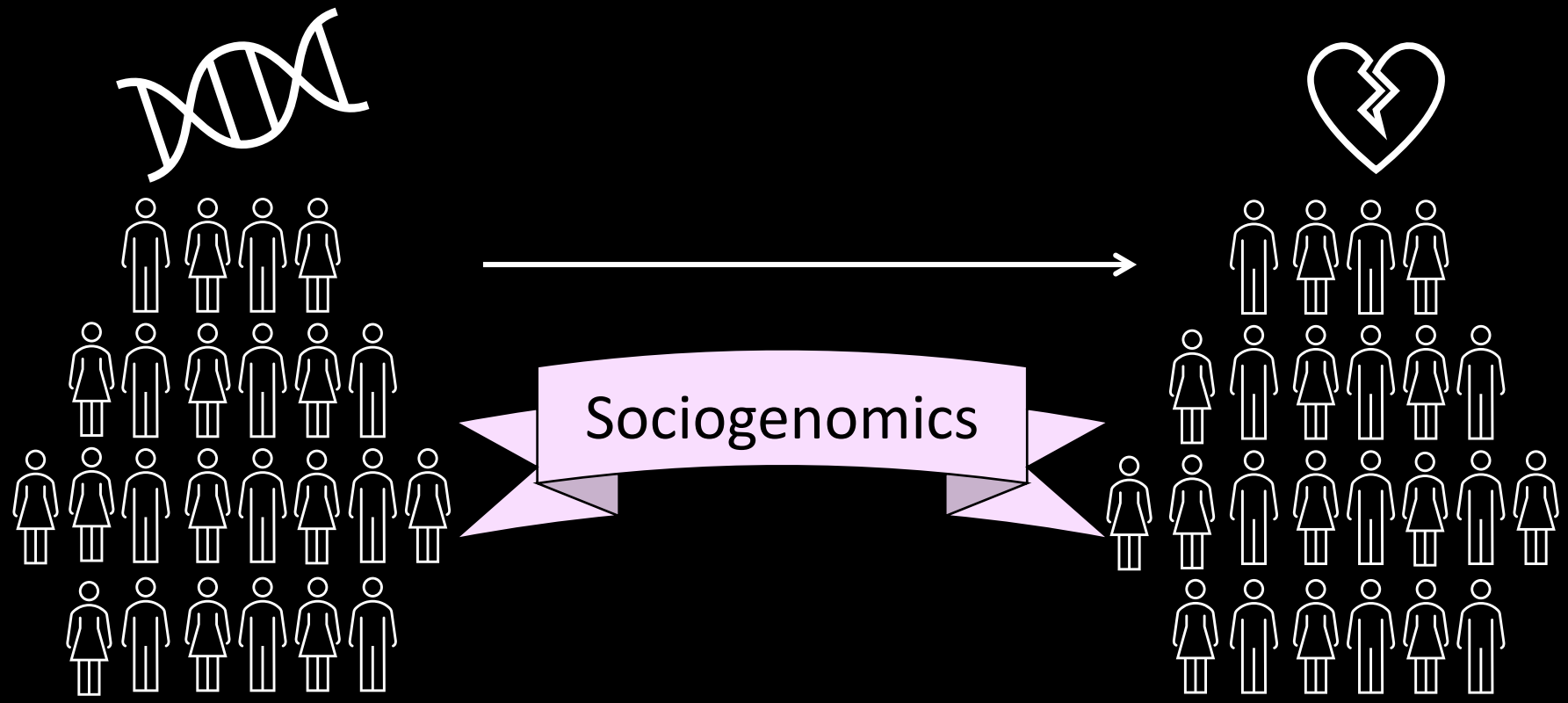
What can we learn from sociogenomic research on partnership dissolution?



Skagerrak
Demographic series
Ruth Eva Jørgensen

Your genes predict whether your relationship lasts





Plan for this talk

1. How did we get here?
   Measuring genetics indirectly:
   Example paper: *Parental divorce and children's partnership dynamics*

2. The arrival of modern sociogenomics:
   Measuring genetics directly:
   Example paper: *The genetics of partnership dissolution*

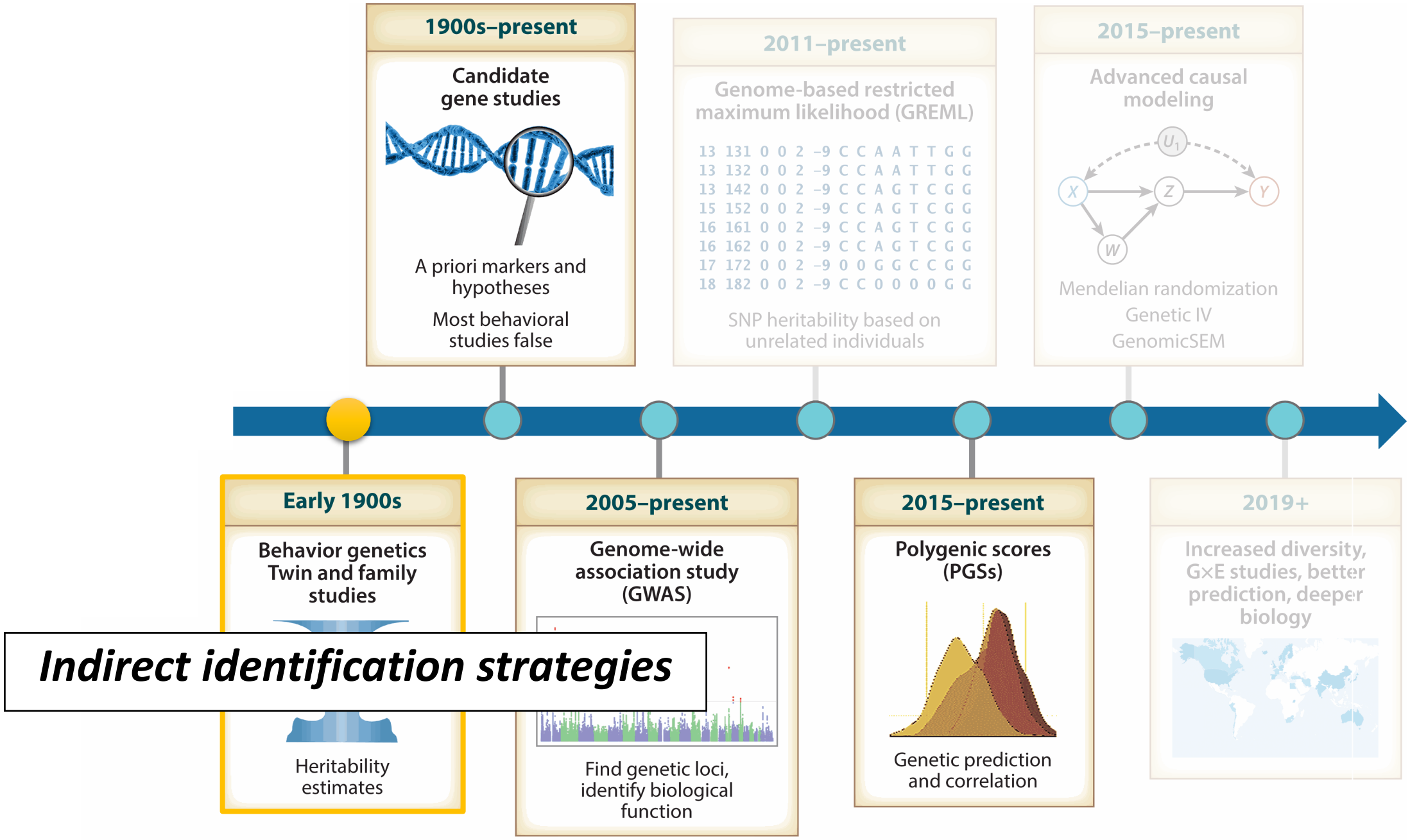
3. Cross-cutting limits

Plan for this talk

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   Measuring genetics indirectly:
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2. The arrival of modern sociogenomics:
   Measuring genetics directly:
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3. Cross-cutting limits

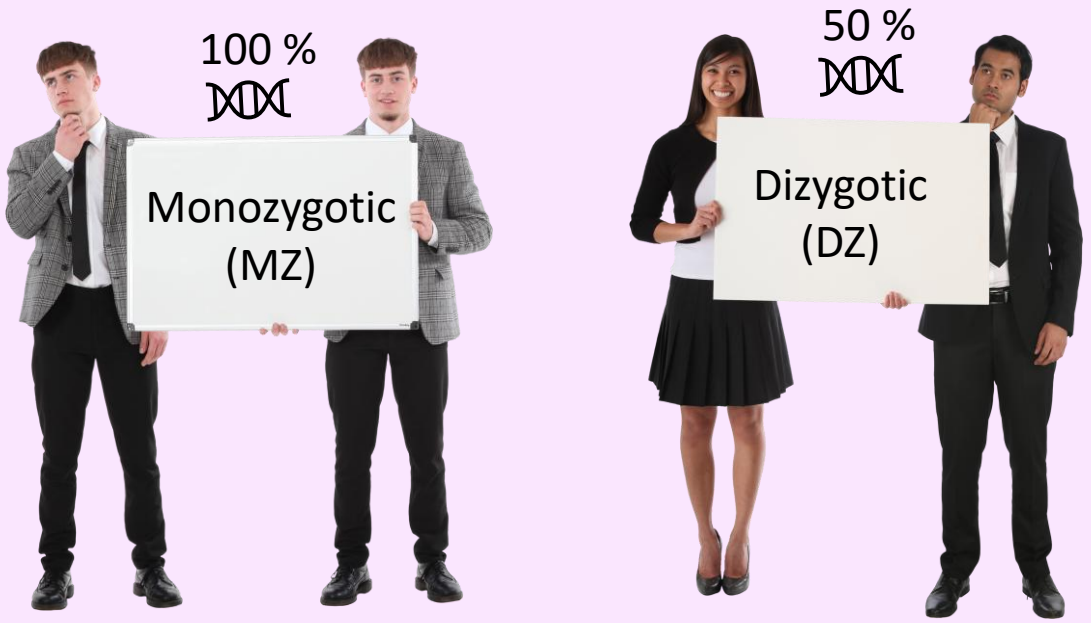


Mills MC, Tropf FC. 2020. *Annu. Rev. Sociol.* 46:553–81

Freese, J. (2018). The Arrival of Social Science Genomics. *Contemporary Sociology: A Journal of Reviews*, *47*(5), 524-536.

Twin studies

- Comparing MZ and DZ twins
  → *variance decomposition*
- Empirical output:
  heritability-estimates
  → How much of the variation in an outcome is explained by genetic factors?



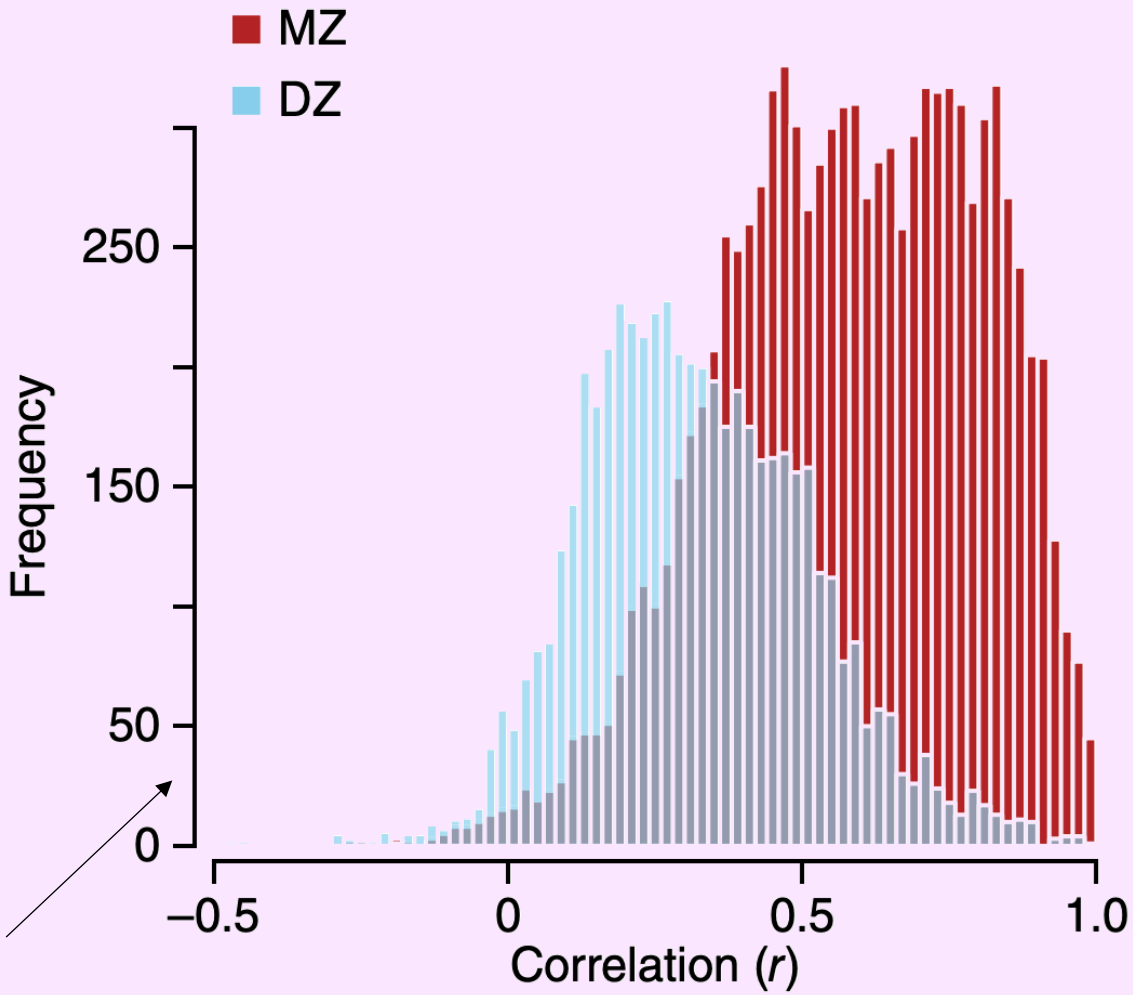
Twin studies

«Everything is heritable»

1st law of behavior genetics, Turkheimer (2000)

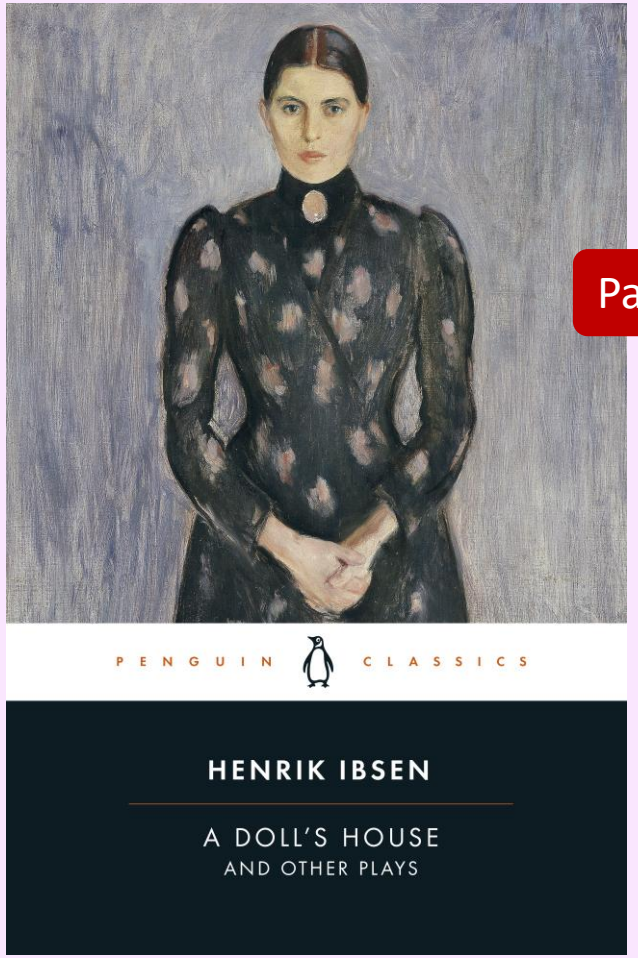
H2 of divorce: 15-53 %

17,804 traits; 2,748 publications; 14,558,903 twin pairs
Polderman et al. (2015)



