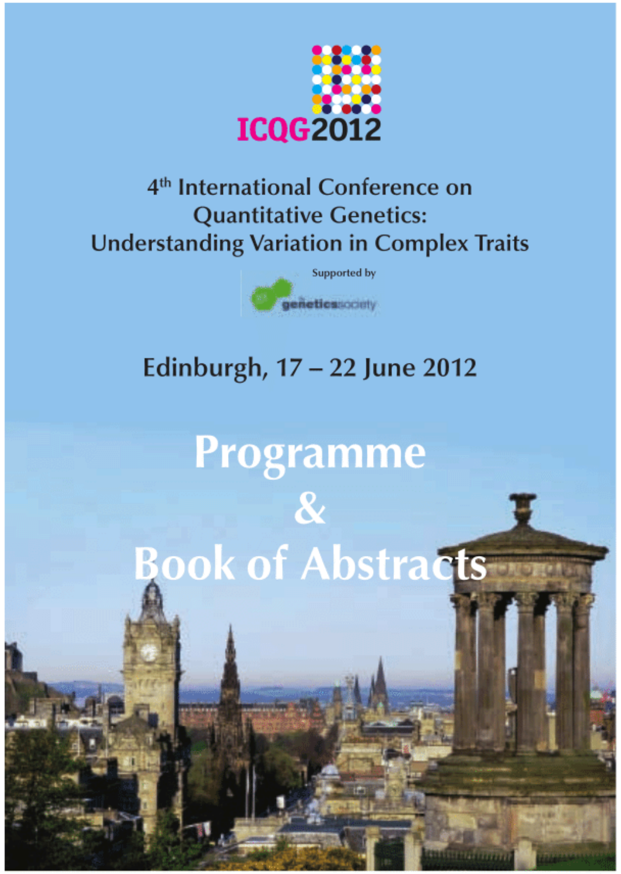
Investigating peer influence using Social/Indirect Genetic Effects

Amelie Baud[1,2], Francesco Paolo Casale[1], Oliver Stegle[1]
1. European Bioinformatics Institute, Cambridge
2. Psychiatry department, University of California San Diego

Background



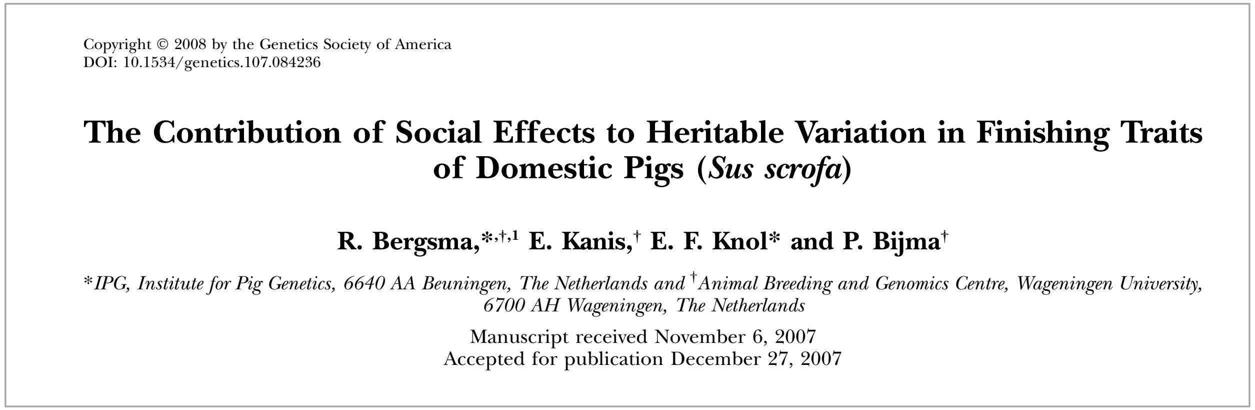
ICQG2012

4th International Conference on
Quantitative Genetics:
Understanding Variation in Complex Traits

