Gene+environment risk models: whys and hows

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- Genes are important
- The environment is important
- Risk models that include both can be useful

Risk models using E

- Framingham risk model (CVD)
- Breast cancer risk assessment tool
- Chronic and acute risk of VTE

Risk models using E

- Framingham risk model (CVD)
- Breast cancer risk assessment tool
- Chronic and acute risk of VTE
- Prostate cancer

Does adding G help?



е



g



g+e





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What functional form should the model have? What variables should be included? How should they be coded?





Linear or logistic regression assuming additive effects within and across genetic and environmental factors

Model ("Y_A(X)") Out



What about non-linear effects (aka interactions)? School of hard knocks: linear terms pick up most of the signal, potential gains from including non-linear terms swamped by degrees of freedom.

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This model choice has implications for *extrapolated* risks in the tails.



The assumed logadditive relative risk model has notable implications for individuals in the tails of the genetic risk distribution,

More work is needed to verify that this model is a good fit *in the tails*.

Genetic Risk Score

Kraft (2017) J Clin Oncol



Joshi (2014) Am J Hum Genet

Testing calibration of risk models at extremes of disease risk

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Biostatistics (2015)

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Constraining GxE effects may improve model fit (assuming SNP-E interactions are mostly in the same direction). Increasing exposure variance may as well.



Exposure

What if G is Mediated thru E?



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If <u>all</u> of G's effect is mediated thru E and we've measured E <u>without error</u>, then genetic terms b₁,...,b_K go to 0.

What if G is Mediated thru E?



CVD

Breast Cancer



Dudbridge (2018) Genet Epidemiol

So, is it useful?

- Spreading risk distribution
- Identifying subgroups where G is actionable



Can increase the gradient of predicted risks by including G, but utility will depend on context—e.g. on the "action threshold" where expected benefits of intervention outweigh risks.

RR



Adding G can identify 2x as many folks with RR>2



Adding G can identify >10x as many folks with RR>2

RR



Figure 1. Cutaneous squamous cell carcinoma risk with increasing Polygenic Risk Score.

Women < 40 years old



Preliminary results from CARRIERS consortium, presented at AACR 2019 Gao, Couch, Goldgar, Nathanson, Couch, Kraft et. al.

Determining clinical utility

- RCTs
- In the absence of large, expensive, and time consuming RCTs, we can simulate effectiveness using a model of disease natural history w/ or w/o intervention

Determining clinical utility



https://cisnet.cancer.gov/modeling/

Determining clinical utility

Example: stratified breast cancer screening

(preliminary work from CISNET breast cancer working group —van den Broek et al.)







ife years gained:	118
Breast cancer deaths averted:	6.7

ife years gained:	196
Breast cancer deaths averted:	9.7

More can be better



- Qx risk factors
- Mammographic density

PRS

• Emerging biomarkers

Garcia-Closas (2014) JNCI

Misc Issues

- Implementing "complicated" E models
 —good locally, maybe not globally
- Including biology in risk models

