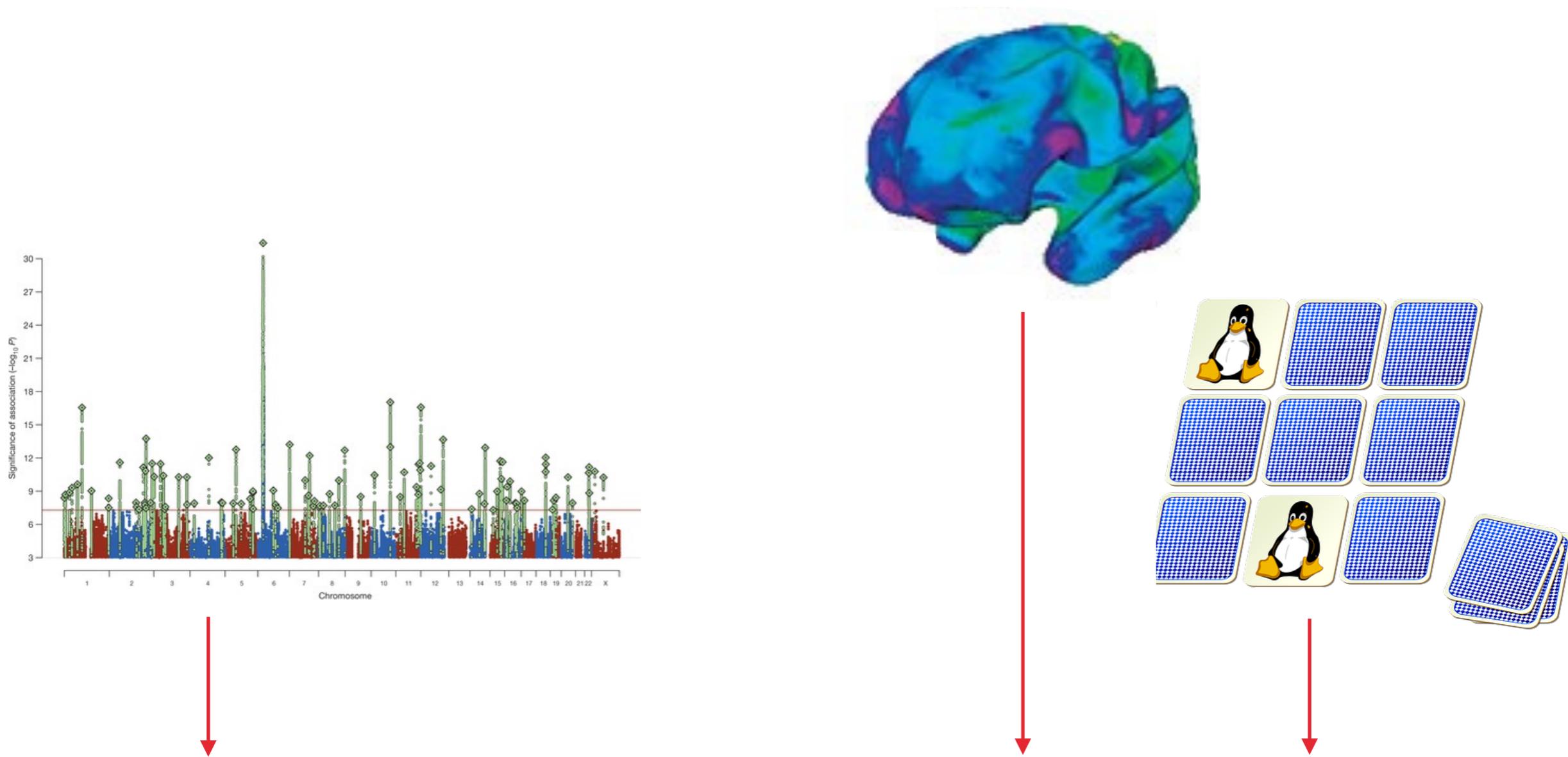
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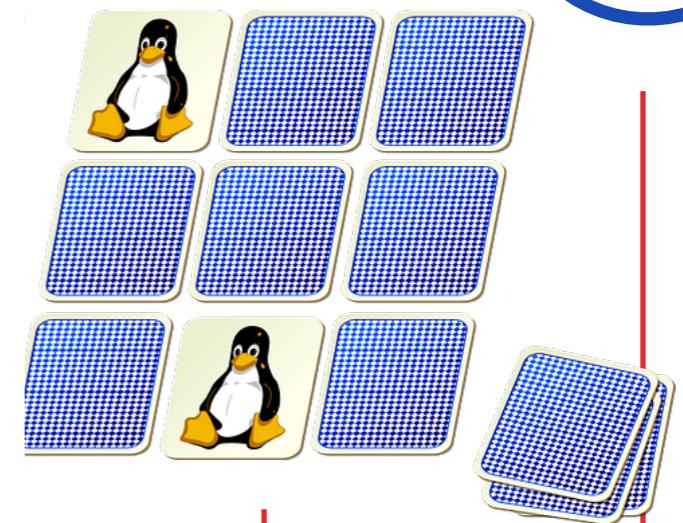