Supported by
geneticssociety

Edinburgh, 17 – 22 June 2012

Programme
&
Book of Abstracts



Copyright © 2008 by the Genetics Society of America
DOI: 10.1534/genetics.107.084236

The Contribution of Social Effects to Heritable Variation in Finishing Traits of Domestic Pigs (*Sus scrofa*)

R. Bergsma,*,†,1 E. Kanis,† E. F. Knol* and P. Bijma†

**IPG, Institute for Pig Genetics, 6640 AA Beuningen, The Netherlands and †Animal Breeding and Genomics Centre, Wageningen University, 6700 AH Wageningen, The Netherlands*

Manuscript received November 6, 2007
Accepted for publication December 27, 2007

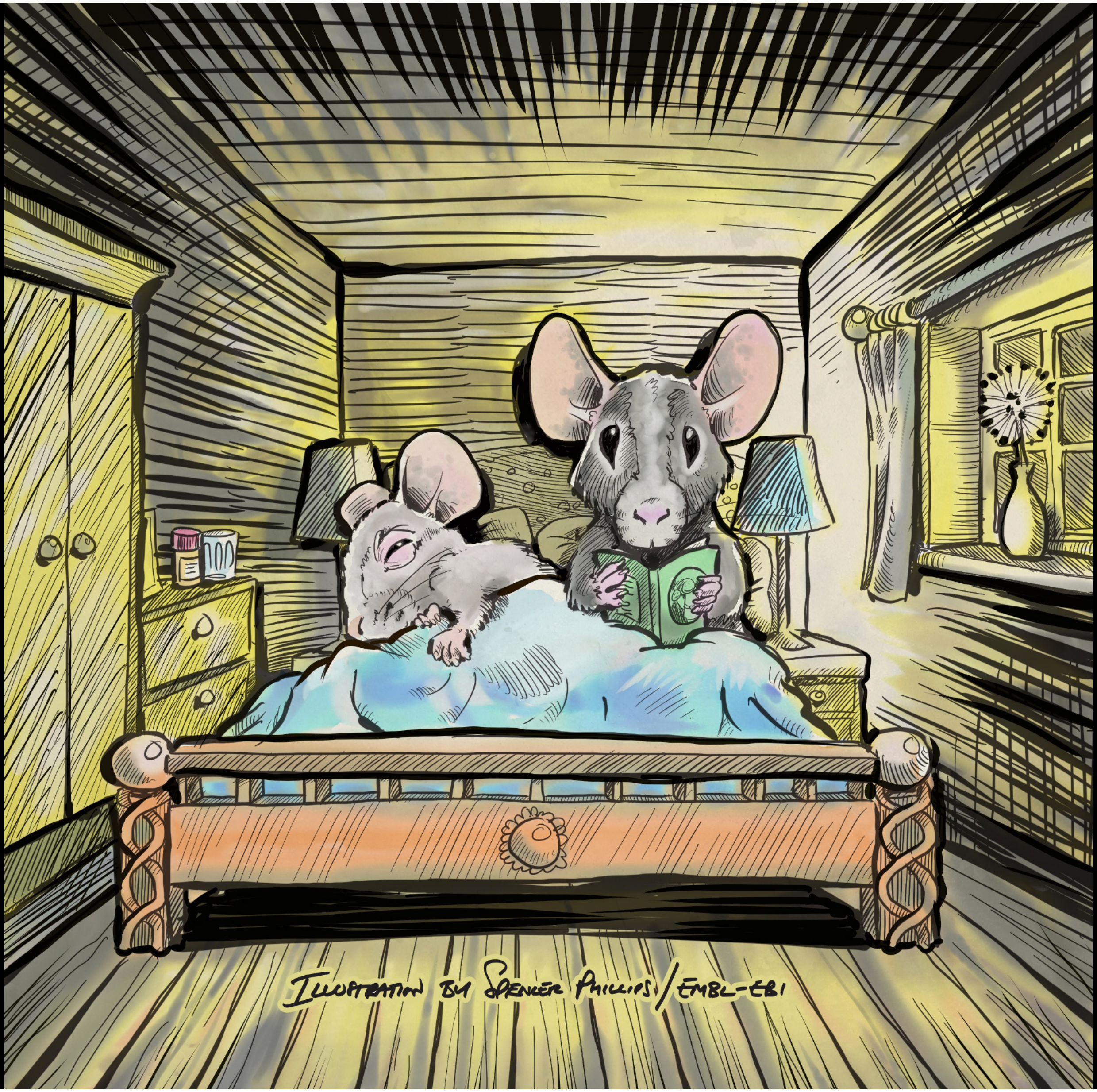
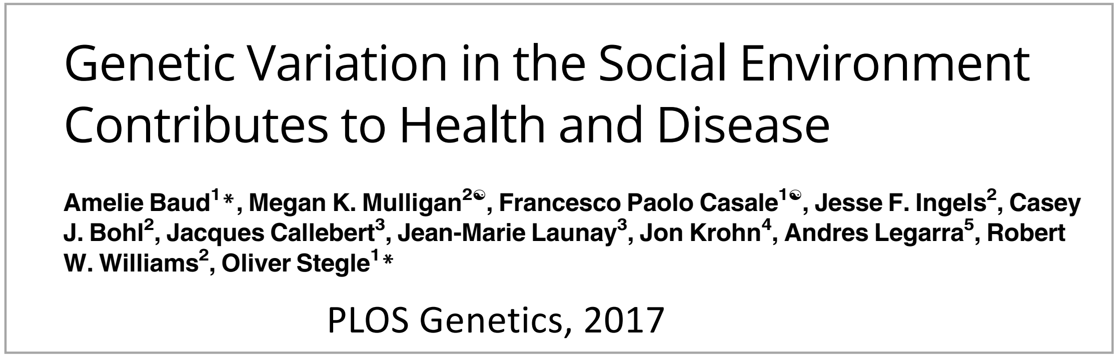


