

## BINSCATTER

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Binscatter, o diagrama de dispersión agrupada, es una herramienta muy popular en microeconomía aplicada. Proporciona una forma flexible de visualizar y resumir la media, el cuantil y otras funciones de regresión no paramétricas en grandes conjuntos de datos. También puede utilizarse para analizar linealidad o monotonicidad. En esta charla se abordará un análisis del Binscatter en donde se discutirán resultados teóricos y prácticos que ayudaran a comprender las prácticas usuales como también a orientar futuras aplicaciones.

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Large scale proteomics datasets are becoming increasingly available in biomedical sciences offering huge potential for better understanding the causal pathways of diseases to develop alternative care treatments. Unfortunately, protein expression levels can be strongly influence by the environment, which may confound potential causal effects on a response of interest. Mendelian Randomization is a popular approach used to control for this confounding and identify causal effects by leveraging valid genetic variants as instrumental variables. We develop a two-stage regularized instrumental variable estimator to select valid instruments as well as causal proteins from high-dimensional -omics datasets. To reduce the risk of selecting non-valid instruments, we develop our estimator to be robust to violations to three required instrumental variables conditions. We call this estimator the Thrice-Robust Instrumental Variable Estimator (THRIVE). We examine important properties of our estimator in a large-scale simulation study and compare its performance to that of competing estimators. We use our estimator in a relevant prostate cancer dataset from The Cancer Genome Atlas (TCGA) and identify 2 proteins as potentially having a causal effect on the severity of a prostate cancer tumour.

*Joint work with Joe Watson (University of British Columbia) and David Kepplinger (George Mason University).*