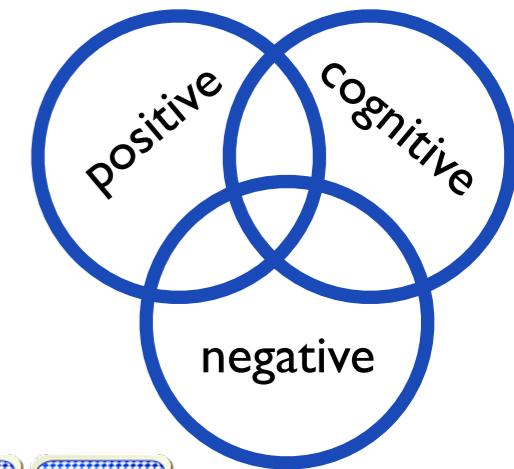
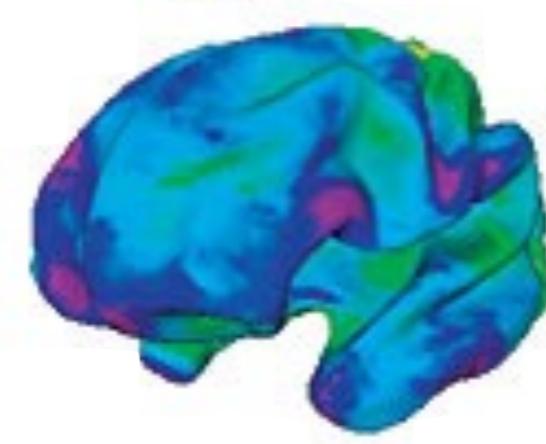
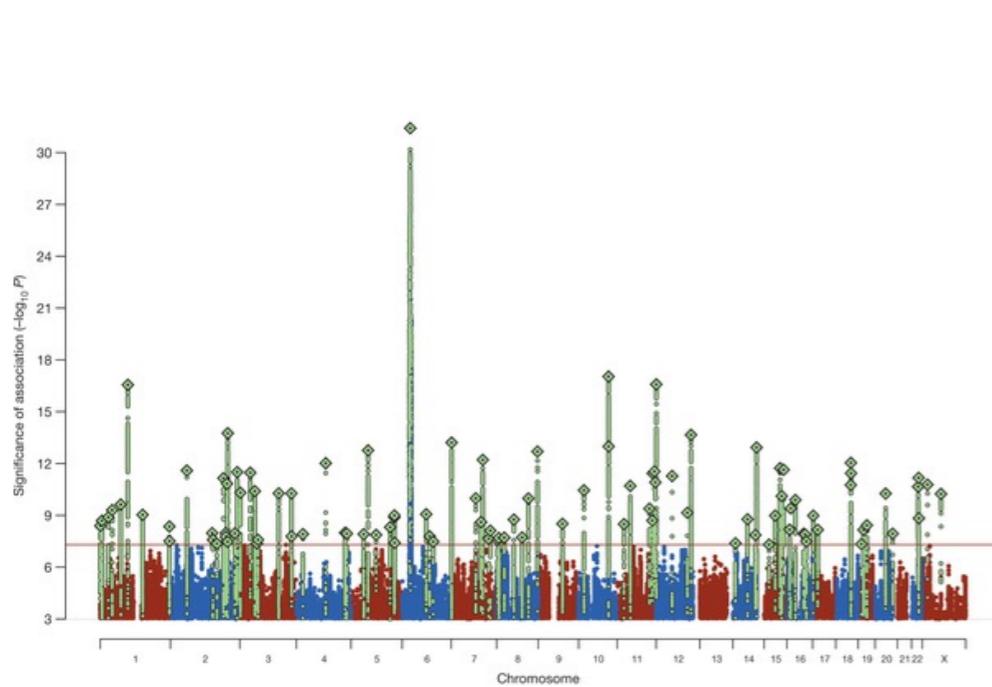
FUNCTIONAL IMPLICATIONS



