# Polygenic score construction with mean field variational inference to model SNP-SNP interactions

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# Polygenic score

- Uses genome-wide SNP allele counts to produce a number that summarizes genetic risk for a disease of interest, like coronary artery disease
- Polygenic scores typically rely on SNP effect estimates from genome-wide association studies
- Current uses include risk stratification for preventive interventions

# SNP-SNP interactions

- Existing polygenic score construction methods consider only SNP main effects and neglect SNP-SNP interactions
- We hypothesize that our variational inference methods, and the associated reduction in computing requirements, will enable construction of polygenic risk scores that model SNP-SNP interactions
- We expect polygenic risk scores that model SNP-SNP interactions (and include SNP main effects) to outperform current methods in predictive accuracy
- Our collection of statistical models that use both SNP-SNP interactions and SNP main effects contains the collection of statistical models that use only SNP main effects

# Significance

- Current PRS methods, with only SNP main effects, poorly predict disease risk
- Others have shown that SNP-SNP interactions contribute to risk for some diseases
- We expect our PRS methods, with both SNP main effects and SNP-SNP interactions, to outperform existing methods

# Innovation

*The proposed research is innovative, in our opinion, because it represents a substantive departure from the status quo by developing and assessing polygenic risk score methods that leverage SNP-SNP interactions in addition to SNP main effects.*

# New Horizons

- Clinical & public health research
- Biostatistics & statistical genetics research