Use of Biomarkers in Propensity Score Matching to Mitigate Channeling Bias in a Retrospective Cohort of ESRD Patients

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INTRODUCTION

Retrospective analyses of medical data are inherently subject to channeling bias because clinicians choose treatments based on a patient's heath status. Pseudo-randomization via techniques such as propensity score matching (PSM) can help mitigate this bias. However, PSM is often done solely using administrative claims data. We tested the hypothesis that claims plus relevant biomarkers provide superior matching when compared to claims alone.

METHODOLOGY

- We used databases from a large dialysis organization to obtain two cohorts of dialysis patients, prescribed different drug therapies within the same class to control phosphorus and normalized protein catabolic rate (nPCR).
- The treatment cohorts were first matched on demographics and comorbidities only.
- The same cohorts were then re-matched, adding baseline biomarkers to the PSM: albumin, corrected calcium, nPCR, parathyroid hormone (PTH), Kt/V and phosphorus.
- We used generalized linear mixed models (GLMM) to determine if treatment was associated with lab outcomes 4 months after treatment initiation.
- We ran the GLMM separately for both matched cohorts and compared results to determine whether the addition of biomarker data to the PSM would meaningfully change the estimates of association between treatment and outcome.

RESULTS

Table 1. Biomarker Values in Cohort Matched on Demographics and Comorbidities

Baseline Values	Drug Therapy 1	Drug Therapy 2	P-value
Albumin (g/dL)	3.93	3.94	0.34
Corrected calcium (mg/dL)	9.07	9.09	0.57
nPCR (g/kg/day)	1.12	1.11	0.28
PTH (pg/mL)	358	344	0.49
Kt/V	1.63	1.63	0.70
Phosphorus (mg/dL)	**6.14**	**5.82**	**<0.01**
Month Four Values (GLMM)	Drug Therapy 1	Drug Therapy 2	P-value
Phosphorus (mg/dL)	**5.95**	**5.67**	**<0.01**
nPCR (g/kg/day)	**1.09**	**1.04**	**<0.01**

Table 2. Biomarker Values in Cohort Matched on Demographics, Comorbidities and Biomarkers

Baseline Values	Drug Therapy 1	Drug Therapy 2	P-value
Albumin (g/dL)	3.92	3.93	0.96
Corrected calcium (mg/dL)	9.07	9.09	0.55
nPCR (g/kg/day)	1.13	1.13	0.59
PTH (pg/mL)	360	358	0.89
Kt/V	1.63	1.63	0.98
Phosphorus (mg/dL)	6.14	6.16	0.76
Month Four Values (GLMM)	Drug Therapy 1	Drug Therapy 2	P-value
Phosphorus (mg/dL)	5.95	5.77	0.08
nPCR (g/kg/day)	1.09	1.07	0.21

SUMMARY of RESULTS

- The PSM cohorts matched only on demographics and comorbidities did not differ on included variables, but differences existed in 1 key biomarker (phosphorus) of the 6 baseline biomarkers not included in the match ($p < 0.01$; Table 1).
- When biomarkers were included in the PSM, there were no significant differences between groups on any baseline measure. (Table 2)
- At month 4, GLMM analysis showed a significant association between drug and lab outcomes for the cohort matched on demographic and comorbid information only (all p-values < 0.01).
- There was no significant association between drug and lab values in the cohort matched on biomarkers plus comorbid and demographic variables (all p-values > 0.05).

KEY LEARNINGS

- ✓ PSM using administrative claims alone left subtle but leveraged channeling bias in the sample, and erroneous conclusions were drawn from subsequent GLMM analysis.
- ✓ Inclusion of biomarkers in the PSM removed this bias and yielded non-significant GLMM results.
- ✓ Administrative claims data without biomarkers may not be sufficient for conducting PSM.

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