

## GRAND ROUNDS

Sponsored by: The Division of Biostatistics

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**Thursday, October 16, 2014**  
**12:00PM-1:00PM**  
**Campus Services Building Room 679**

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### **Assessing Incremental Values of Biomarkers in Cohort Studies**

*Comprehensive risk prediction models are critical for identifying populations at different levels of risks that should be recommended for preventive or treatment strategies that vary in intensity. As more putative biomarkers or genetic markers become available to assist in risk prediction, it is important to rigorously evaluate their incremental values (IncV) in improving existing risk models because of the potential cost associated with measuring these markers. However, practical complications and challenges are often involved in biomarker evaluation.*

*In this talk, I will focus on three practical issues. One is that many promising biomarkers, while strongly associated with clinical outcomes, may show limited capacity in improving risk prediction over and above routine clinical variables at the population-average level since the IncV of these biomarkers often vary across subgroups. We have proposed a novel statistical procedure for systematically identifying potential subgroups in whom it might be beneficial to measure both the new biomarkers and traditional markers.*

*Nested case-control (NCC) sampling designs have been often employed in large cohort studies due to high cost for biomarker measurement. As scientific questions evolve over time, multiple NCC studies might be conducted sequentially with different sets of biomarkers measured on different sub-cohorts. Statistical analyses of multi-phase NCC studies become challenging since the design introduces complex data structure. We develop robust statistical procedures for making inferences about the IncV of biomarkers accommodating complex sampling designs as well as other complications such as time-varying biomarker effects and model misspecification.*

*I will also talk about how to construct risk prediction models accounting for age-specific effects of longitudinally-collected risk factors. This work is motivated by the Framingham risk model for cardiovascular disease where age is included as one of the standard risk factors with simple effects, while other risk factors are assumed to have a static effect on the risk. However, important risk factors such as BMI might have a substantially different effect on future risks, depending on the age. To incorporate such age-varying effects, we introduce an alternative approach that estimates the age-specific risk directly via a flexible varying-coefficient model.*

*Lunch will be provided. Please contact Anne Rudwick at [stemwede@ohsu.edu](mailto:stemwede@ohsu.edu) if you have a dietary restrictions.*