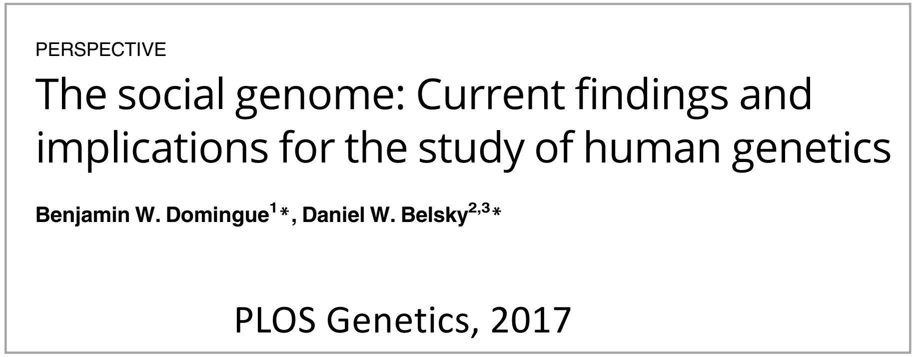
Illustration by Spencer Phillips / EMBL-EBI



Genetic Variation in the Social Environment Contributes to Health and Disease

Amelie Baud[1]*, Megan K. Mulligan[2], Francesco Paolo Casale[1], Jesse F. Ingels[2], Casey J. Bohl[2], Jacques Callebert[3], Jean-Marie Launay[3], Jon Krohn[4], Andres Legarra[5], Robert W. Williams[2], Oliver Stegle[1]*

PLOS Genetics, 2017

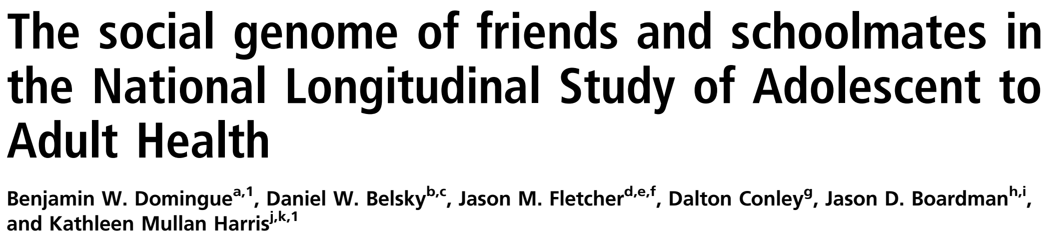


PERSPECTIVE

The social genome: Current findings and implications for the study of human genetics