GENES → proteins → cells → circuits → networks → BEHAVIOR

BACKGROUND

FUNCTIONAL IMPLICATIONS

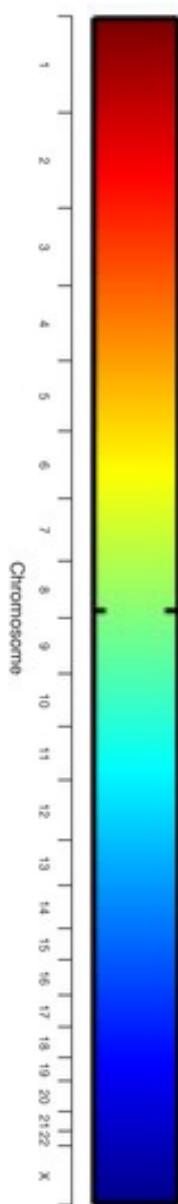


GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

GENOTYPIC PATTERNS

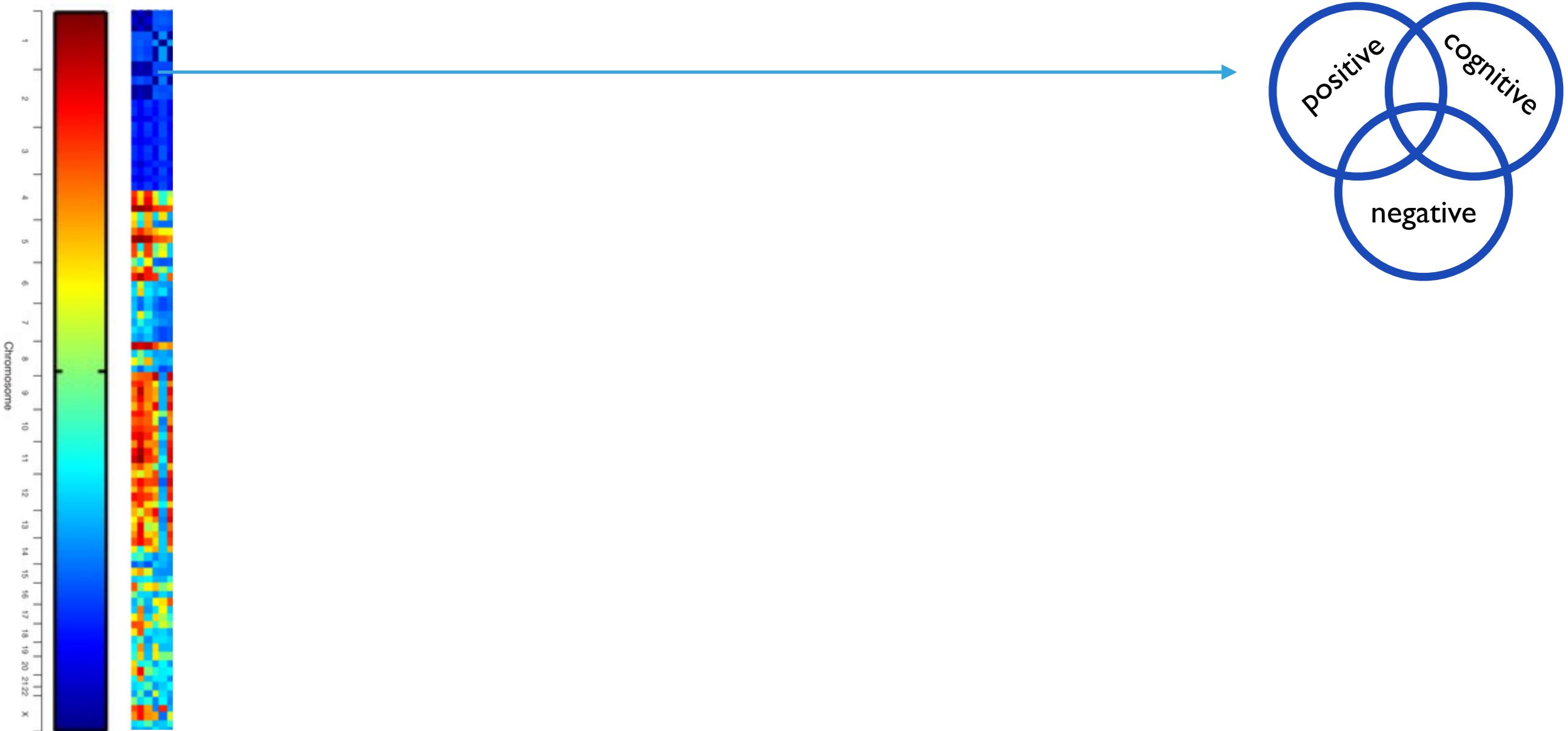
GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