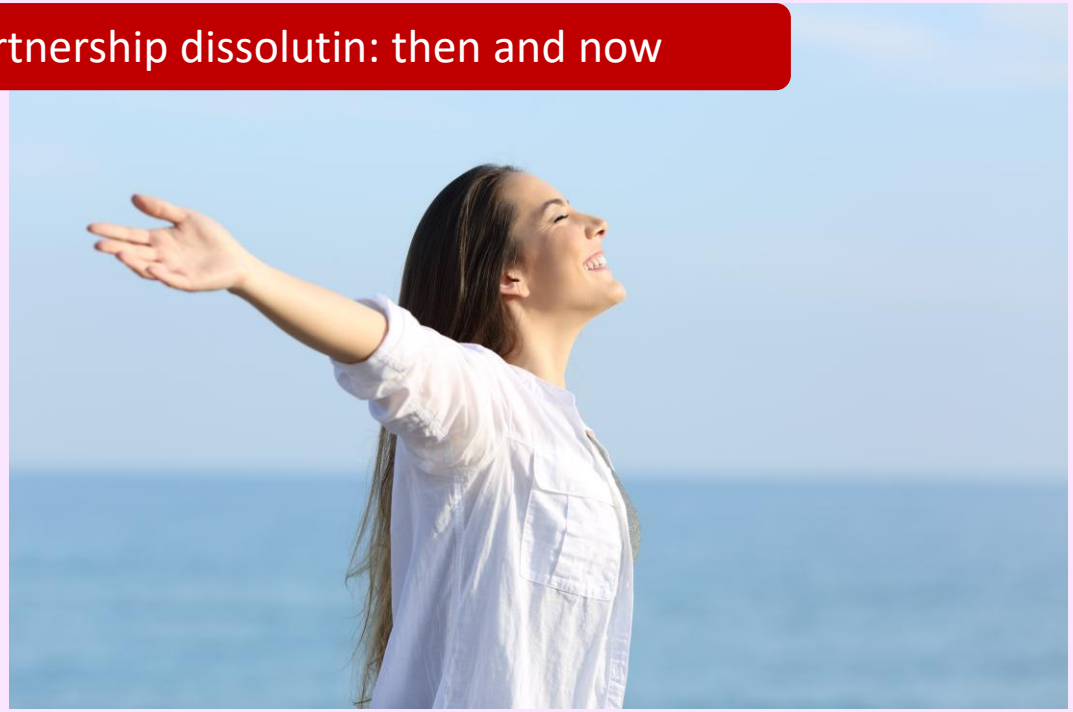


Twin studies



- **Outcome (not essence) heritability:**
  Not a fixed property of a trait, but of variation in a trait in a population

Partnership dissolutin: then and now



ILLUMINATE

- Everything is partly heritable
- Not purely environmental influence
- Non-shared environments also matter!
- GxE interaction

The divorce cycle

Parental Divorce & Children's Partnership Dynamics

Ruth Eva Jørgensen, Arno Van Hootegem &
Torkild H. Lyngstad

UNIVERSITY
OF OSLO

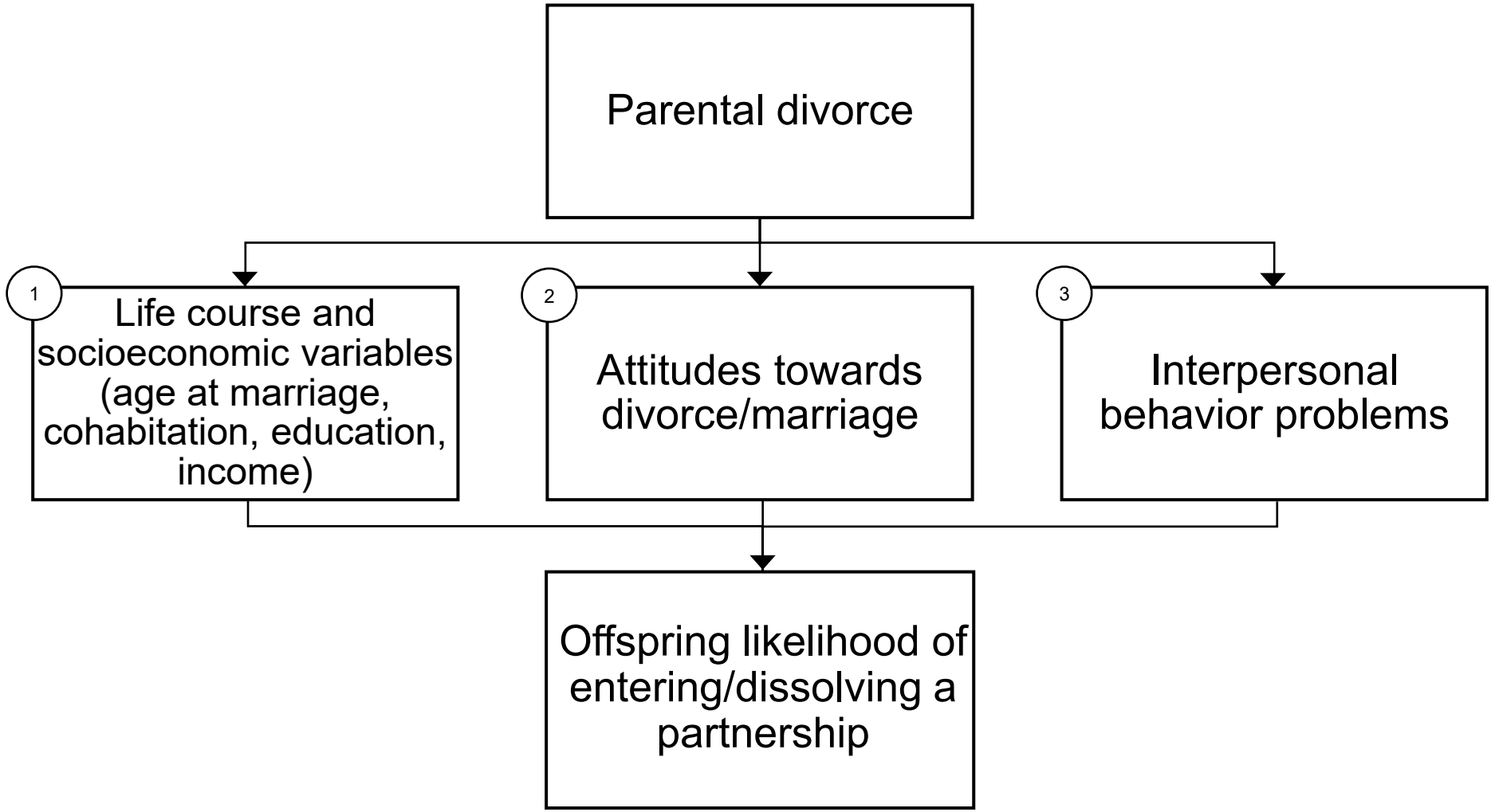


Background

- Rising instability of partnerships → more children experience parental union dissolution
- Children of divorce
  - More likely to leave home early, partner early, choose cohabitation over marriage (Kuperberg, 2014; Sassler et al., 2009)
  - Higher risk of partnership dissolution (Amato, 2000; Lyngstad & Jalovaara, 2010; Stanfors & Bergvall 2024; Wolfinger, 2005)
- → Causal impact vs. selection?

Theoretical perspectives

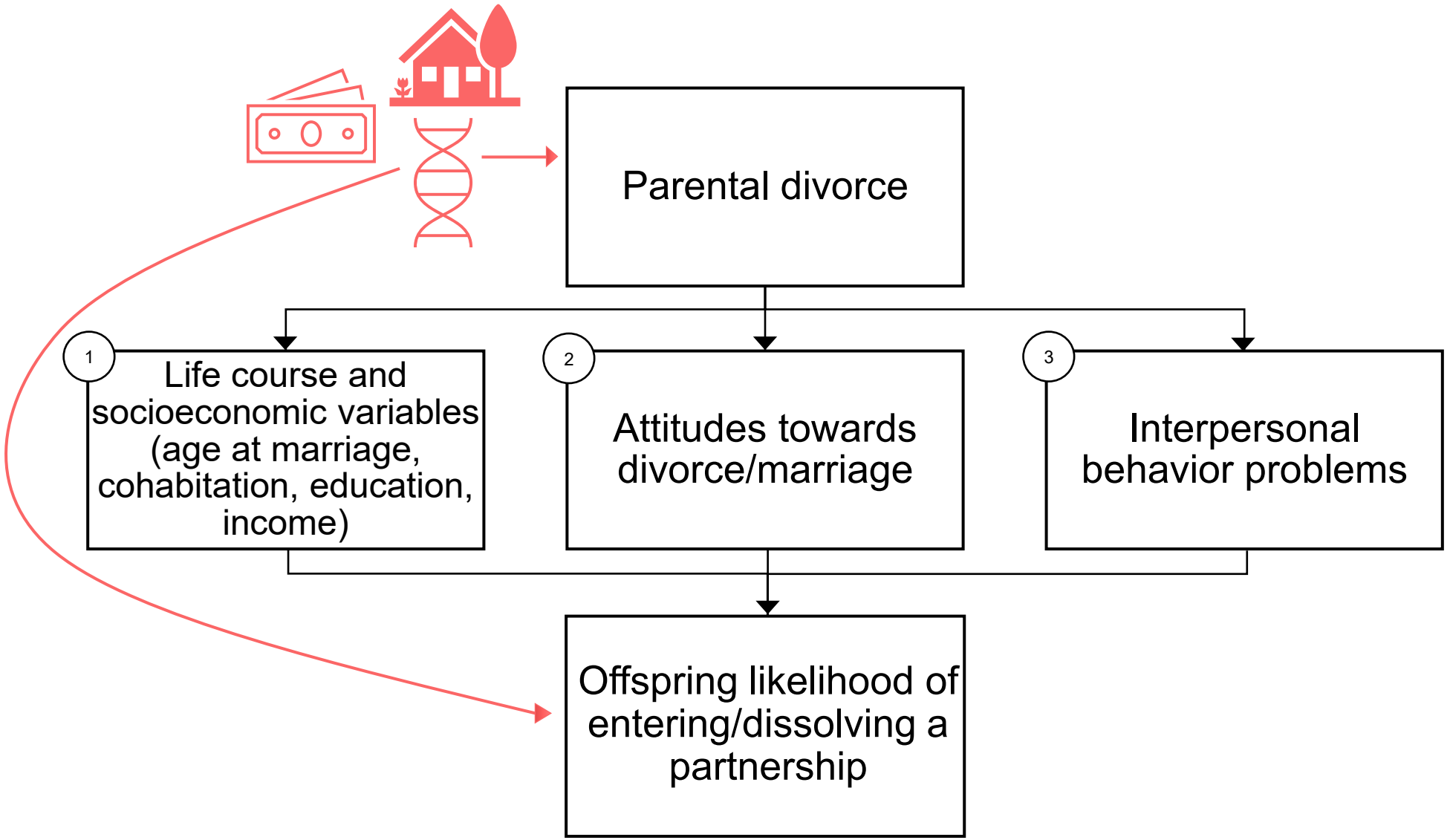
- **Family environment model**:
  disrupted family processes, social learning, economic strain
  (Amato 1996)



Adapted from Amato 1996

Theoretical perspectives

- **Family environment model:**
  disrupted family processes, social learning, economic strain
  (Amato 1996)
- **Selection Perspective:**
  shared dispositions, genetics, family background factors
  (McGue & Lykken 1992; D'Onofrio et al., 2007; Salvatore et al. 2018)



Adapted from Amato (1996)

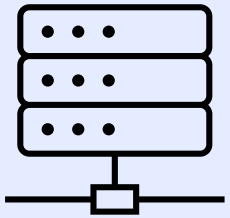
Research Questions

Does parental divorce affect children's:

1. Likelihood of entering co-residential partnerships?
2. Likelihood of dissolving such partnerships?

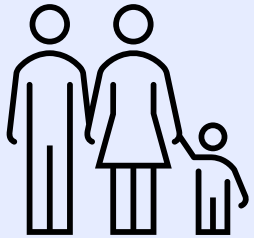
Data

Norwegian population registers



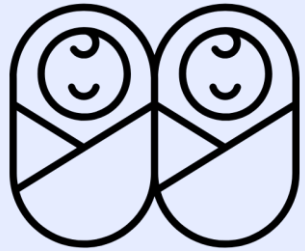
Full coverage

Adoptive families



Indirect identification strategy → Discrepancies birth country

Twin registers



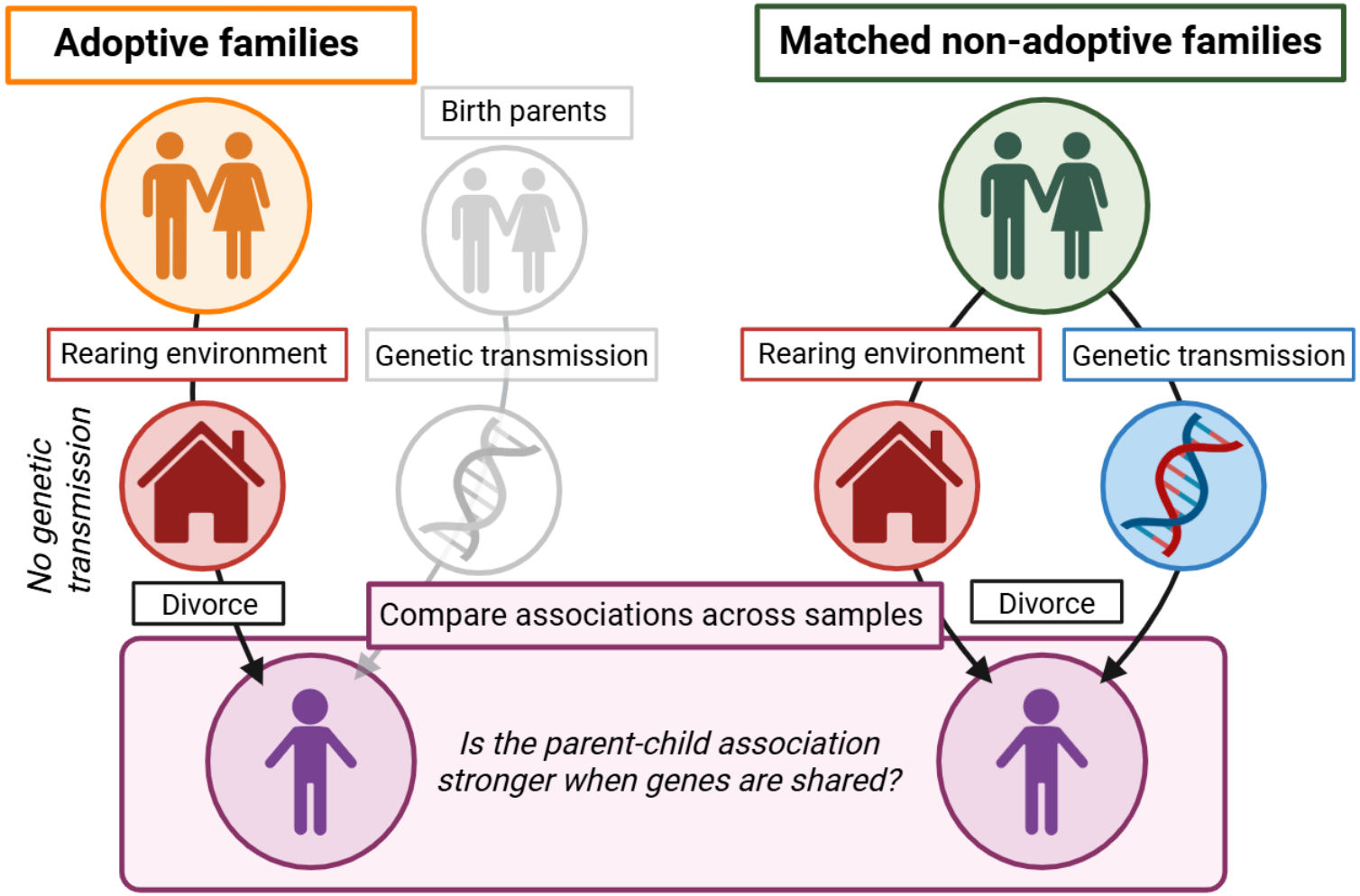
Adult twins and their children

Adoption Design

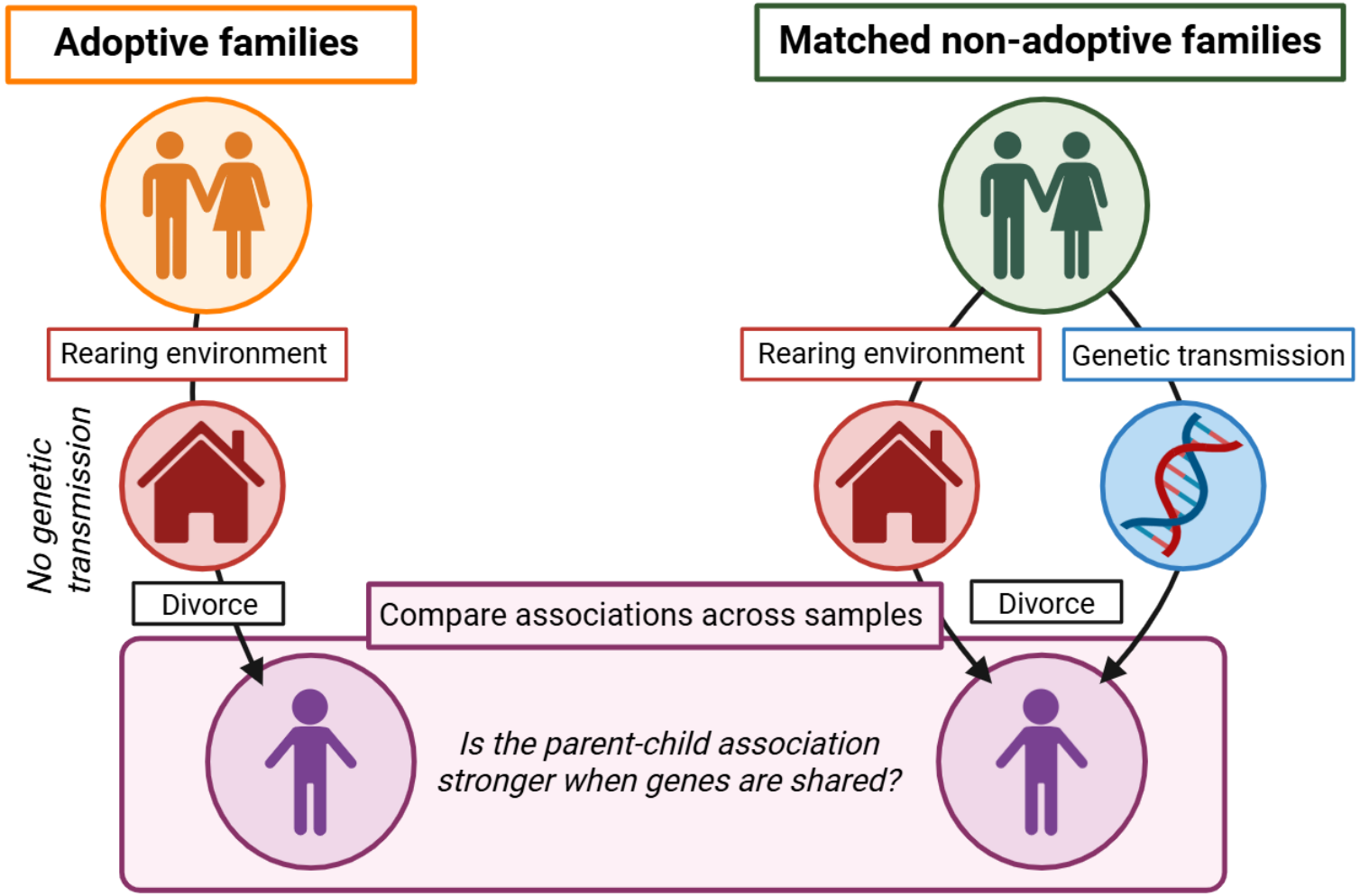
- Sample: South Korean adoptees: (N≈2,150) vs. Matched Norwegian peers (N≈2,150)
  - Born from 1965-1985
  - End of follow-up: 2023
- 1:1 Nearest neighbor matching:
  - Gender, birth year, birth order, number of children, parents' education, parents' income rank, parents' occupational status, mother's and father's birth year
- Method: discrete time event-history models

$$log\left(\frac{P(dissolution = 1)}{1 - P(dissolution = 1)}\right) = \beta 0 + \beta 1 mother_{divorced} + \beta 2 age^{2}_{centered})$$

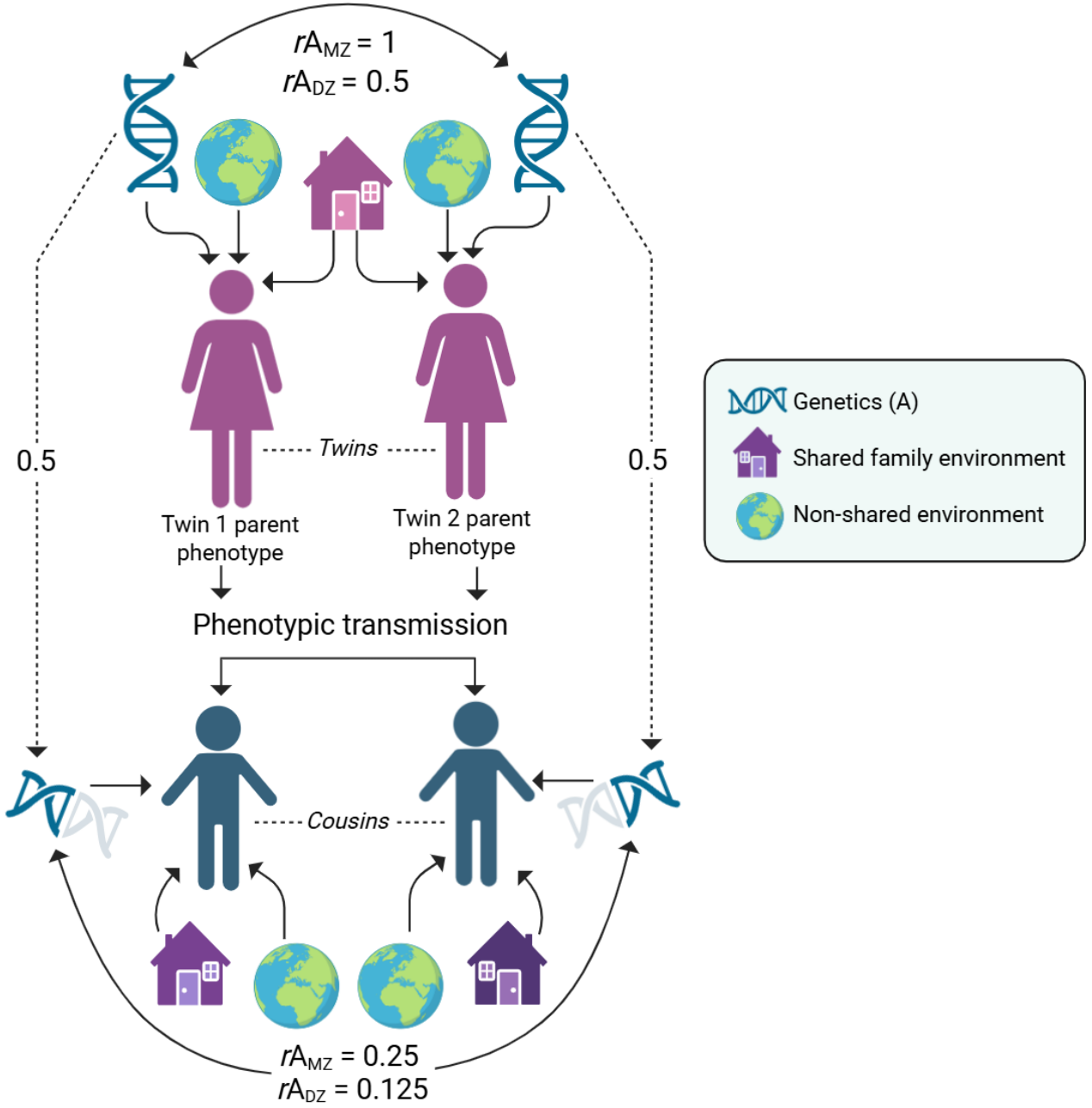
Adoption Design



Adoption Design



Children of Twins-Design (CoT)



Children of Twins-Design (CoT)

MZ and DZ twins (N≈28,500) + children

$$\log(y_{ijk}) = \beta_0 + \beta_1 Within_{jk} + \beta_2 Between_k + \beta_3 DZ_{jk} + \beta_4 (Within_{jk} * DZ_{jk})$$

Parent	Twin Pair	Divorce	Between	Within
101	1001	1	0.5	0.5
102	1001	0	0.5	-0.5
103	1002	0	0	0
104	1002	0	0	0
105	1003	1	1	0
106	1003	1	1	0
107	1004	0	0.5	-0.5
108	1004	1	0.5	0.5

Children of Twins-Design (CoT)

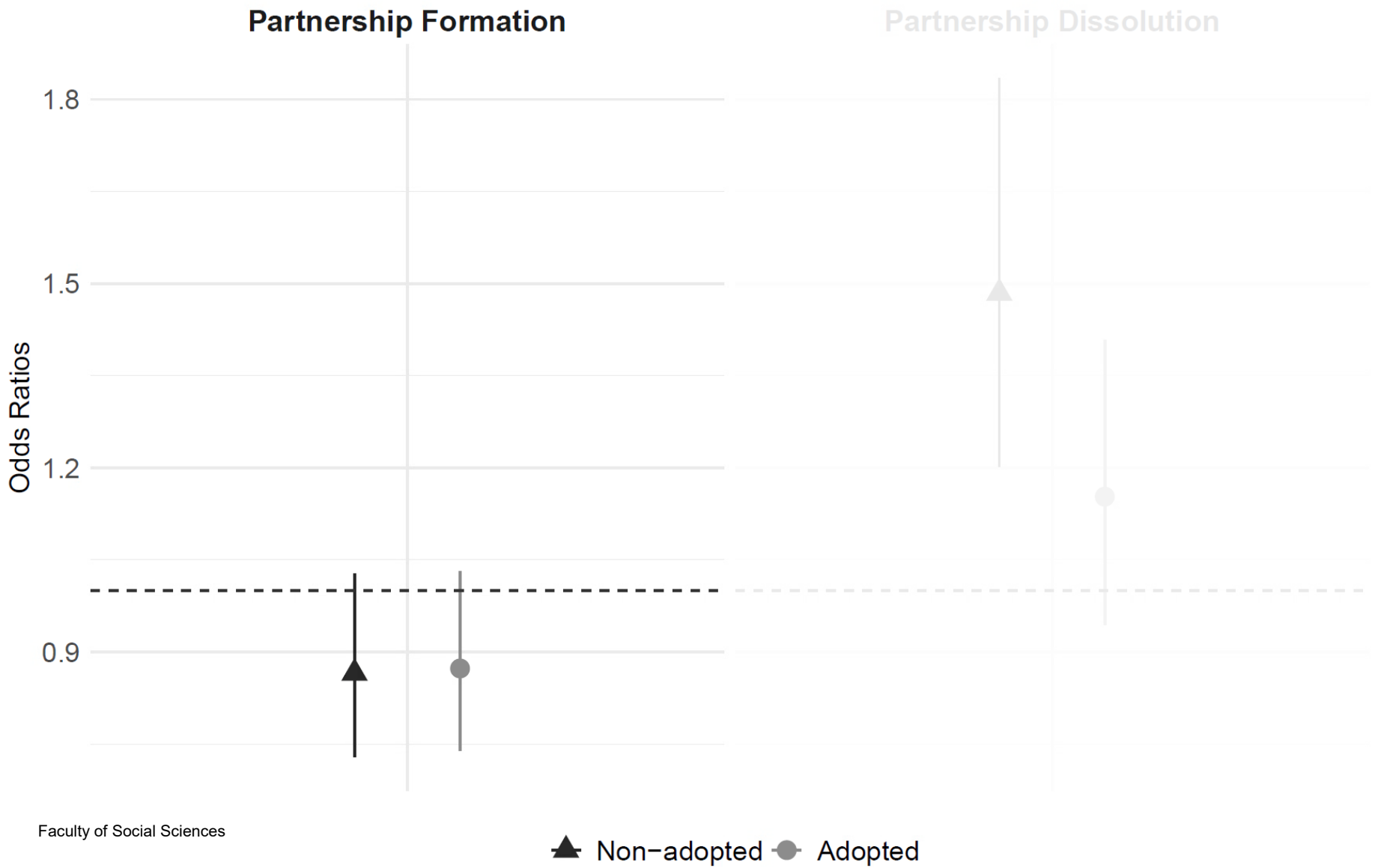
MZ and DZ twins (N≈28,500) + children

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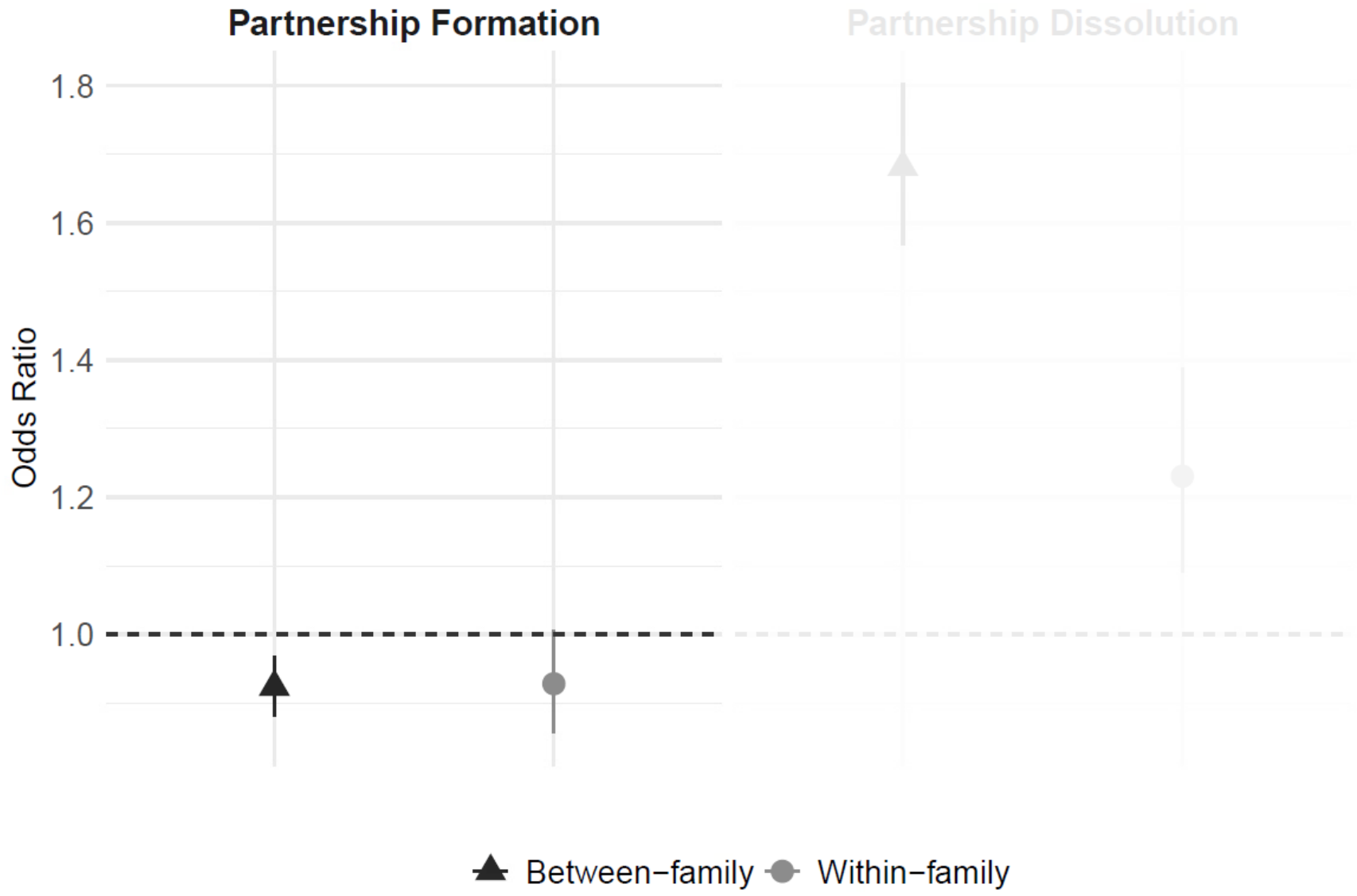
Parent	Twin Pair	Divorce	Between	Within
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104	1002	0	0	0
105	1003	1	1	0
106	1003	1	1	0
107	1004	0	0.5	-0.5
108	1004	1	0.5	0.5