Benjamin W. Domingue[1]*, Daniel W. Belsky[2,3]*

PLOS Genetics, 2017



The social genome of friends and schoolmates in the National Longitudinal Study of Adolescent to Adult Health

Benjamin W. Domingue[a,1], Daniel W. Belsky[b,c], Jason M. Fletcher[d,e,f], Dalton Conley[g], Jason D. Boardman[h,i], and Kathleen Mullan Harris[j,k,1]

PNAS, 2018

New Results

Comment on this paper

Genetic Nature or Genetic Nurture? Quantifying Bias in Analyses Using Polygenic Scores

Sam Trejo, Benjamin W. Domingue

doi: https://doi.org/10.1101/524850

This article is a preprint and has not been certified by peer review [what does this mean?].

REVIEW

Deconstructing the sources of genotype-phenotype associations in humans

Alexander I. Young[1,2,*], Stefania Benonisdottir[1], Molly Przeworski[3,4,*], Augustine Kong[1,*]

+ See all authors and affiliations

Science 27 Sep 2019:
Vol. 365, Issue 6460, pp. 1396-1400
DOI: 10.1126/science.aax3710

Key questions for SGE research

1) quantify the impact of SGE on an outcome of interest
2) understand how SGE arise

Approach taken by others

Domingue et al. 2018; Kong et al. 2018, Bates et al. 2018,…

- in cohort 1: estimate the $\hat{\beta}$ for phenotype A
- in cohort 2: calculate PRS for social partners (friends or parents) and correlate with phenotype A’ of focal individuals

Only looking at SGE mediated by phenotype A

Approach I propose: SGE GREML

$$\underbrace{y_f}_{\text{Phenotype of interest}} = \underline{X_f}\,\underline{b} + \underbrace{a_{D,f}}_{\text{Aggregate DGE}} + e_{D,f} + \underline{W_f}\,\underline{c} + \underbrace{\underline{Z_f}\,\underline{a_S}}_{\text{Aggregate SGE}} + \underline{Z_f}\,\underline{e_S}$$

Advantages:

- makes no assumption as to the traits of social partners mediating SGE
- no prior knowledge required & no PRS required so can be used on *any* phenotype of interest