GENOTYPIC PATTERNS



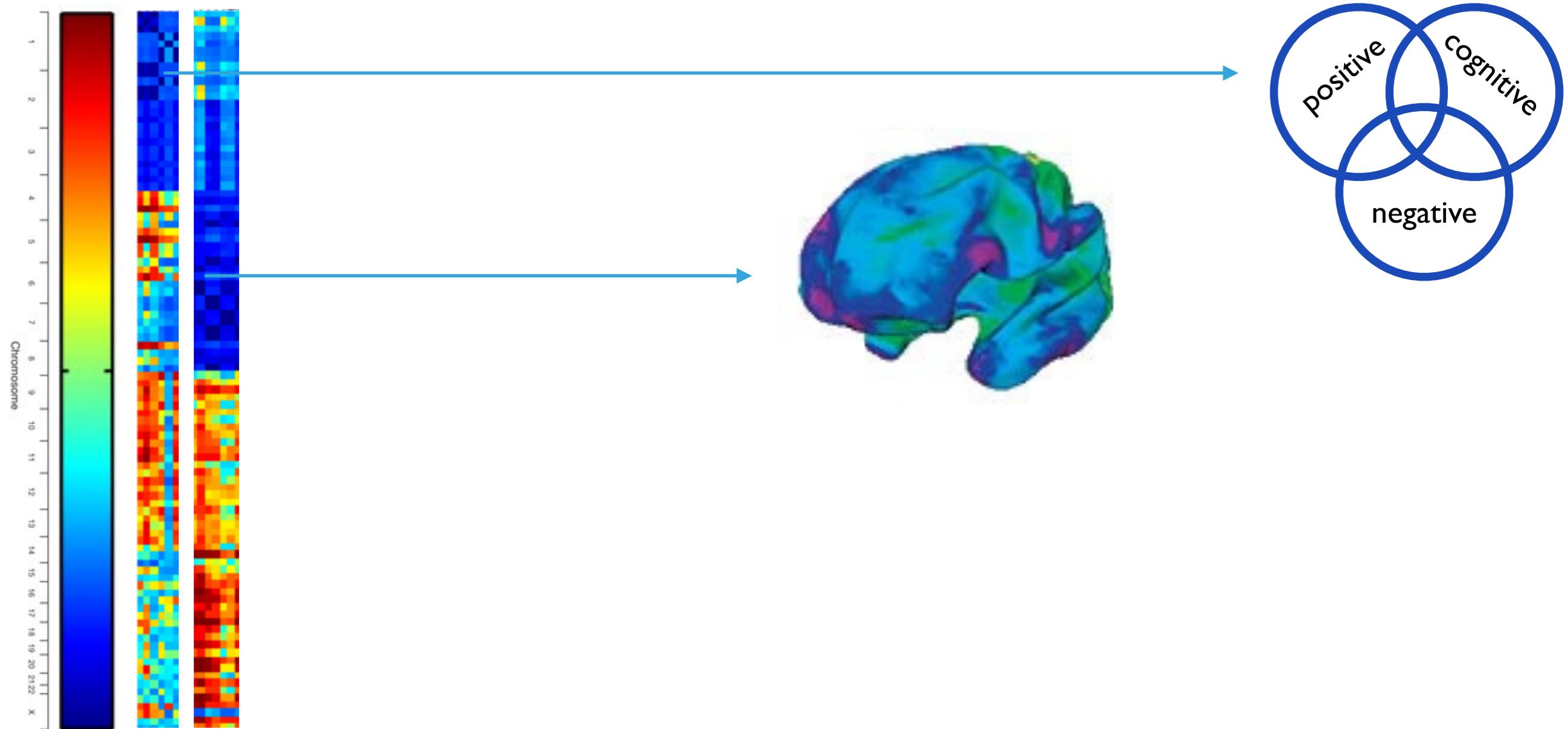
GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