Results

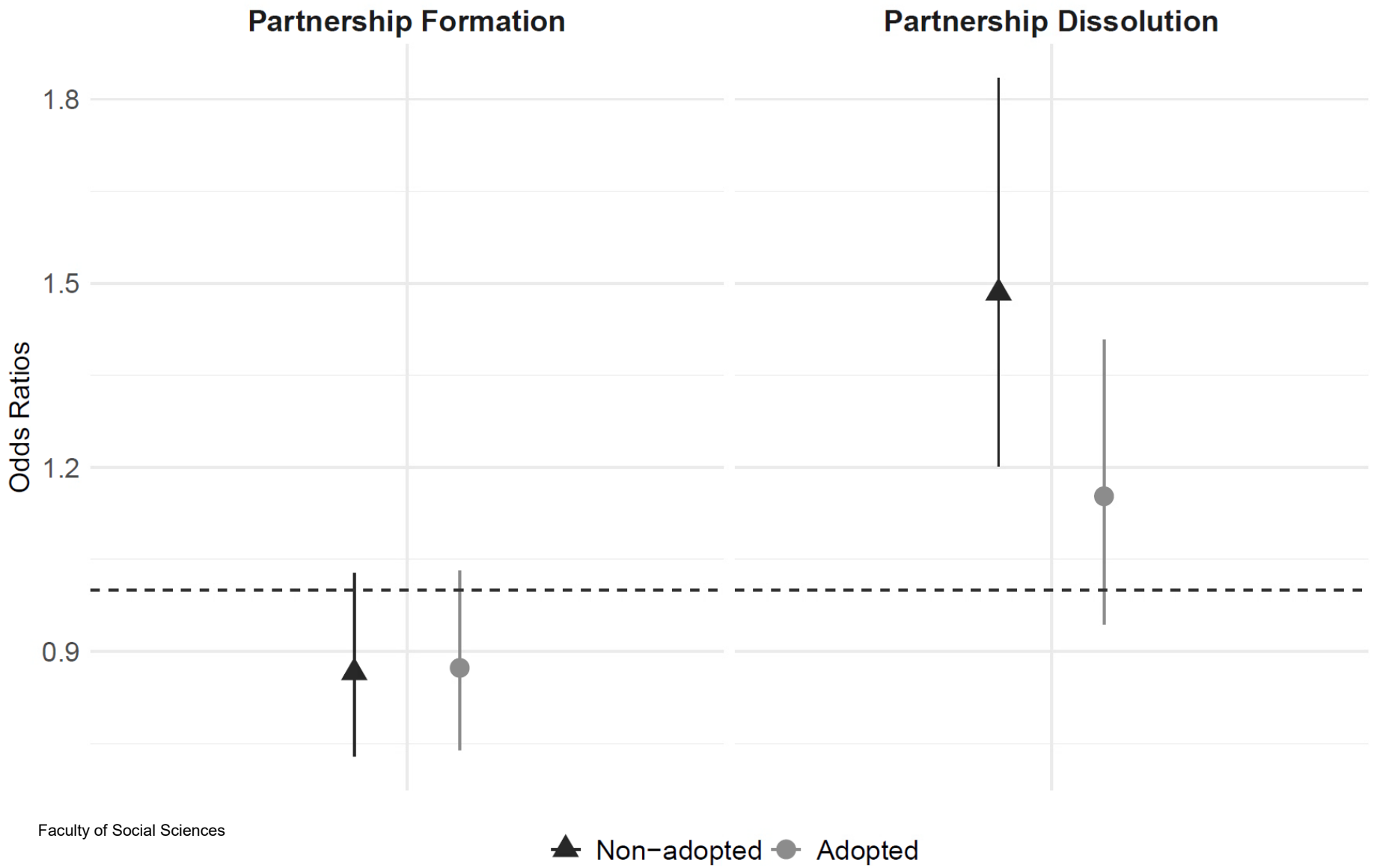
Adoption-results



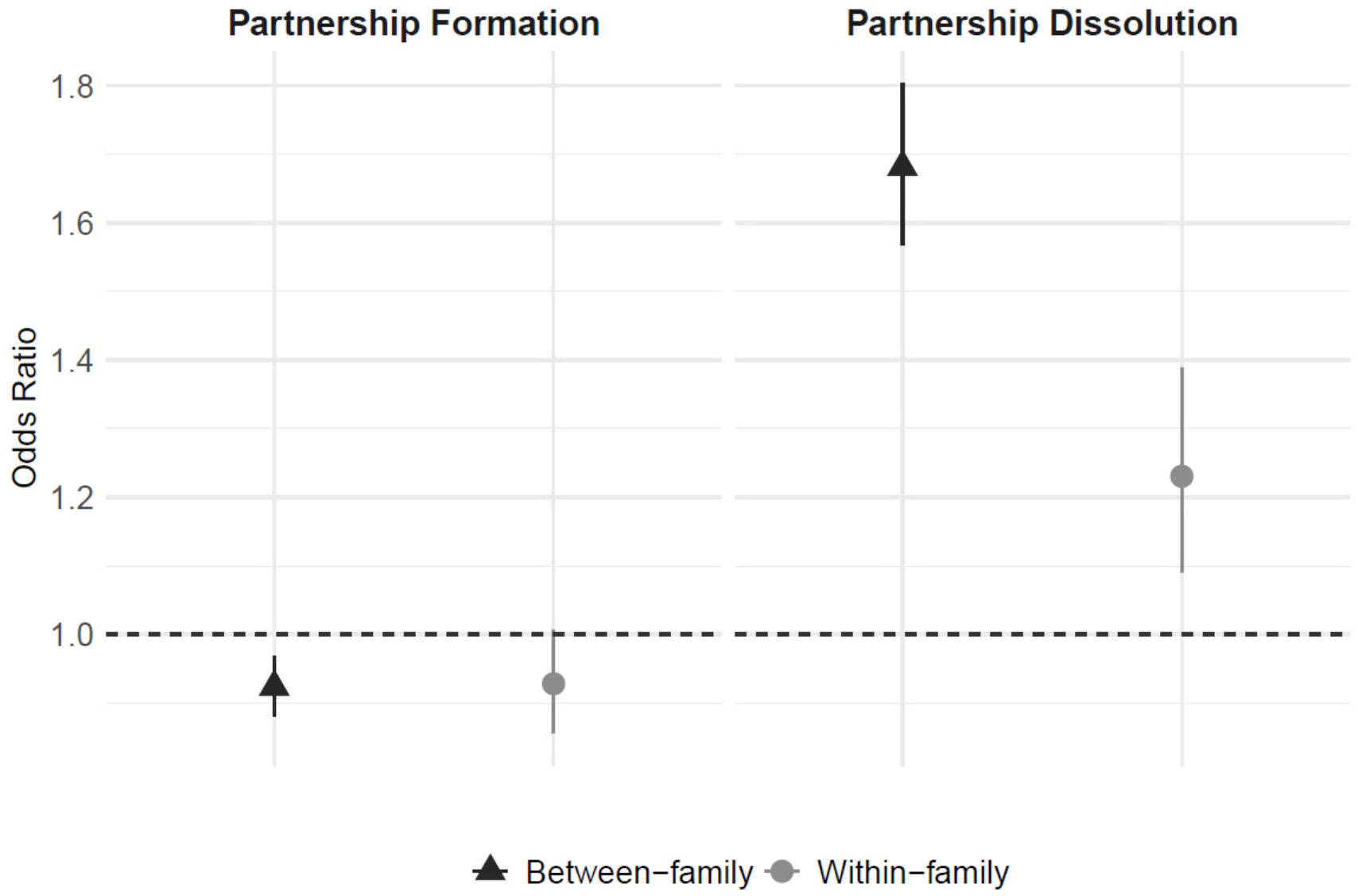
CoT-results

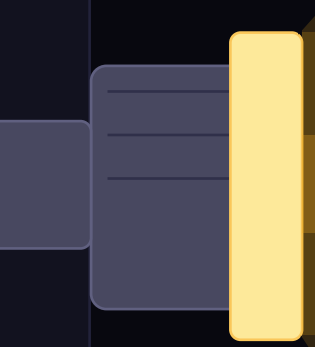

Partnership Formation
Partnership Dissolution
Odds Ratio
1.8
1.6
1.4
1.2
1.0
Between−family
Within−family

Adoption-results



CoT-results


Partnership Formation
Partnership Dissolution
Odds Ratio
1.8
1.6
1.4
1.2
1.0
Between−family
Within−family



WHAT WE LEARN

- **Dissolution: OR ≈ 1.5–1.7 → 1.15–1.25**
- **Over half of the association is selection**
- **Yet a family-environment effect remains**
- **Two designs – one story**

ASSUMPTIONS

- Quasi-random adoption placement
- Equal environments (twins)
- No assortative mating or rGE

...

LIMITS

What they cannot tell us

- Genes matter – but which, and how?
- Generalizability: adoptees & twins unique groups
- Small samples

Useful for asking whether genes confound transmission – not which genes, or how

Plan for this talk

1. How did we get here?
   Measuring genetics indirectly:
   Example paper: *Parental divorce and children's partnership dynamics*

2. The arrival of modern sociogenomics:
   Measuring genetics directly:
   Example paper: *The genetics of partnership dissolution*

3. Cross-cutting limits

1900s–present

Candidate gene studies



A priori markers and hypotheses

Most behavioral studies false

2011–present

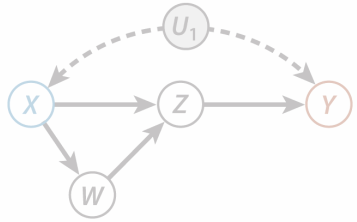
Genome-based restricted maximum likelihood (GREML)

13 131 0 0 2 −9 C C A A T T G G
13 132 0 0 2 −9 C C A A T T G G
13 142 0 0 2 −9 C C A G T C G G
15 152 0 0 2 −9 C C A G T C G G
16 161 0 0 2 −9 C C A G T C G G
16 162 0 0 2 −9 C C A G T C G G
17 172 0 0 2 −9 0 0 G G C C G G
18 182 0 0 2 −9 C C 0 0 0 0 G G

SNP heritability based on unrelated individuals

2015–present

Advanced causal modeling



Mendelian randomization
Genetic IV
GenomicSEM

Early 1900s

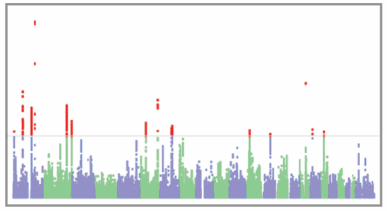
Behavior genetics Twin and family studies



Heritability estimates

2005–present

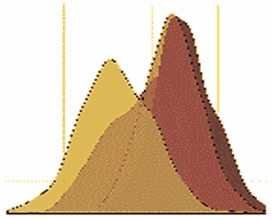
Genome-wide association study (GWAS)



Find genetic loci, identify biological function

2015–present

Polygenic scores (PGSs)



