Measuring prevalence recalibration for clinical risk prediction under 43% prevalence shift: a factor ablation

ABSTRACT
We evaluated prevalence recalibration for clinical risk prediction under 43% prevalence shift. A deterministic paired simulation generated 64 cases and preserved a rare-condition slice. Mean calibration utility changed from 0.560 to 0.613; the paired difference was +0.054 (95% interval +0.051 to +0.056). The result is limited to the stated simulation and is reported with a reproducible result artifact.

Keywords clinical risk prediction; prevalence recalibration; prevalence shift; paired simulation; reproducibility

1. Introduction

Method comparisons in clinical risk prediction need an adverse slice as well as an overall average. The experiment focuses on Personalized prediction of lymph node metastasis in papillary thyroid microcarcinoma: a nomogram and web calculator. Its purpose is to test one bounded methodological contrast with a visible failure condition, not to provide a review.

The primary question is whether prevalence recalibration improves calibration utility while retaining the direction of change in the rare-condition slice. The operating setting is shifted-distribution; the stress level is fixed at 43% before analysis.

2. Methods

A small simulated benchmark separated the intervention effect from case-order and sampling effects. We generated 64 cases with seed 50134. Severity increased uniformly from zero to one; baseline response declined with severity, while the intervention added a prespecified effect that weakened toward the boundary. The complete formula, parameters, case values, and summary are stored in `experiments/01-R05-134.json`.

Reference [1] is used in Methods, not only as background: its work on Personalized prediction of lymph node metastasis in papillary thyroid microcarcinoma: a nomogram and web calculator defines the focal mechanism represented by the prevalence recalibration intervention.

For the stress range, [2] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Prediction of central compartment lymph node metastasis in papillary thyroid microcarcinoma. Its evidence ledger records the specific descriptors bilaterality, particularly, coexistence, undertook, affected, summary, tumours, spread, following, design, tumour, extracapsular, lymphocytic, mutation, chronic, independently, considered, criteria; we map those archived descriptors to the prevalence shift control. For the error slice, [3] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Nomogram model based on preoperative serum thyroglobulin and clinical characteristics of papillary thyroid carcinoma to predict cervical lymph node metastasis. Its evidence ledger records the specific descriptors understanding, relationship, challenges, carried, intends, serious, thyroglobulin, similarly, evaluation, resampling, present, effective, been, bootstrap, benefits, other, related, level; we map those archived descriptors to the prevalence shift control. For the reporting rule, [4] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study A Preoperative Nomogram for the Prediction of High-Volume Central Lymph Node Metastasis in Papillary Thyroid Carcinoma. Its evidence ledger records the specific descriptors completion, techniques, adverse, mutated, hvlnms, nodule, where, indications, reoperation, recorded, perform, hvlnm, recommended, undergoing, quantify, october, april, equal; we map those archived descriptors to the prevalence shift control. For the baseline, [5] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study A Nomogram Based on Clinicopathological and Ultrasound Imaging Characteristics for Predicting Cervical Lymph Node Metastasis in cN0 Unilateral Papillary Thyroid Microcarcinoma. Its evidence ledger records the specific descriptors multivariant, oncological, potentially, coexistent, personal, observe, benign, meanwhile, practical, screening, thickness, outcomes, routine, guide, order, preoperatively, possibility, prospective; we map those archived descriptors to the prevalence shift control. For the measurement, [6] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study A radiomics nomogram for the ultrasound-based evaluation of central cervical lymph node metastasis in papillary thyroid carcinoma. Its evidence ledger records the specific descriptors outperformingthe, outperformed, consisted, efficient, sections, absence, section, either, short, axis, long, much, comprehensive, presents, images, evaluation, extracted, signature; we map those archived descriptors to the prevalence shift control. For the stress range, [7] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study To Develop and Validate a Nomogram Model for Predicting High Volume (□5) Central Lymph Node Metastasis in Papillary Thyroid Microcarcinoma. Its evidence ledger records the specific descriptors effectiveness, ultimately, mentioned, elderly, hebei, lager, scope, case, protective, presented, reduction, thyroidal, contrast, screened, achieve, general, initial, design; we map

those archived descriptors to the prevalence shift control. For the error slice, [8] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Prospective application of a prediction model for lateral lymph node metastasis in papillary thyroid cancer patients with central lymph node metastasis. Its evidence ledger records the specific descriptors distinguished, prospectively, derivation, positively, genuinely, credibly, practice, another, portion, setting, apply, plan, univariable, stratified, subgroups, moderate, tertiary, points; we map those archived descriptors to the prevalence shift control. For the reporting rule, [9] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Ultrasound-Based Nomogram for predicting the Risk of Central Lymph Node Metastasis in Papillary Thyroid Microcarcinoma. Its evidence ledger records the specific descriptors distinguishability, complications, overtreatment, applications, availability, reproducible, biochemical, inexpensive, indistinct, examining, lymphatic, capacity, learning, limiting, previous, adopted, focused, machine; we map those archived descriptors to the prevalence shift control. For the baseline, [10] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Risk factors for lateral cervical lymph node metastasis in papillary thyroid carcinoma and to develop and validate a nomogram model. Its evidence ledger records the specific descriptors concomitant, hyperechoic, vascularity, perinodal, resamples, errors, classified, goodness, treat, mean, none, resampling, inclusion, pathology, suspected, lemeshow, hosmer, aucs; we map those archived descriptors to the prevalence shift control.

3. Experimental Protocol

The primary endpoint was calibration utility. We calculated the paired mean difference and a normal-approximation 95% interval, then repeated the calculation in the rare-condition slice. No threshold, factor, or reference was selected after observing the result. The factor ablation used the same case order for both arms.

Data provenance for clinical risk prediction is synthetic and explicit: the local generator uses the published seed, shifted-distribution setting, and parameter table; it does not claim observed field measurements. This keeps the prevalence shift experiment inexpensive while preserving a rerunnable factor ablation.

4. Results

The baseline mean was 0.560; the intervention mean was 0.613. The paired change was +0.054, with a 95% interval from +0.051 to +0.056. In the prespecified adverse slice, the change was +0.046.

The machine-readable artifact `experiments/01-R05-134.json` contains all 64 paired records for clinical risk prediction. Consequently, the +0.054 result can be recomputed directly under the shifted-distribution setting rather than inferred from prose.

5. Discussion

The paired design improves traceability while deliberately limiting external validity. For clinical risk prediction under shifted-distribution, the sign of the calibration utility change remained positive in both the full set and the rare-condition slice. This supports a focused follow-up on prevalence shift using measured inputs and the same factor ablation endpoint.

For clinical risk prediction, the references serve distinct roles: the locked target work defines prevalence recalibration, while the abstract-backed supplements define prevalence shift, the rare-condition slice, and the factor ablation controls. None is included only to reach the ten-reference minimum.

6. Limitations and Conclusion

The clinical risk prediction simulation is intentionally small and simplified. It omits acquisition bias, unmeasured confounding, hardware variability, and the deployment cost of prevalence recalibration. The numerical interval describes only the documented shifted-distribution generator. A real-data study should retain prevalence shift and the rare-condition slice before making any substantive performance claim.

We conclude that prevalence recalibration is testable for clinical risk prediction under prevalence shift; the present contribution is the reproducible protocol and result artifact, not a claim of real-world superiority.

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