GENOTYPIC PATTERNS



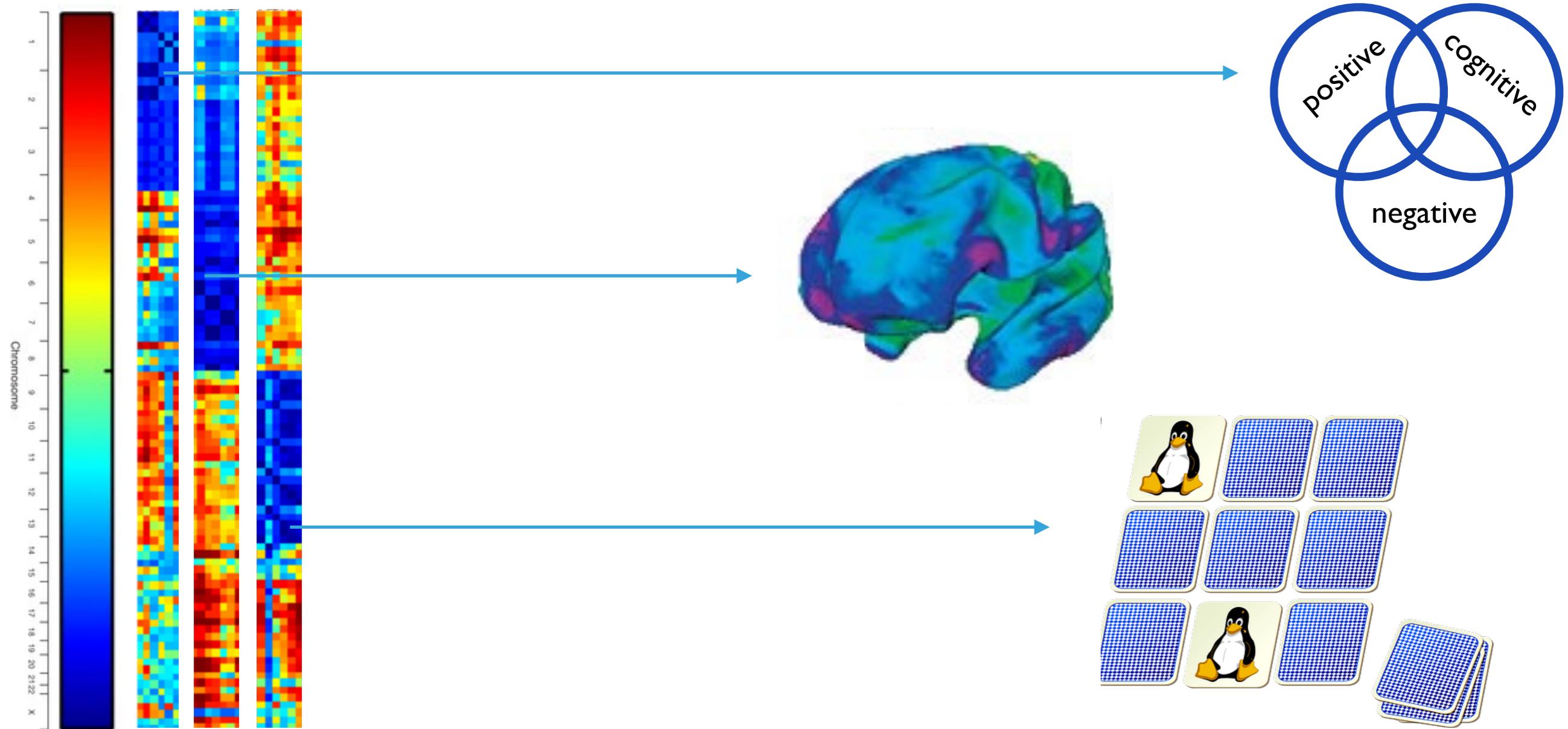
GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

GENOTYPIC PATTERNS



GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

GENOTYPIC PATTERNS



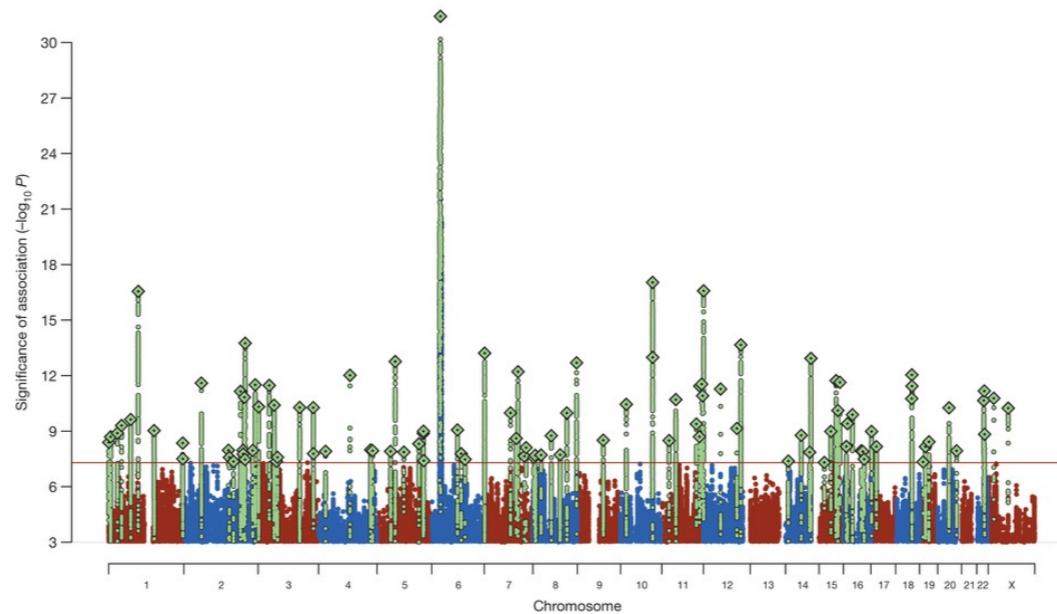
GENES ▶ proteins ▶ cells ▶ circuits ▶ networks ▶ BEHAVIOR