http://github.com/limix/SGE

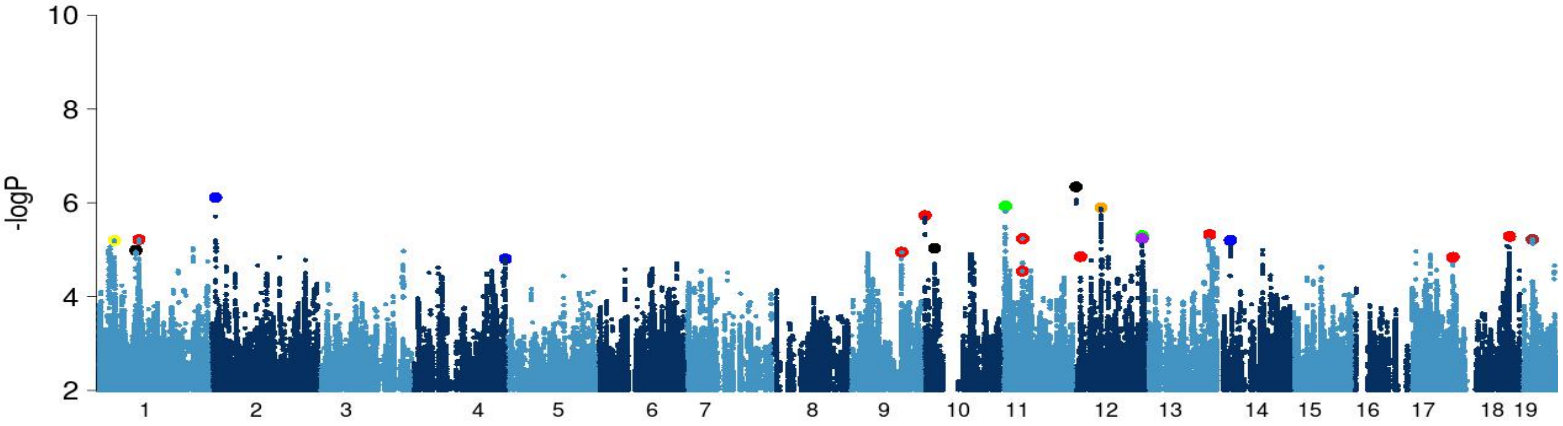
Results *in mice*

- SGE between cage mates affect a broad range of phenotypes including anxiety, immune system activation, body weight, **lung function**, **blood biochemistry** (e.g. LDL levels), and **rate of wound healing**
- SGE can be substantial: up to 29% of variance in lymphocytes proportions and SGE > DGE for 8 / 100 phenotypes
- correlation between DGE and SGE acting on the same phenotype is generally positive
- failing to account for SGE leads to biased estimates of DGE heritability

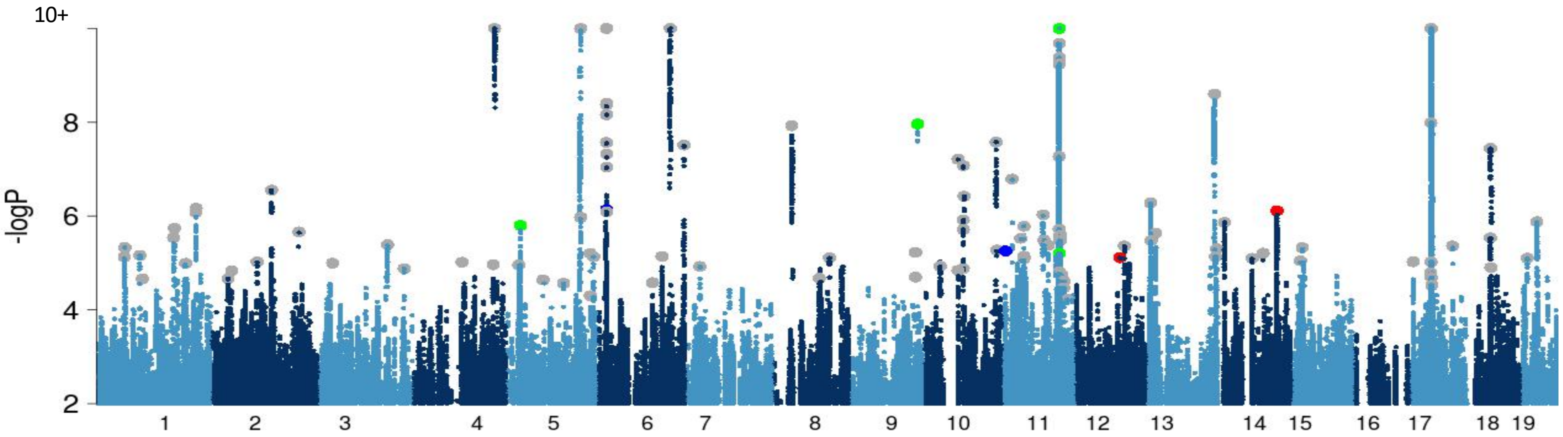
Baud *et al., Genetic variation in the social environment contributes to health and disease,* PLOS Genetics (2017);

Once step further: SGE GWAS to understand how SGE arise

170 SGE GWAS:
21 SGE loci (FDR < 10%)



170 DGE GWAS:
118 DGE loci (FDR < 10%)



Baud *et al.,* bioRxiv (2019); http://github.com/limix/SGE