Genetic prediction and correlation

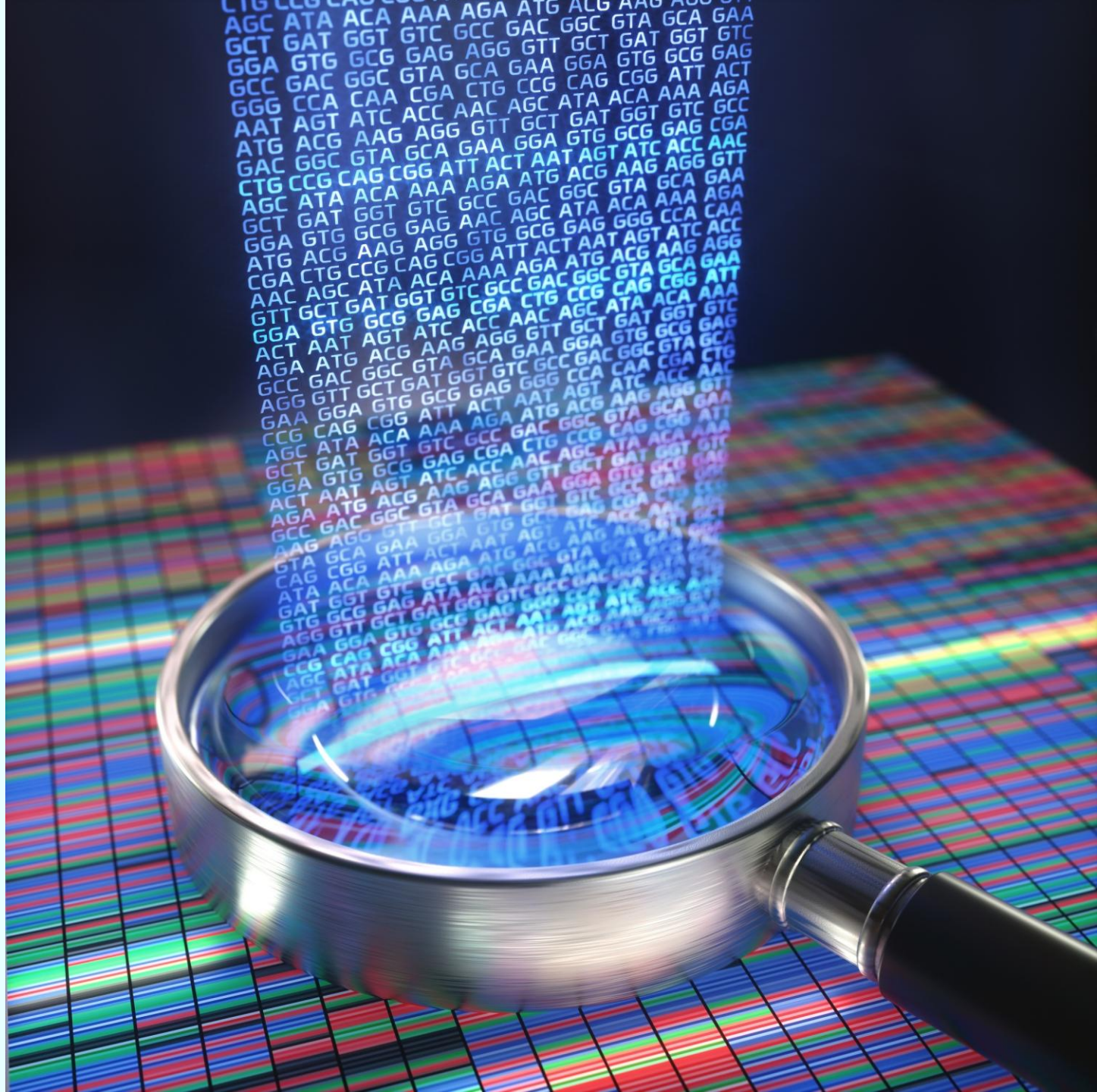
2019+

Increased diversity, G×E studies, better prediction, deeper biology

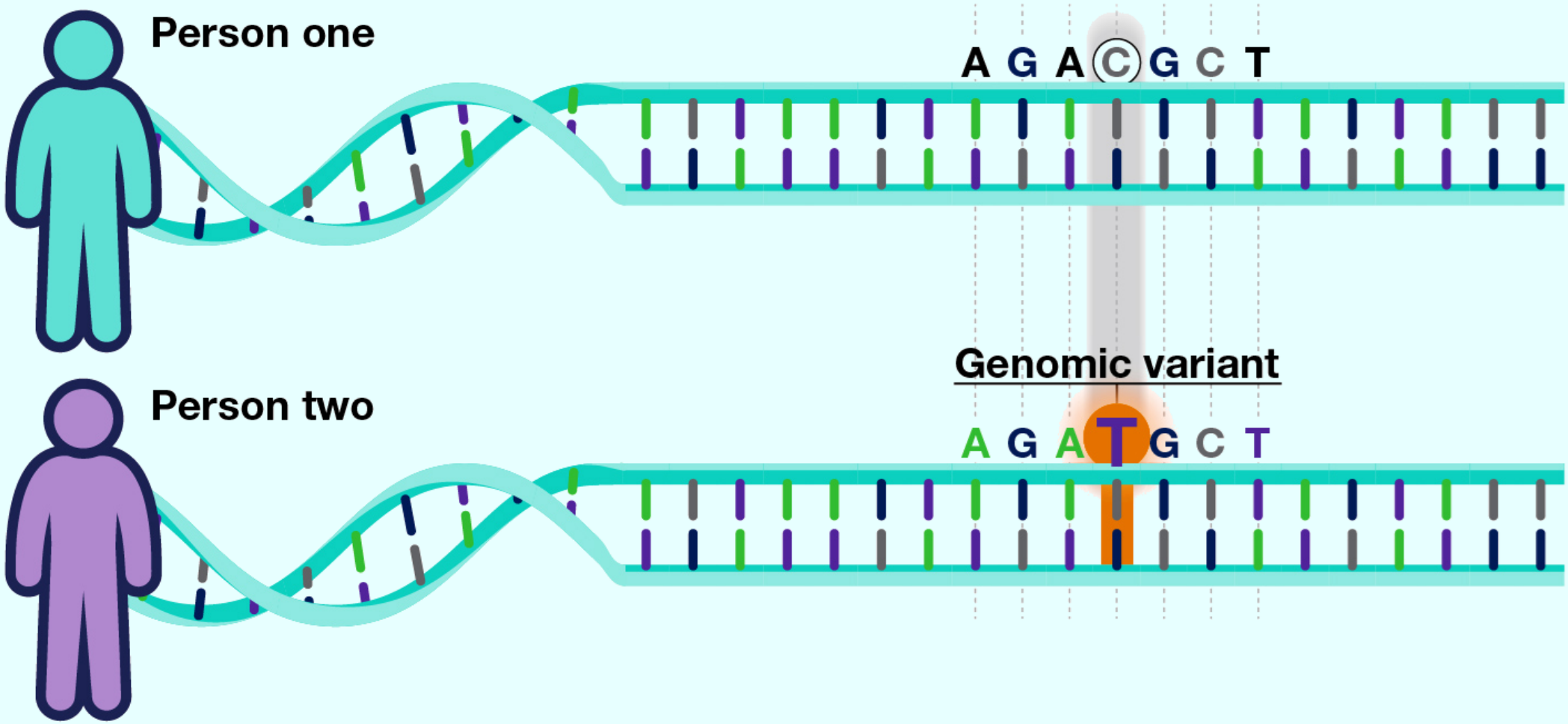
Mills MC, Tropf FC. 2020.
Annu. Rev. Sociol. 46:553–81

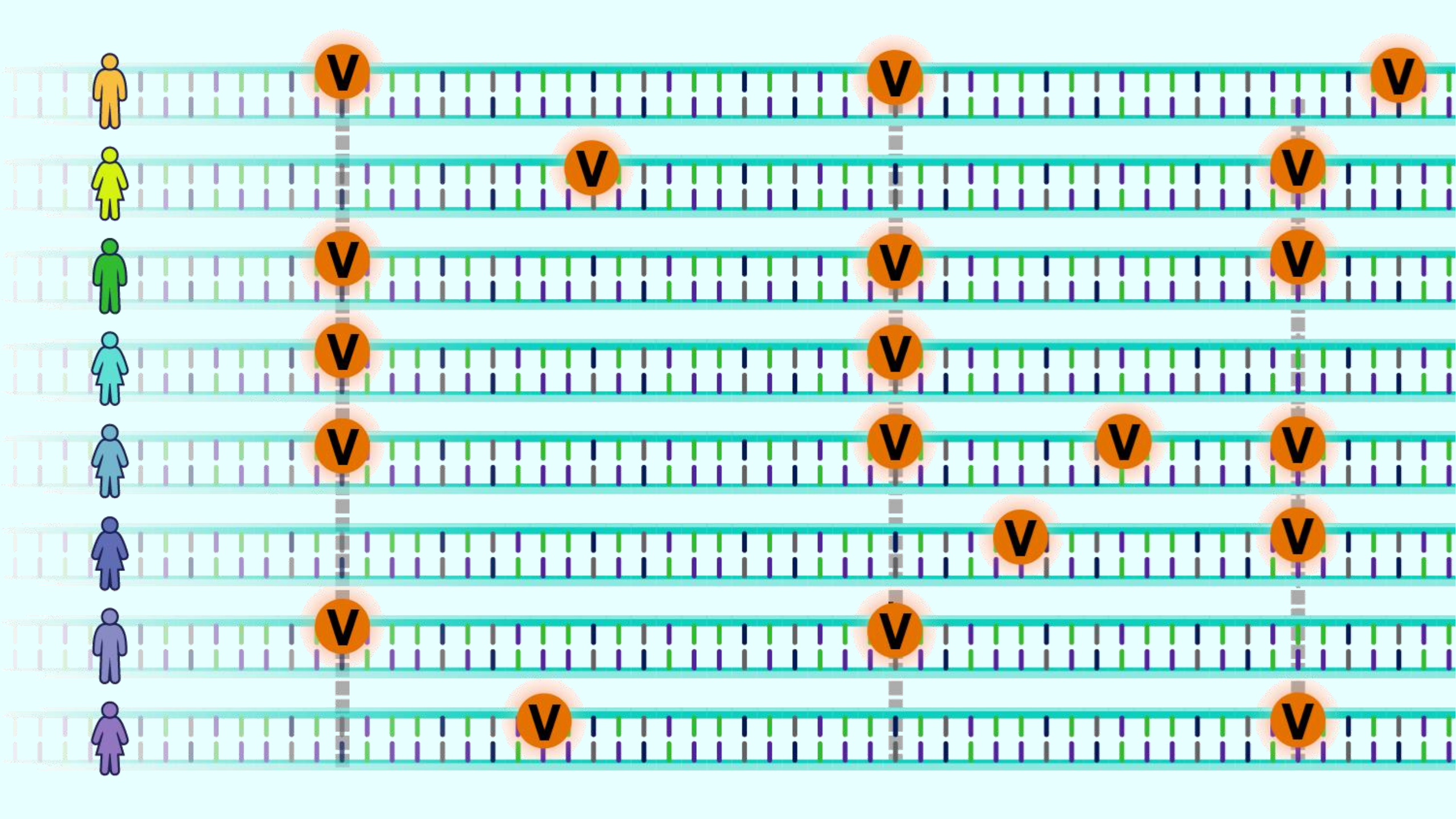
“Today we are learning the language in which God created life (…) With this profound new knowledge, humankind is on the verge of gaining immense new power to heal”.

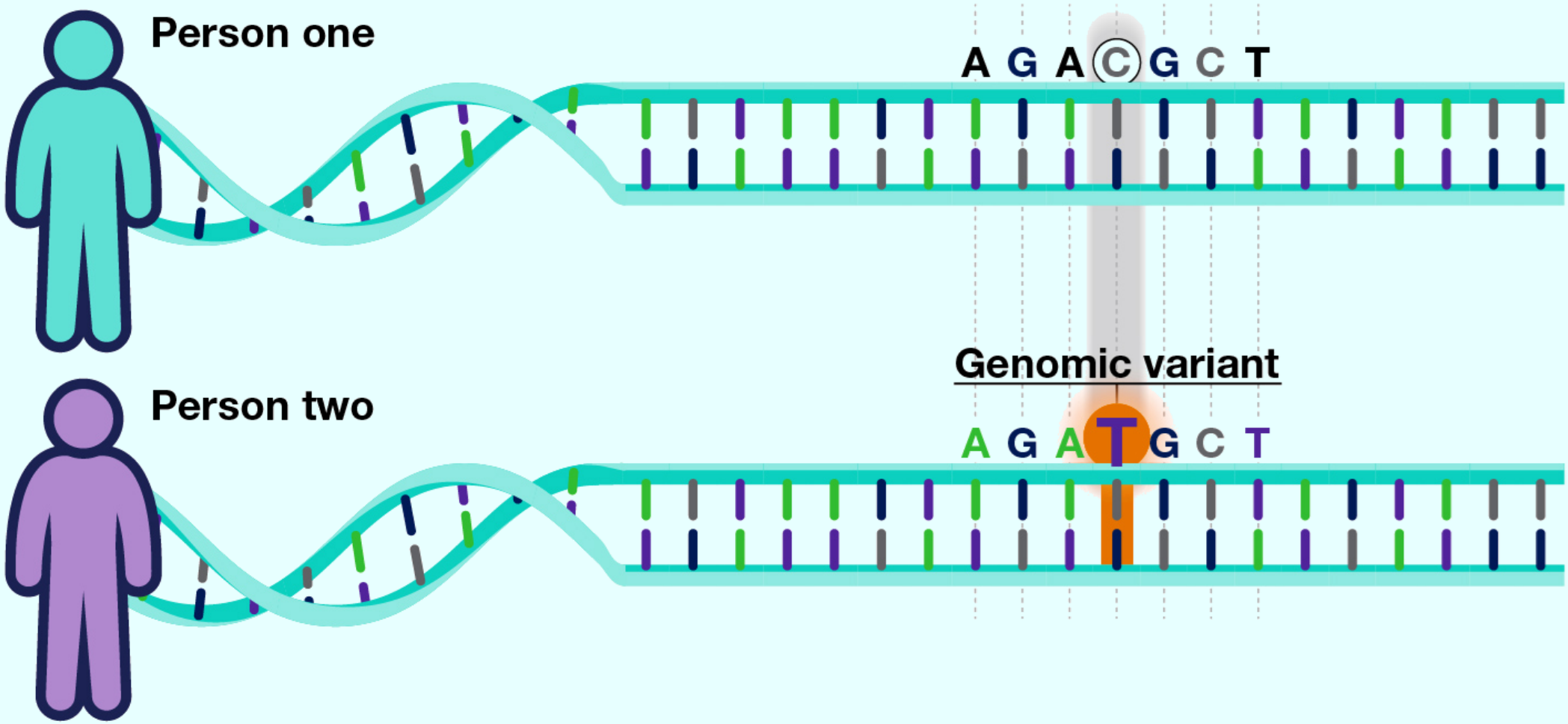
Bill Clinton, 2000





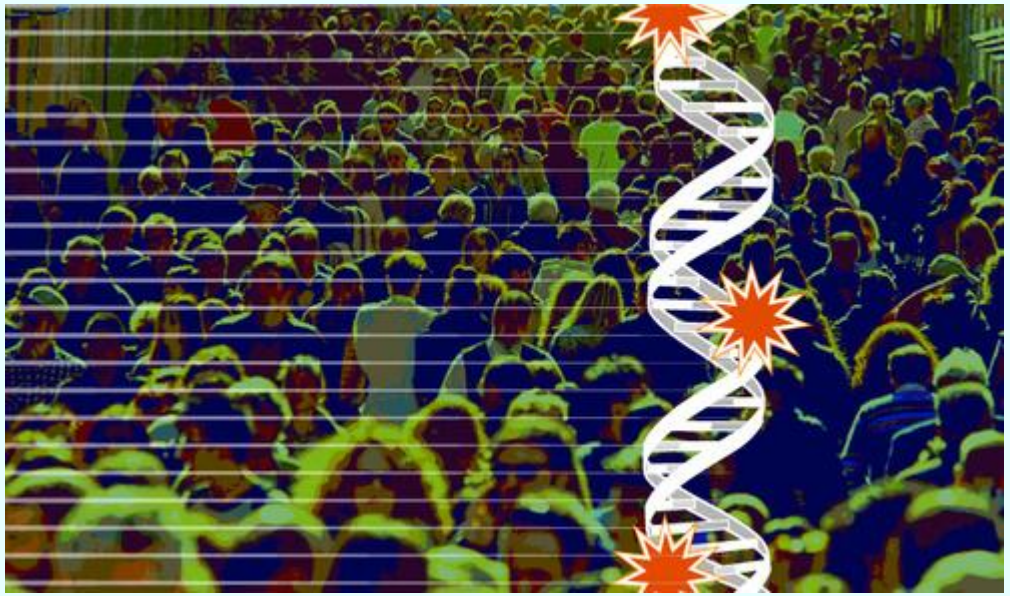

Person one
A G A C G C T
Genomic variant
Person two
A G A T G C T


V


Person one
A G A C G C T
Genomic variant
Person two
A G A T G C T

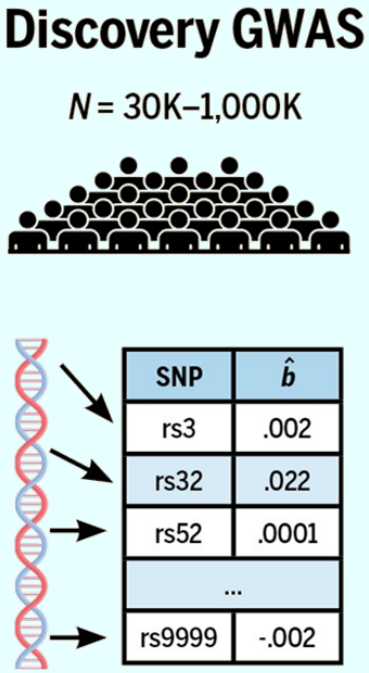
Genome-wide association studies (GWAS)

- Hypotheses-free approach



Credit: Lauren Solomon, Broad Communications/Photo by iStock.com/Maxiphoto

Genome-wide association studies (GWAS)



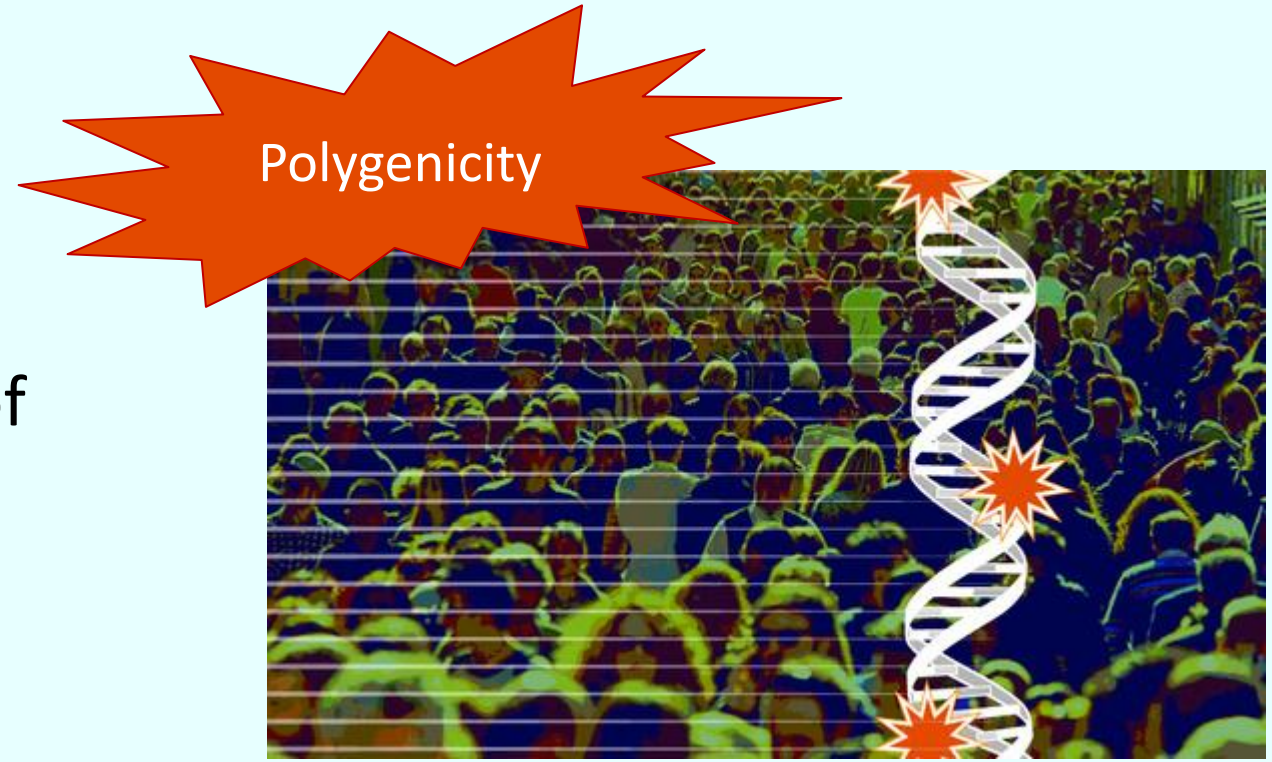
Hart, S., Little, C., & van Bergen, E. (2020). Polygenic score. figshare https://doi.org/10.6084/m9.figshare.12751019.v2