BACKGROUND

FUNCTIONAL CHARACTERIZATION

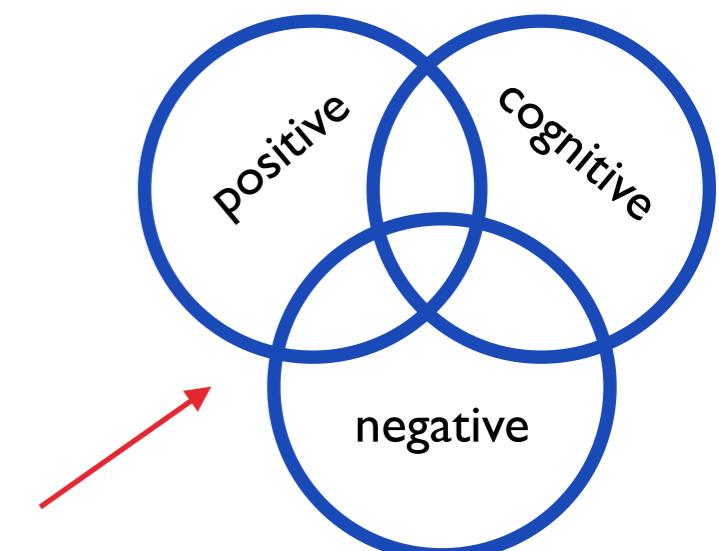
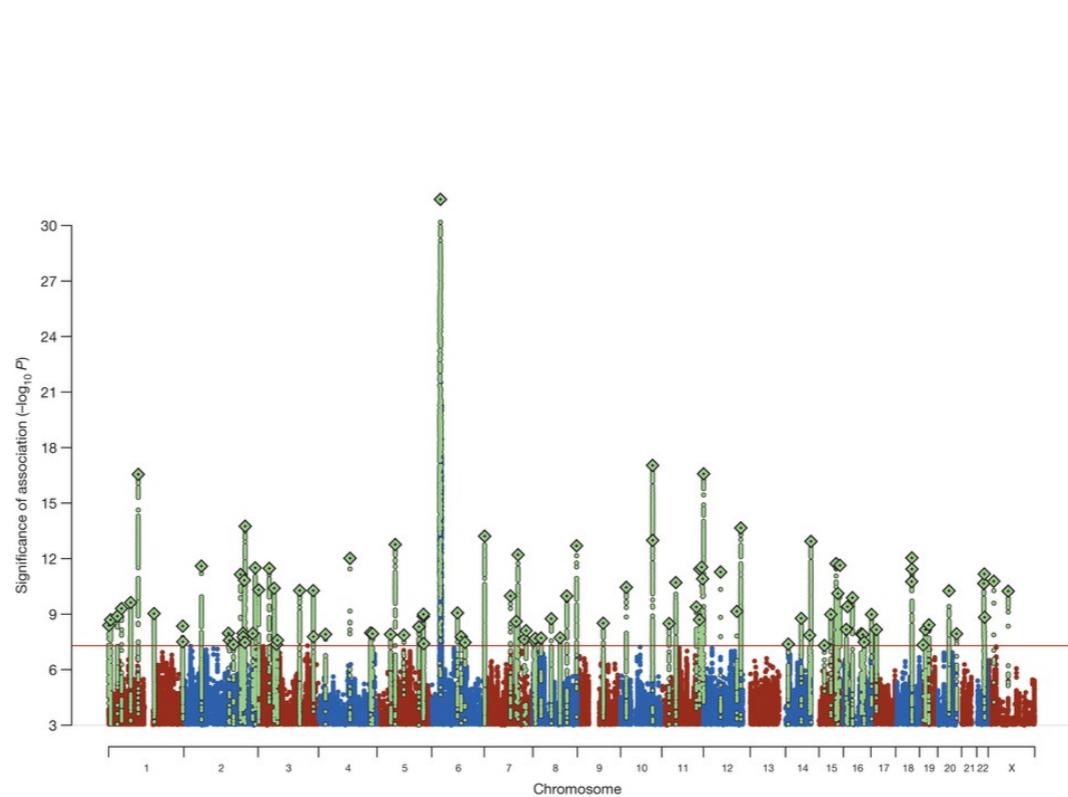
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FUNCTIONAL CHARACTERIZATION

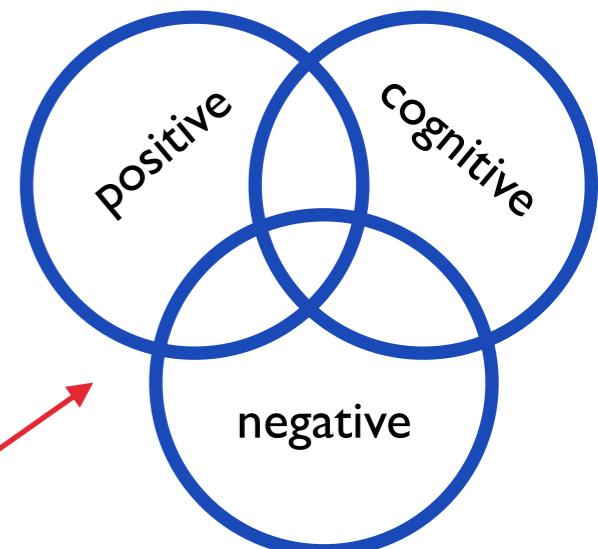
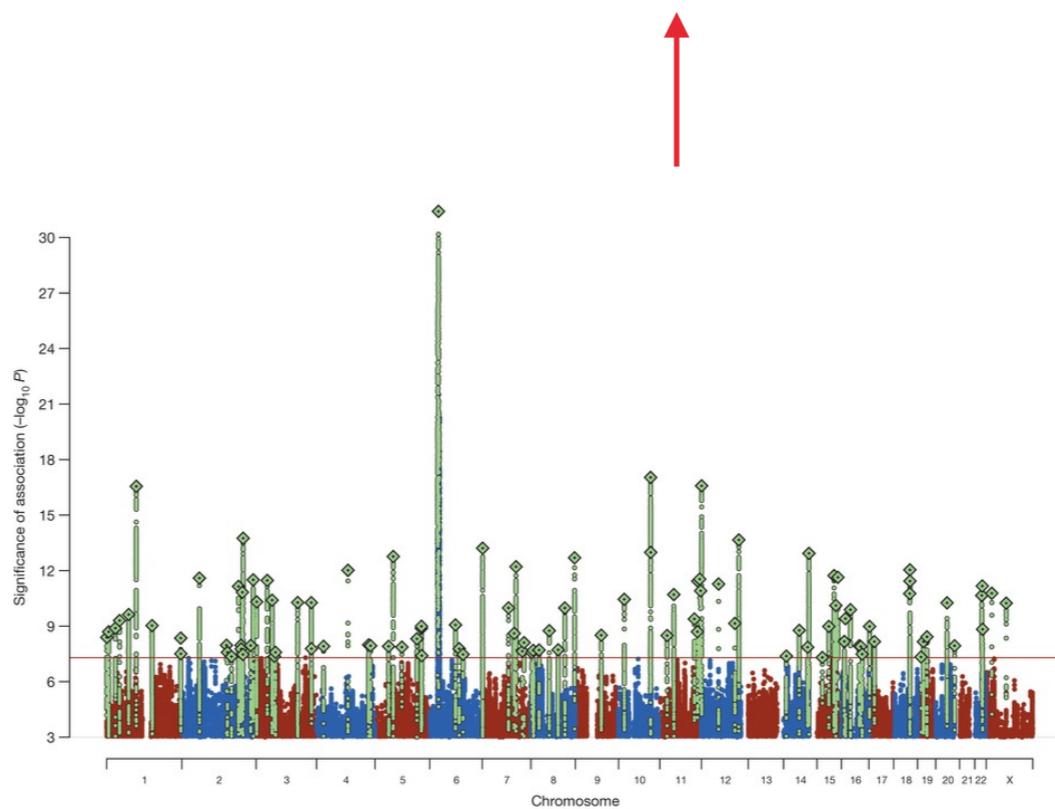
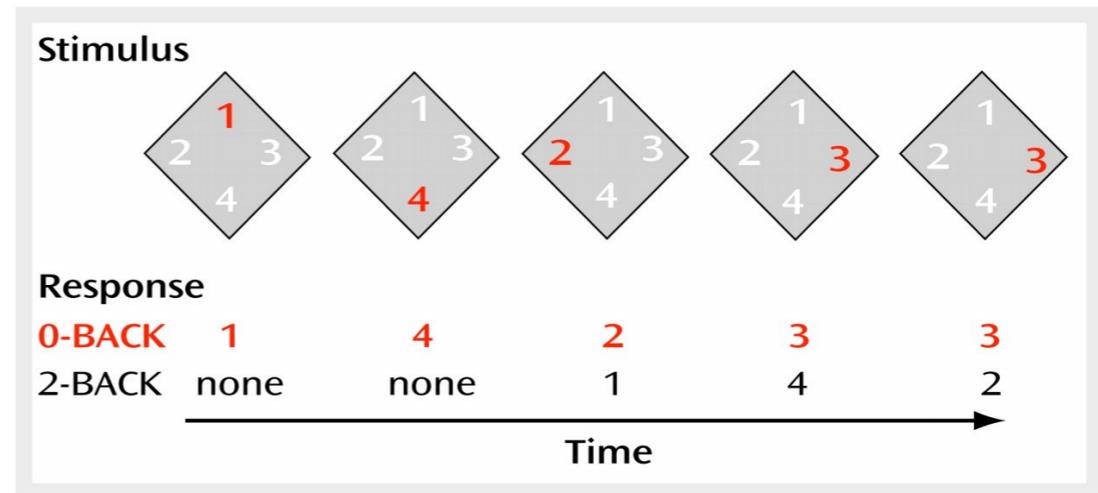


Derks et al., 2012, *PLoS One*; Fanous et al., 2012, *AJP*; Martin et al., 2015, *Psych Res*; Lencz et al., 2014, *Mol Psych*; Hatzimanolis et al., 2015, *AJMG B Neuropsych Gen*; Kauppi et al., 2015, *Schizophrenia Bull*; Whalley et al., 2013, *Biol Psych*; van Scheltinga et al., 2013, *Biol Psych*; Heck et al., 2014, *Neuron*