Genome-wide association studies (GWAS)

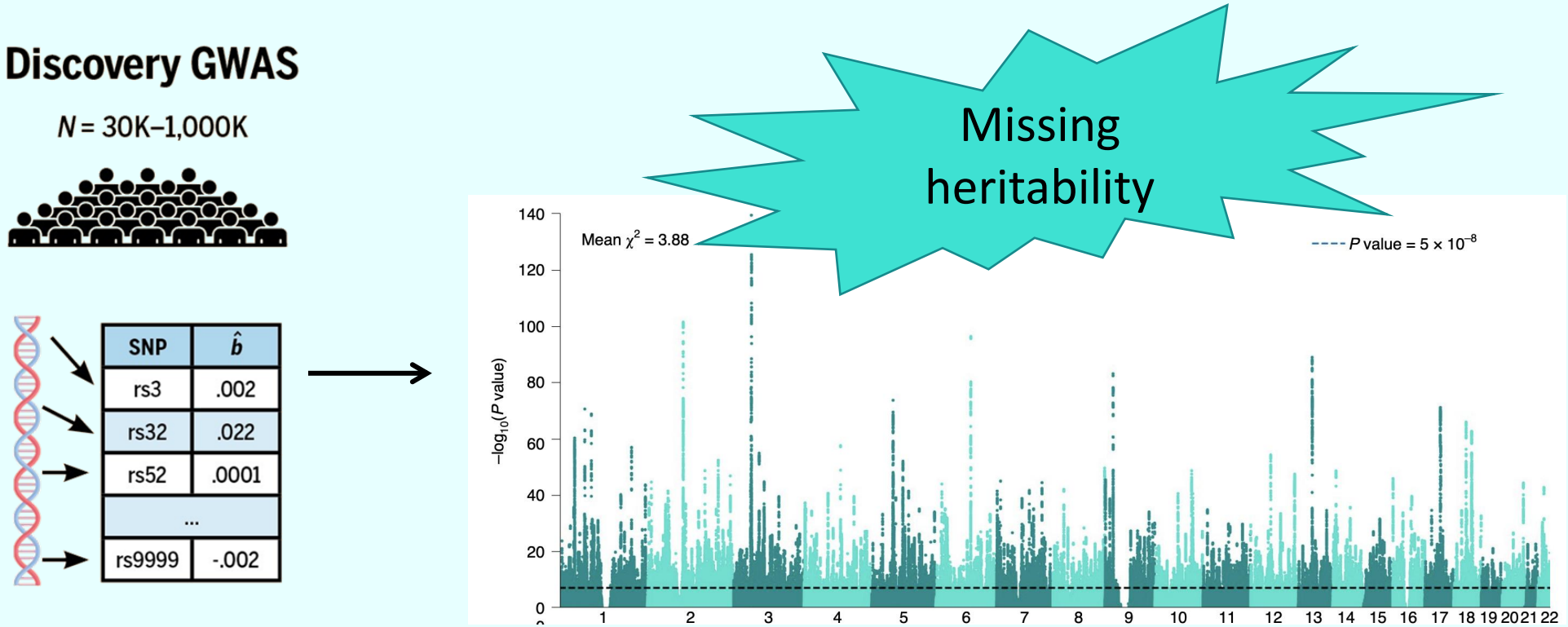
- Hypotheses-free approach

- "A typical human behavioral trait is associated with very many genetic variants, each of which accounts for a very small percentage of the behavioral variability"

  - Fourth law of behavior genetics (Chabris et al. 2015)

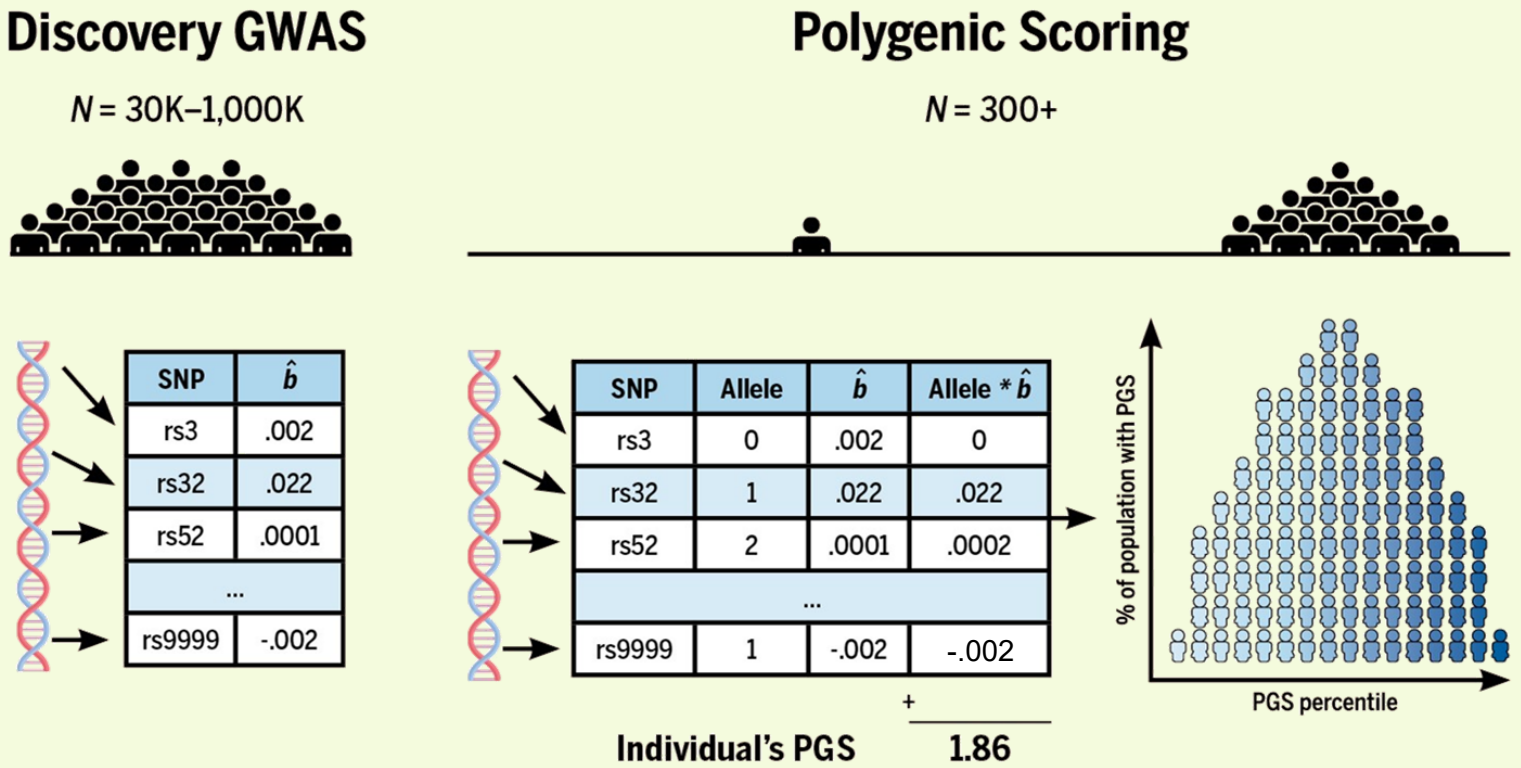


Credit: Lauren Solomon, Broad Communications/Photo by iStock.com/Maxiphoto



Hart, S., Little, C., & van Bergen, E. (2020). Polygenic score. figshare https://doi.org/10.6084/m9.figshare.12751019.v2

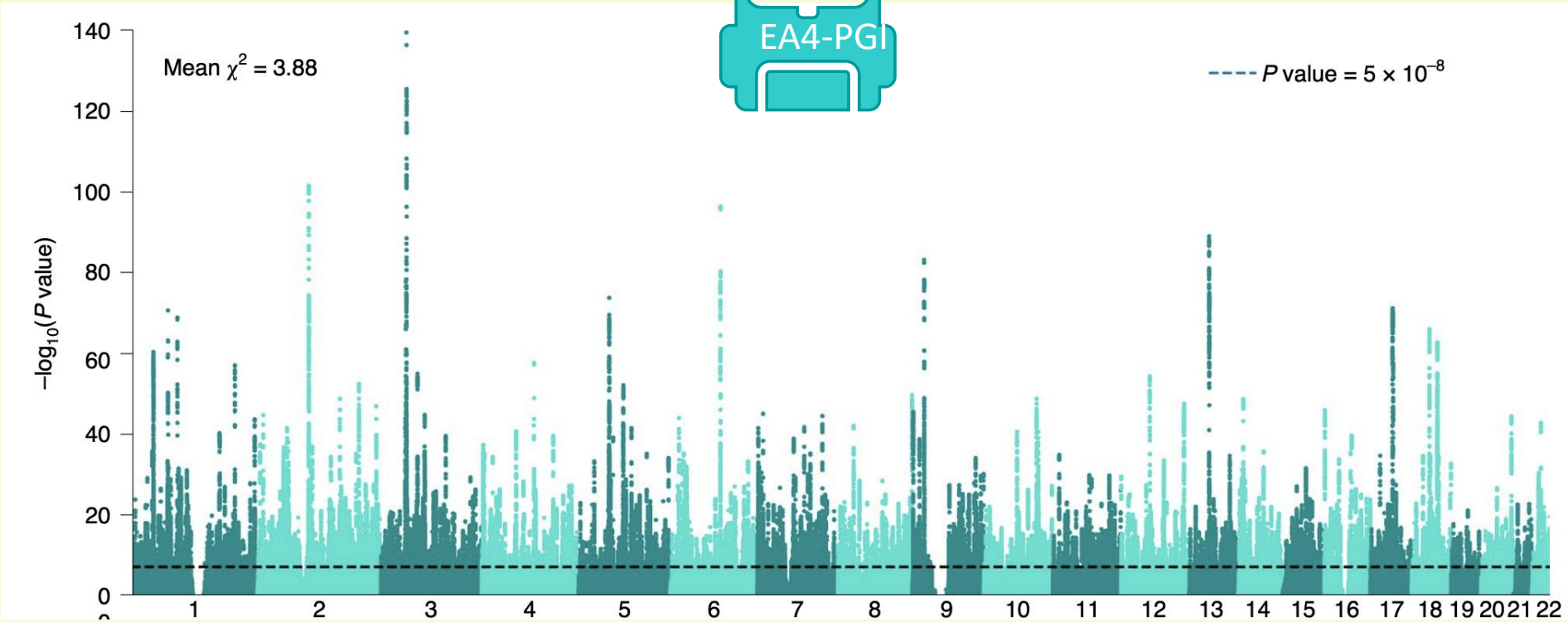
Polygenic Index (PGI)



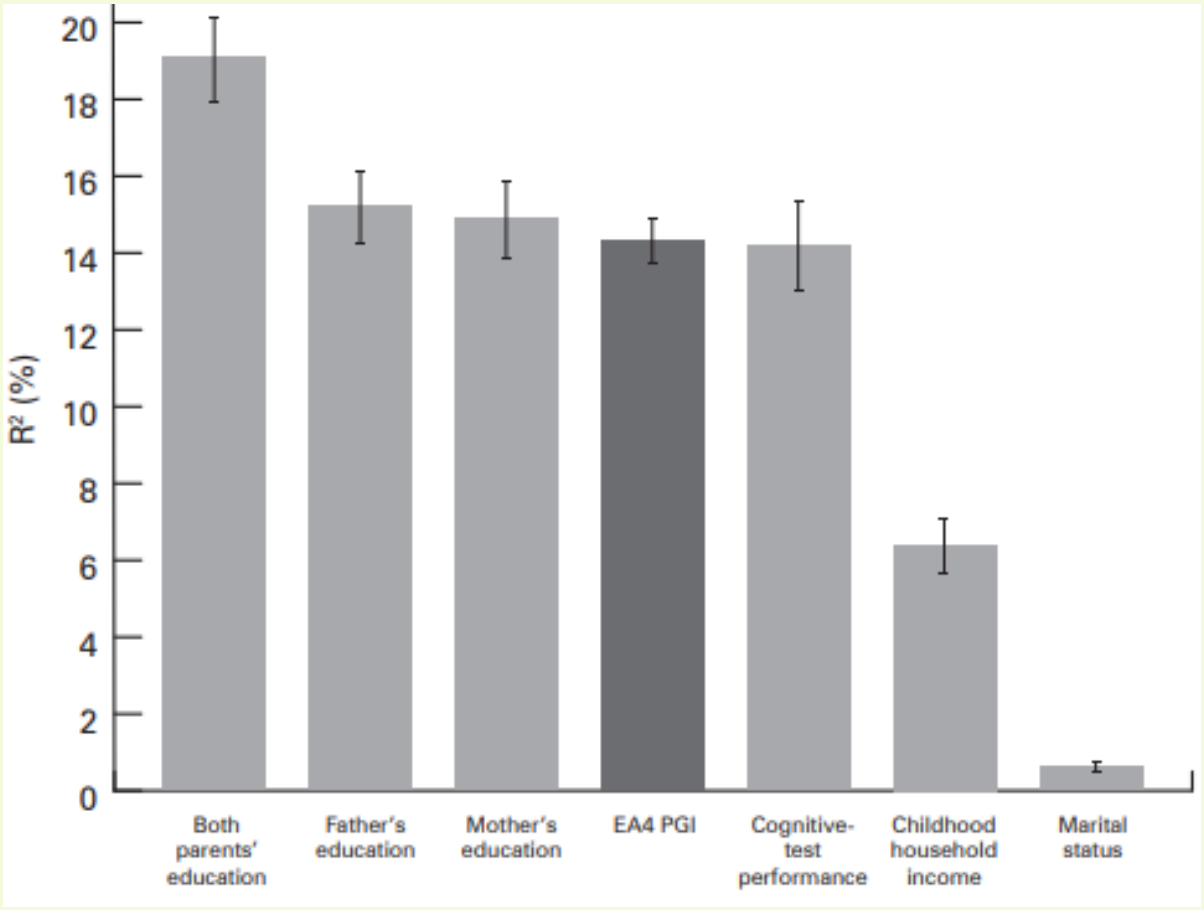
Hart, S., Little, C., & van Bergen, E. (2020). Polygenic score. figshare https://doi.org/10.6084/m9.figshare.12751019.v2

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Polygenic Index



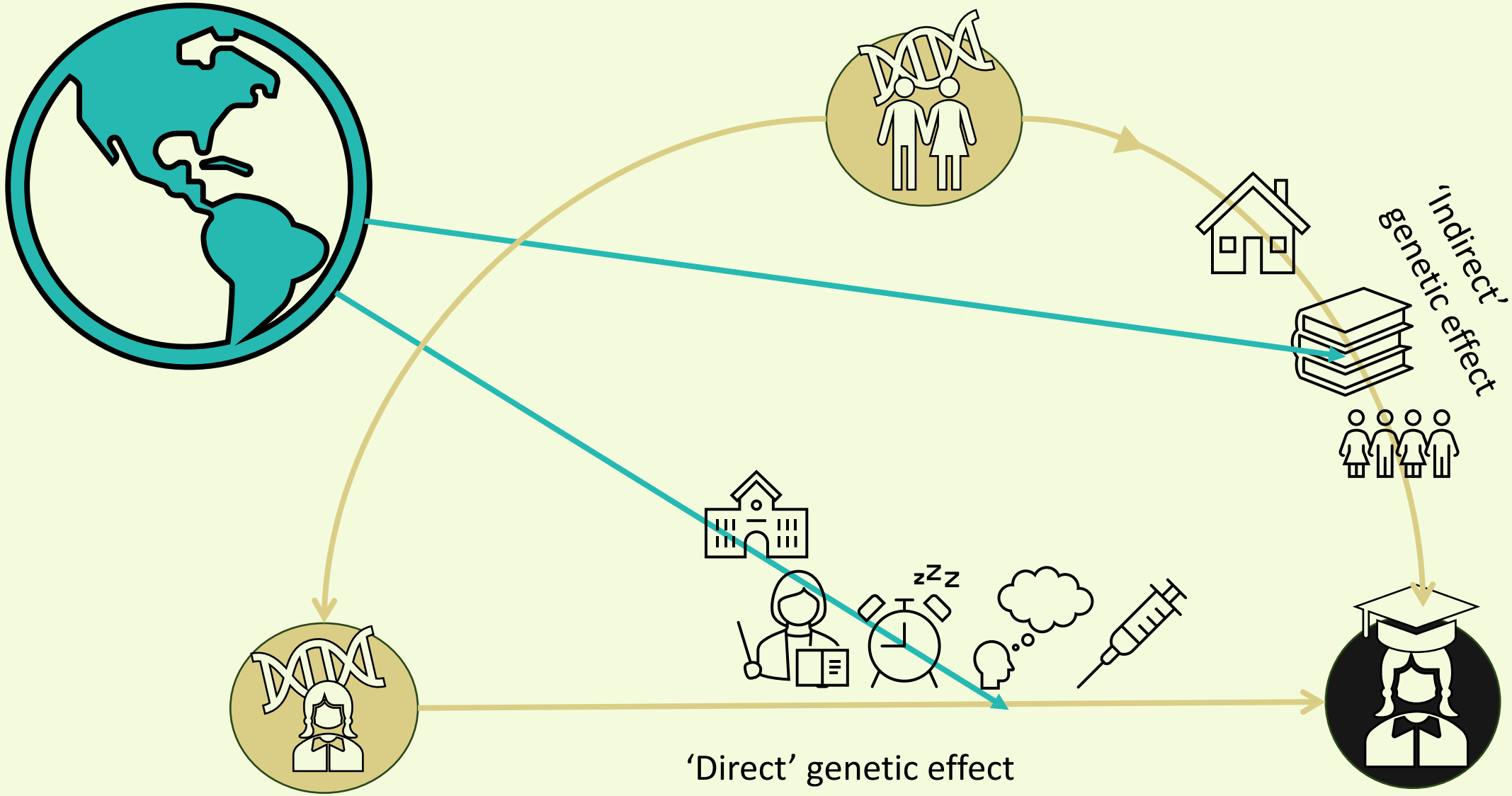
Polygenic Index

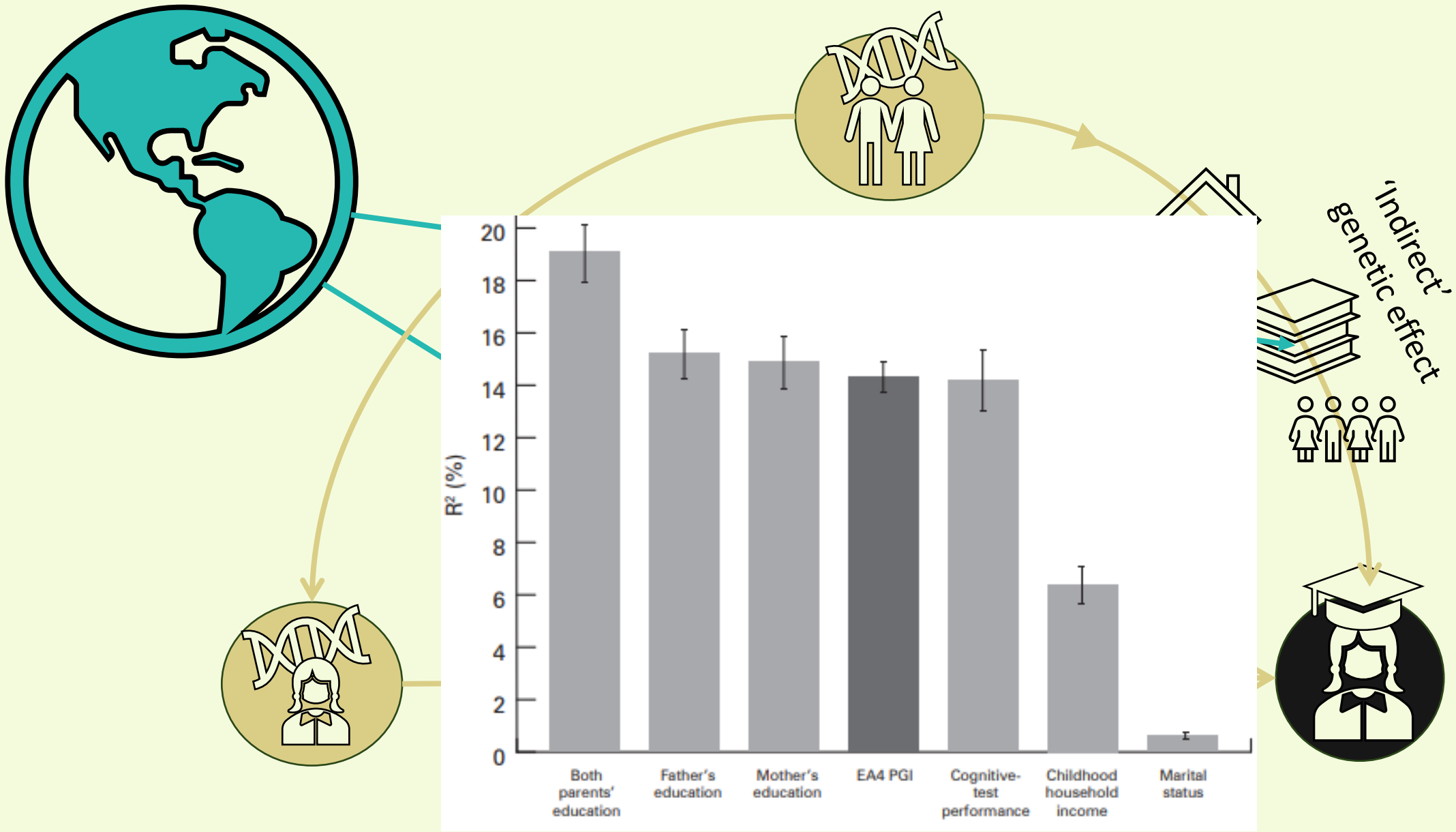


Polygenic Index

Advantages:

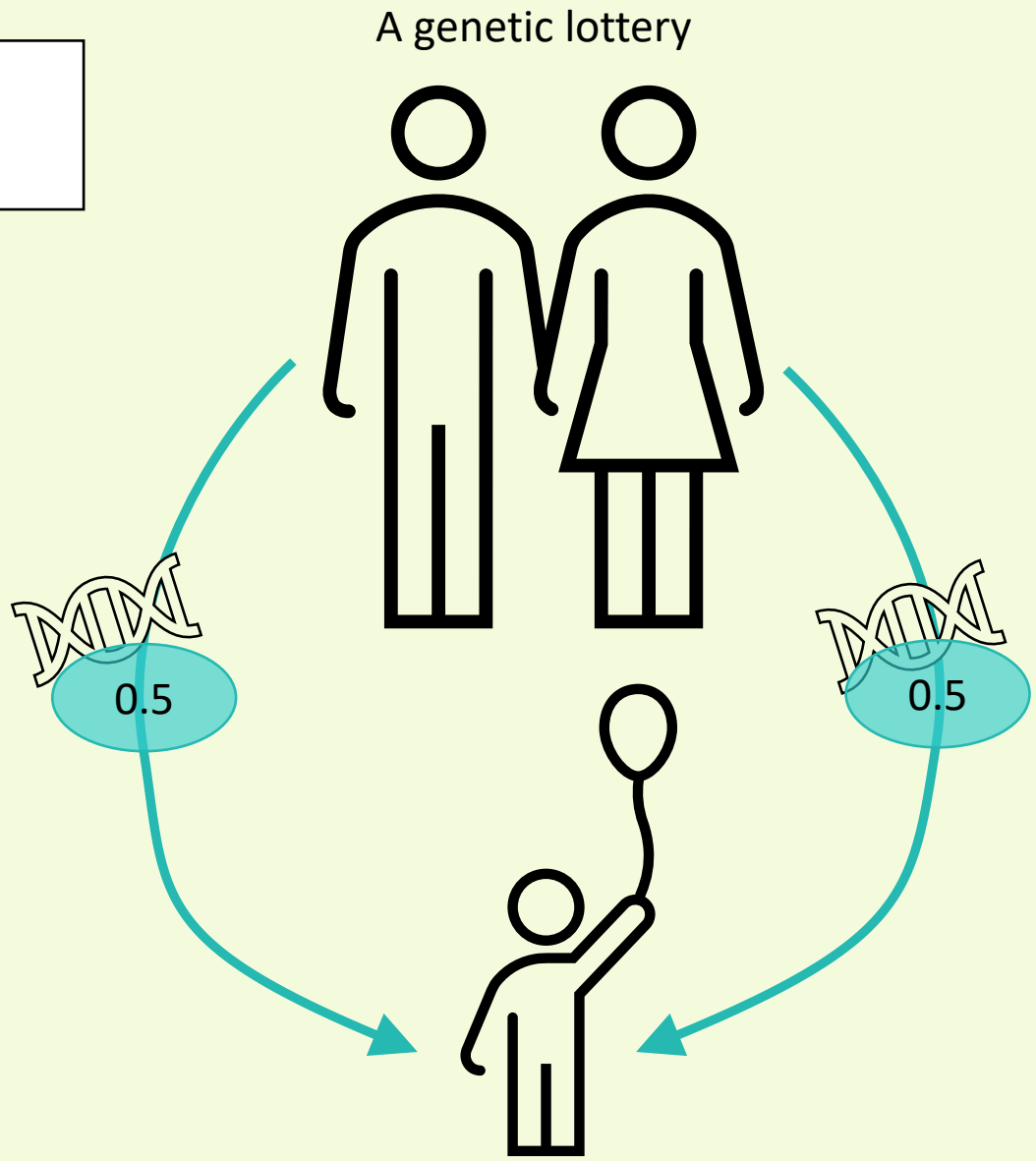
- Predict from birth
- Stable source of individual variation
- One-time cost
- Can access rare traits


'Indirect' genetic effect
'Direct' genetic effect


'Indirect' genetic effect
R^2 (%)
0
2
4
6
8
10
12
14
16
18
20
Both parents' education
Father's education
Mother's education
EA4 PGI
Cognitive-test performance
Childhood household income
Marital status

Within-family designs

- A natural experiment
- Trio-data: can be used to address causal questions





Sociological Science

THE GENETICS OF PARTNERSHIP DISSOLUTION

Ruth Eva Jørgensen, Rosa C. G. Cheesman,
Ole Andreassen & Torkild H. Lyngstad

UNIVERSITY
OF OSLO

OPENFLUX

European Research Council
Established by the European Commission

Background

- Twin and adoption studies: divorce is partly heritable (15–53 %)
  (McGue & Lykken 1992; D'Onofrio et al. 2007; Salvatore et al. 2018)
- But heritability is a black box
  - Which heritable traits are involved – and how?
  - No "divorce gene": many traits, many tiny effects
- Known predictors of divorce are themselves partly heritable
  (Lyngstad & Jalovaara 2010; Bartels 2015; Røysamb & Nes 2019)
- → What do genetic dispositions add to the story of who breaks up?

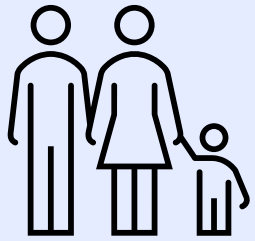
Research Questions

Using measured genotypes:

1. How much of the variation in partnership dissolution do common genetic variants capture?
2. Which genetically influenced traits predict dissolution?
3. Do these associations hold within families?