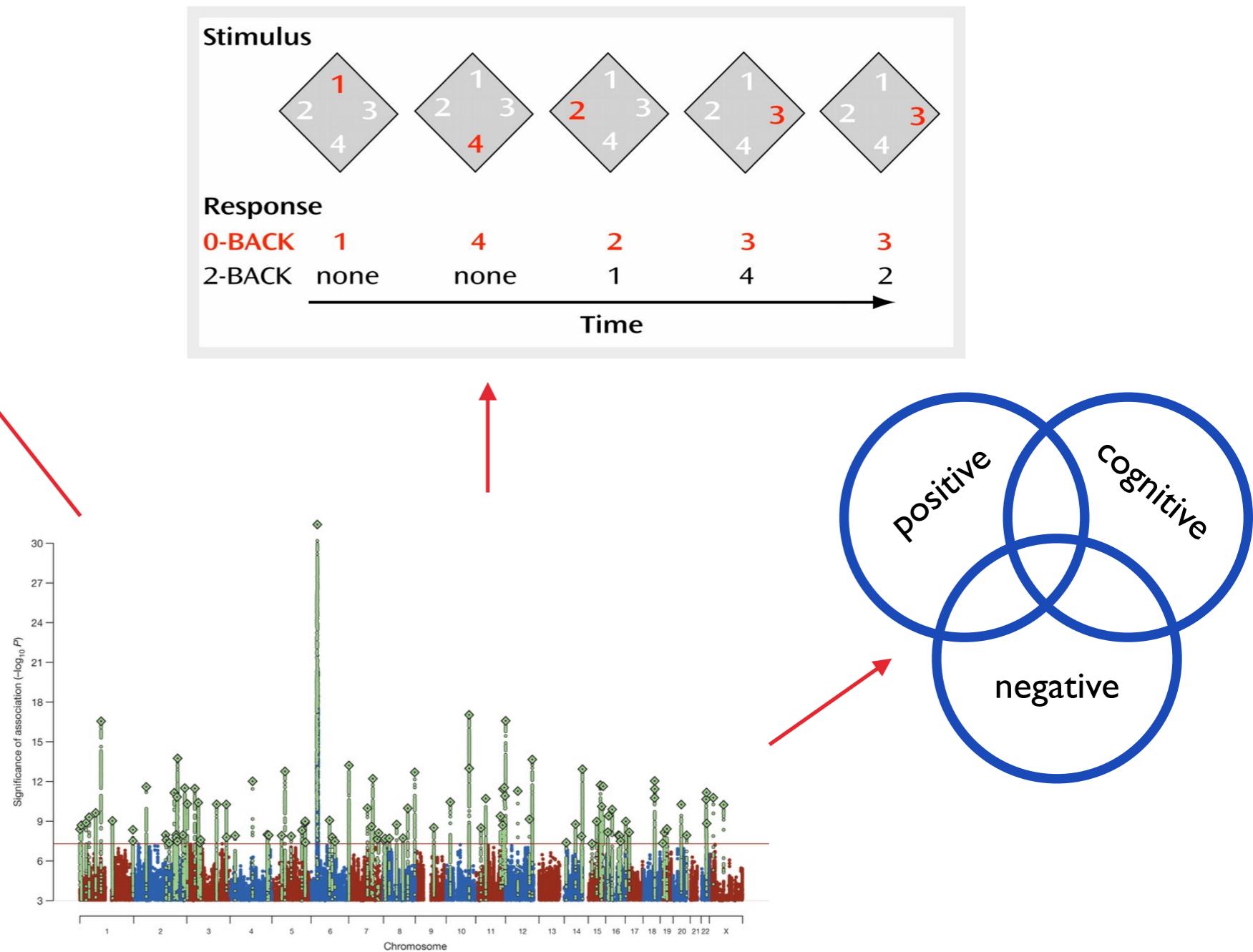
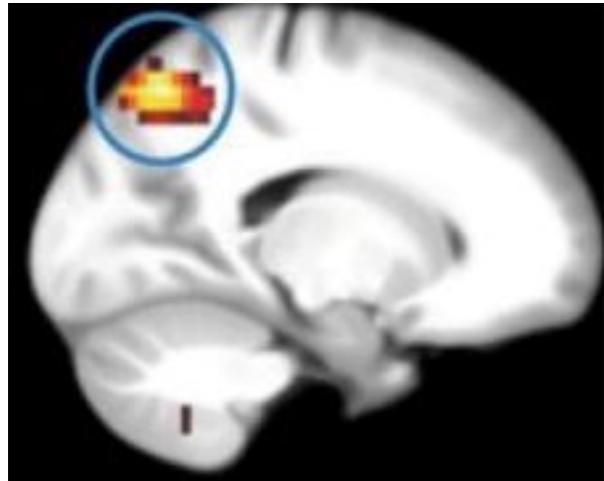
FUNCTIONAL CHARACTERIZATION



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BACKGROUND

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