Data

MoBa genotypes

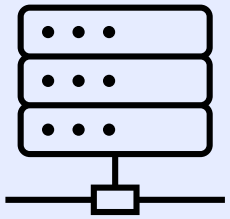


≈128,000 parents

76,441 women, 52,035 men

GWAS → SNP-heritability

Population registers

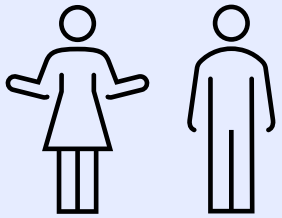


1.5 M person-years

Married + cohabiting

Event-history models, 16 PGIs

Siblings in MoBa



20,622 adults

With a sibling in MoBa

Sibling fixed effects

Heritability-results

9 %

SNP-heritability
women

3.5 %

SNP-heritability
men

0.75

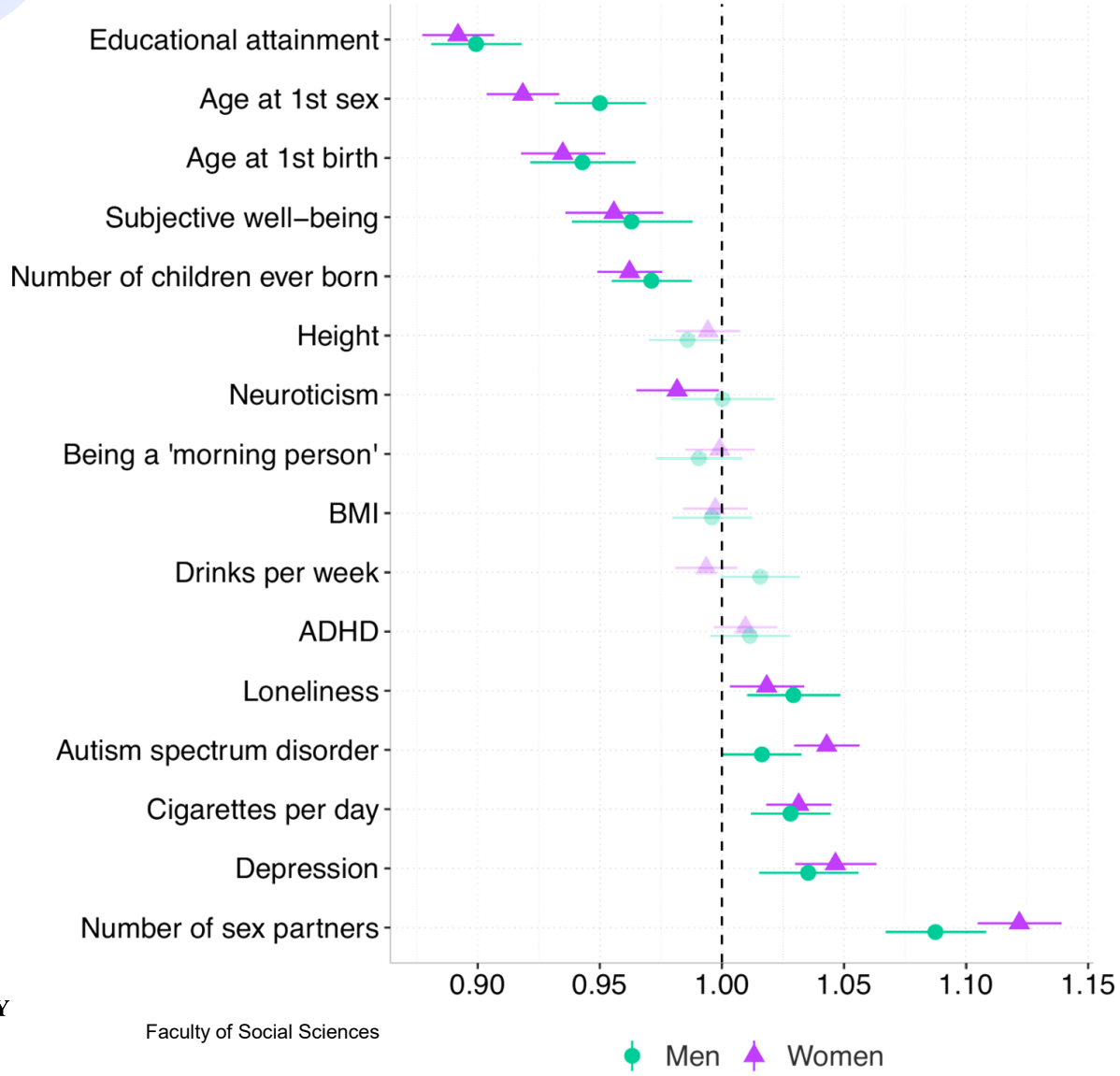
Genetic correlation
women–men

Twin studies: 15–53 % → **“missing heritability”**

Small but significant – and higher for women than for men

GWAS + LD score regression, liability scale, N = 128,476

PGI-results

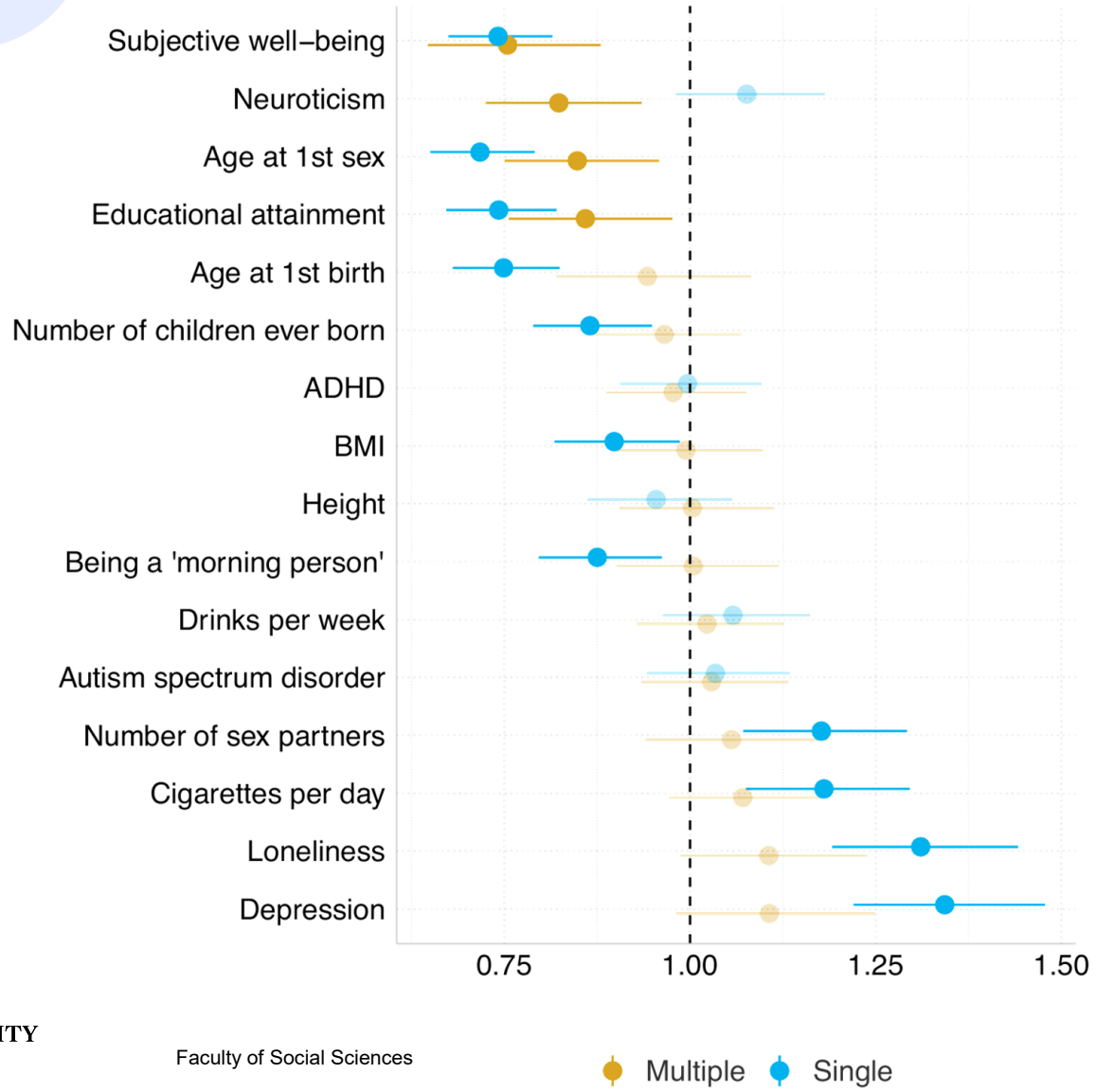


1 SD higher PGI for …

- Education: ≈10 % lower odds of dissolution
- Later sex & first birth, well-being, more children: lower odds
- Number of sex partners (9–12 %), depression, smoking, loneliness: higher odds
- Very similar for women and men

Odds ratios, discrete-time event-history models. All 16 PGIs in the same model; 1.5 M person-years.

Within-sibling results



Comparing siblings

- One PGI at a time (blue): most associations remain within families
- All PGIs together (orange): four remain
  - Well-being (OR 0.75), neuroticism (0.82), age at first sex (0.85), education (0.86)
- Closer to causal – but not “purely biological”

Sibling fixed-effects logit, 20,622 adults; women and men pooled.

Take-aways

- Partnership dissolution is modestly heritable
  - SNP-heritability 3–9 % – far below twin estimates (as expected -> missing heritability
- Genetic selection runs through familiar traits
  - Education, well-being, timing of sex and family formation, mental health
- Part of it holds within families
  - Genetic dispositions are part of “selection” – not only family background
- → Genes are a small piece of the puzzle – and context-specific
  - Norway, parents with a shared child, today

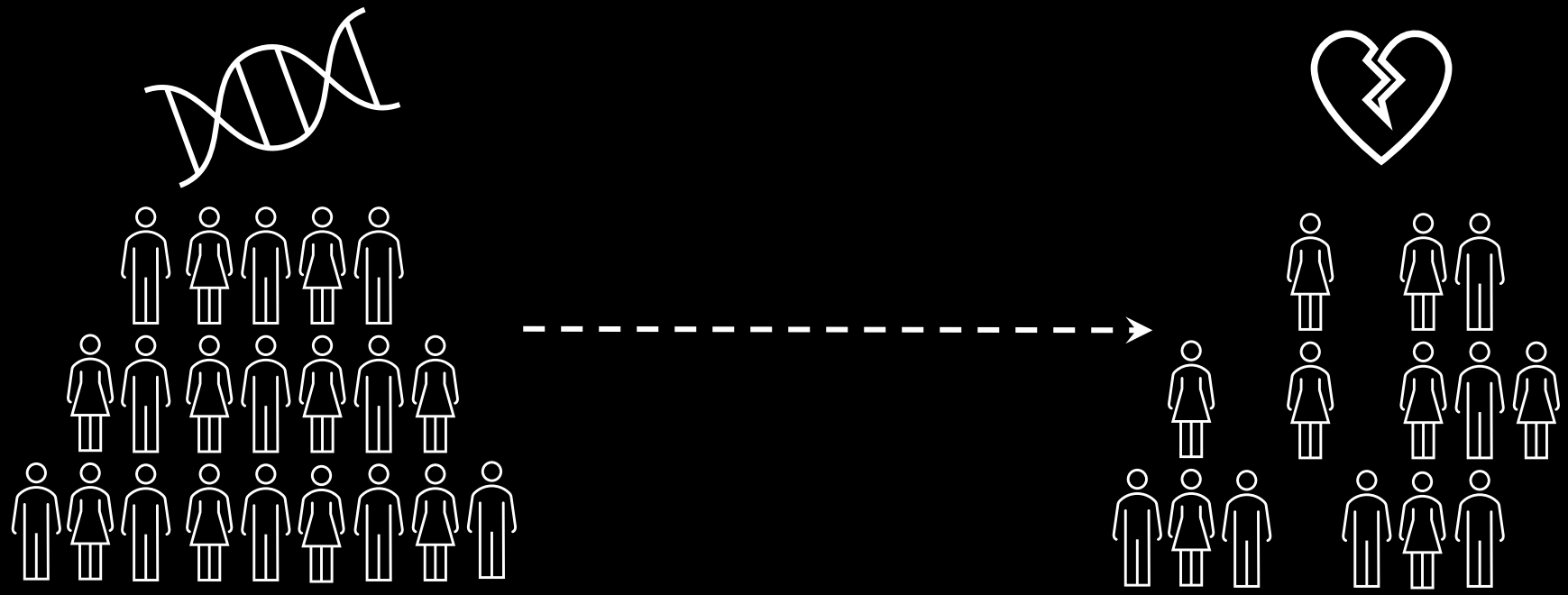
Plan for this talk

1. How did we get here?
   Measuring genetics indirectly:
   Example paper: *Parental divorce and children's partnership dynamics*

2. The arrival of modern sociogenomics:
   Measuring genetics directly:
   Example paper: *The genetics of partnership dissolution*

3. Cross-cutting limits

Prediction vs. explanation





PROMISE

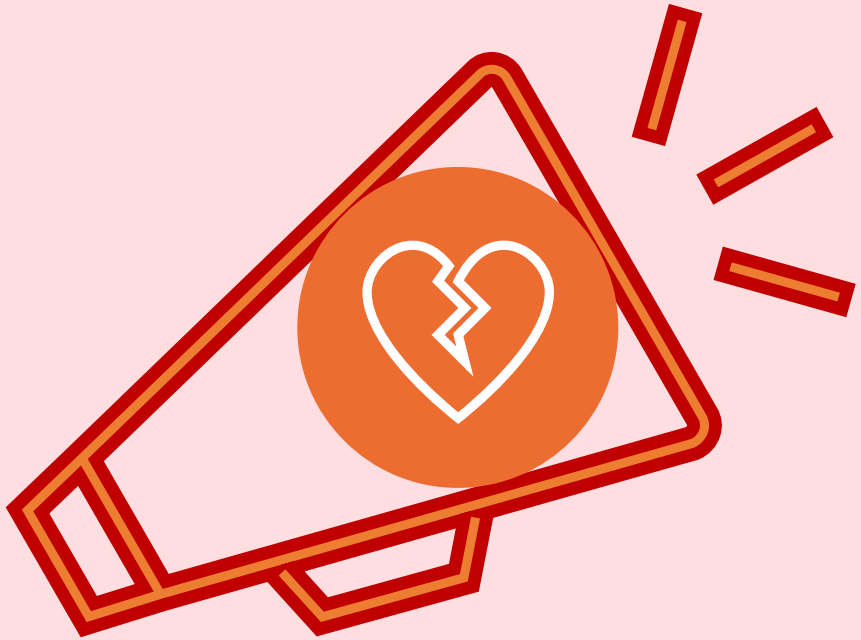
- **Measure traits that registers lack**
- **Natural experiments within families**
- **Genetic controls for selection**
- **How context shapes genetic influence (GxE)**

PITFALLS

- Small effects
- Portability
- Selected samples
- Indirect effects
- Assortative mating

DEEPER LIMITS

- No mechanisms – why?
- Time- and place-specific
- Not biological insight
- No individual prediction
- Downward causation



Communicative & ethical limits

Genetic myths

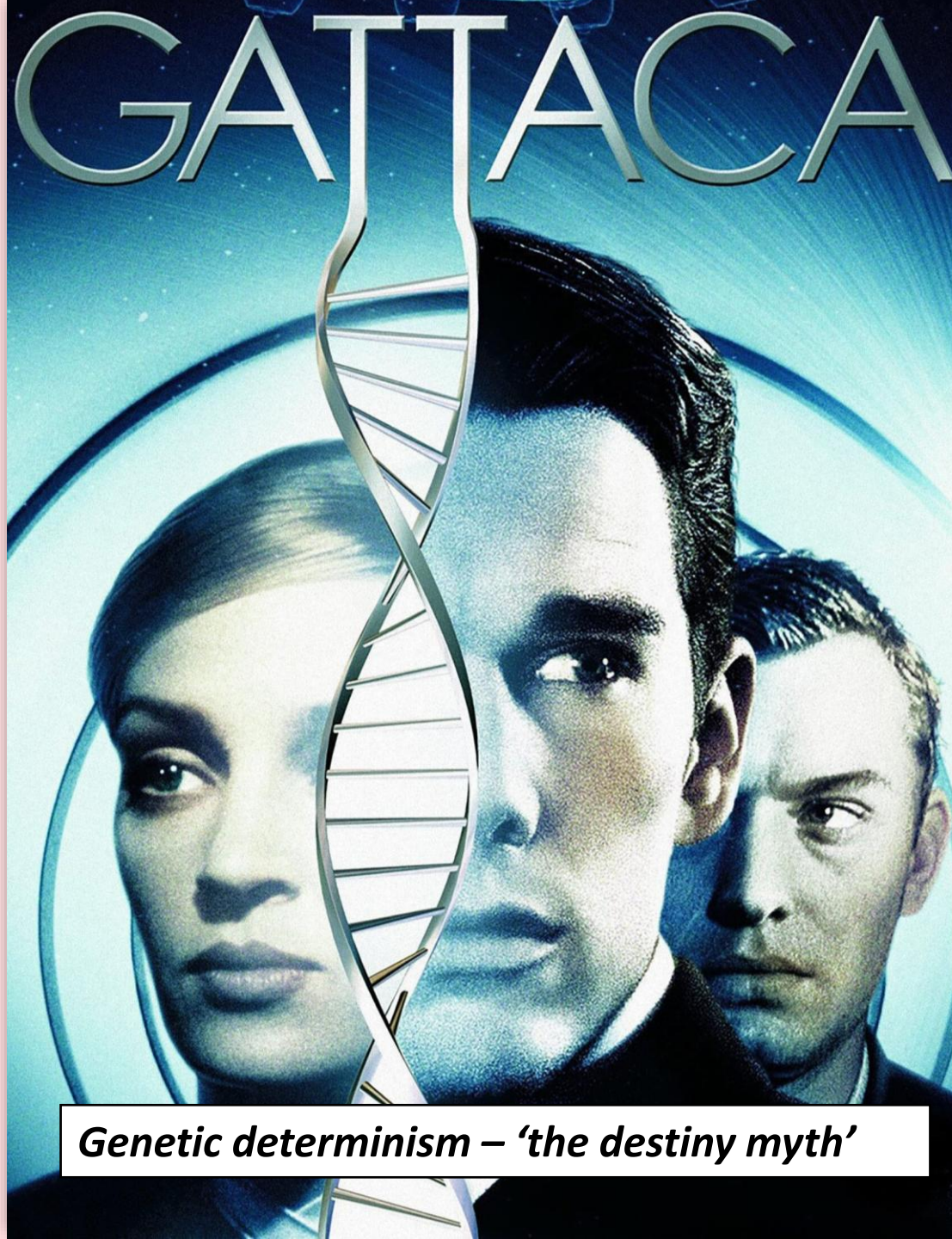
The ‘divorce gene’?

- Communication
  - No divorce gene – name the trait the PGI was built for
  - Report absolute effects: small, and context-dependent
  - Risk of genetic fatalism – and distraction from social causes
- Commercialization
  - DNA matchmaking and ‘compatibility’ tests

GENEPARTNER · 2008

“Love is no coincidence”

Critique: Smithsonian Magazine (2018), “The Dubious Science of Genetics-Based Dating”



Genetic determinism – ‘the destiny myth’

How I think these methods are best used

You cannot intervene on the gene

Interventions work through environments: families, schools, policy

Genetics as a tool

- A control for selection – separating genes from family environment
- A measure of traits our registers lack
- As methodological tools
- A window on how context shapes genetic influence

Not as a target

- Predicting individual couples
- Selecting partners – or embryos
- Replacing social explanations


Thank you!

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Papers cited · Sources · Image credits

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Example papers, data & other sources

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Image & figure credits

Slide	Image / figure	Source
6, 33	Timeline of genetics and sociogenomics	Mills & Tropf (2020), Annual Review of Sociology, Fig. 1
8	Distribution of MZ and DZ twin correlations	Polderman et al. (2015), Nature Genetics, Fig. 2a
9	Book cover, A Doll's House and Other Plays	Penguin Classics (2016), transl. D. Dawkin & E. Skuggevik
15, 17	Pathways of divorce transmission	Adapted from Amato (1996)
19	Twins icon	From the Noun Project (CC BY 3.0) https://thenounproject.com/icon/twins-7952136/
12, 20–30	Design diagrams and results figures	Jørgensen, Van Hootegem & Lyngstad (2026), JMF
36–38	Genomic-variant illustrations	National Human Genome Research Institute, genome.gov "Polygenic Risk Scores"
39, 41	Crowd with DNA double helix	Lauren Solomon, Broad Communications / iStock.com/Maxiphoto
40, 42, 43	GWAS and polygenic-scoring schematic	Hart, Little & van Bergen (2020), figshare (CC BY 4.0)
42, 44	Manhattan plot, EduYears GWAS	Okbay et al. (2022), Nature Genetics, Fig. 1
45, 48	Predictive value of EA4 PGI vs. non-genetic controls	Based on Okbay et al. (2022)
54-56	Results figures	Jørgensen, Cheesman, Andreassen & Lyngstad (2025), Sociological Science

Other illustrations: power-point icons and pictures, stock images and colourbox.