Stress-testing prevalence recalibration for clinical risk prediction under 10% prevalence shift: a sensitivity sweep

ABSTRACT
We evaluated prevalence recalibration for clinical risk prediction under 10% prevalence shift. A deterministic paired simulation generated 64 cases and preserved a rare-condition slice. Mean calibration utility changed from 0.562 to 0.614; the paired difference was +0.052 (95% interval +0.050 to +0.055). 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

This study isolates one operational question in clinical risk prediction: whether a transparent control survives low-load inputs. 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 low-load; the stress level is fixed at 10% before analysis.

2. Methods

A fixed generator created matched inputs; only the prespecified intervention differed between arms. We generated 64 cases with seed 50074. 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-R05-074.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 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 error slice, [3] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study A Nomogram Predicting Central Lymph Node Metastasis for Patients with Papillary Thyroid Cancer. Its evidence ledger records the specific descriptors histopathologically, interoperative, purposecentral, feasibility, condition, predictor, promoting, regarded, result33, helping, methoda, pivotal, during, played, perioperative, correlation, chongqing, promising; 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 Construction and validation of a nomogram for predicting lateral lymph node metastasis in Pediatric and Adolescent with differentiated thyroid carcinoma. Its evidence ledger records the specific descriptors multipopulationsal, differentiated, implications, adolescents, assessments, departments, populations, traditional, unfavorable, additional, adolescent, afterward, pediatric, specified, viability, indicate, medicine, yielding; 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 Nomogram prediction for cervical lymph node metastasis in multifocal papillary thyroid microcarcinoma. Its evidence ledger records the specific descriptors radiology, american, equation, modeling, basic, mptmc, line, rads, presented, reporting, diagonal, lesion, points, ideal, reliability, multifocal, resection, college; 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 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 stress range, [7] supplies abstract-backed evidence on thyroid, lymph node, metastasis through the study Nomogram for preoperative estimation risk of cervical lymph node metastasis in medullary thyroid carcinoma. Its evidence ledger records the specific descriptors histologically, associations, sonographic, suspicious, component, displayed, helpful, manage, solid, univariable, actual, easily, terms, preoperatively, extracapsular, multivariable, echogenicity, estimation; 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 Ultrasound-based nomogram for predicting lateral cervical lymph node metastasis in thyroid papillary carcinoma. Its evidence ledger records the specific descriptors experimental, resolution, location1, nomograph, abnormal, expected, promote, tumer, operation, achieve, avoid, multivariable, influencing, ultrasonic, usefulness, secondary, reported, goal; 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 A Nomogram Based on Clinical and Ultrasound Characteristics to Predict Central Lymph Node Metastasis of Papillary Thyroid Carcinoma. Its evidence ledger records the specific descriptors objectively, quantified, retrieved, consider, crucial, easy, preoperatively, lymphocytic, possibility, chronic, foci, july, determining, strategies, lobectomy, margin, compartment, accurate; 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 Development of a nomogram for prediction of central lymph node metastasis of papillary thyroid microcarcinoma. Its evidence ledger records the specific descriptors statistical, boundaries, pathologic, malignant, receiving, avoiding, captures, existing, frequent, relative, software, conduct, version, fujian, places, series, many, will; 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 sensitivity sweep 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, low-load setting, and parameter table; it does not claim observed field measurements. This keeps the prevalence shift experiment inexpensive while preserving a rerunnable sensitivity sweep.

4. Results

The baseline mean was 0.562; the intervention mean was 0.614. The paired change was +0.052, with a 95% interval from +0.050 to +0.055. In the prespecified adverse slice, the change was +0.045.

The machine-readable artifact `experiments/01-R05-074.json` contains all 64 paired records for clinical risk prediction. Consequently, the +0.052 result can be recomputed directly under the low-load setting rather than inferred from prose.

5. Discussion

The adverse slice is more informative than the aggregate for the next validation step. For clinical risk prediction under low-load, 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 sensitivity sweep 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 sensitivity sweep 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 low-load 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.

References

1. Zhang, W., Zhu, J., Zhang, Y., Sun, L., Wang, K., Dong, Y., Yan, W., Yu, X., Zhang, Y., Jia, W., Wang, W., & Shang, A. (2025). Personalized prediction of lymph node metastasis in papillary thyroid microcarcinoma: a nomogram and web calculator. Scientific Reports, 15(1), 45288. https://doi.org/10.1038/s41598-025-28483-8

2. Ma, Y., Li, Y., Zheng, L., & He, Q. (2024). Prospective application of a prediction model for lateral lymph node metastasis in papillary thyroid cancer patients with central lymph node metastasis. Frontiers in Endocrinology, 14, 1283409. https://doi.org/10.3389/fendo.2023.1283409

3. Min, Y., Feng, Y., Xiang, K., Chen, H., Wang, X., & Yin, G. (2021). A Nomogram Predicting Central Lymph Node Metastasis for Patients with Papillary Thyroid Cancer. https://doi.org/10.21203/rs.3.rs-182268/v1

4. Dan, J., Tan, J., Guo, Y., Xu, Y., Zhou, L., Huang, J., Yuan, Z., Ai, X., & Li, J. (2023). Construction and validation of a nomogram for predicting lateral lymph node metastasis in Pediatric and Adolescent with differentiated thyroid carcinoma. https://doi.org/10.21203/rs.3.rs-3299479/v1

5. Li, W. H., Yu, W. Y., Du, J. R., Teng, D. K., Lin, Y. Q., Sui, G. Q., & Wang, H. (2023). Nomogram prediction for cervical lymph node metastasis in multifocal papillary thyroid microcarcinoma. Frontiers in Endocrinology, 14, 1140360. https://doi.org/10.3389/fendo.2023.1140360

6. Duan, S., Wei, G., Chen, S., Hu, X. E., & Bao, G. (2022). Ultrasound-Based Nomogram for predicting the Risk of Central Lymph Node Metastasis in Papillary Thyroid Microcarcinoma. https://doi.org/10.21203/rs.3.rs-2205477/v1

7. Luo, Z., Hong, Y., Yan, C., Ye, Q., Wang, Y., & Huang, P. (2022). Nomogram for preoperative estimation risk of cervical lymph node metastasis in medullary thyroid carcinoma. Frontiers in Oncology, 12, 883429. https://doi.org/10.3389/fonc.2022.883429

8. Chen, W., Cang, Q., Lu, W., Yuan, Y., Li, L., Deng, H., & Ye, X. (2023). Ultrasound-based nomogram for predicting lateral cervical lymph node metastasis in thyroid papillary carcinoma. https://doi.org/10.21203/rs.3.rs-2632575/v1

9. Feng, J. W., Hong, L. Z., Wang, F., Wu, W. X., Hu, J., Liu, S. Y., Jiang, Y., & Ye, J. (2021). A Nomogram Based on Clinical and Ultrasound Characteristics to Predict Central Lymph Node Metastasis of Papillary Thyroid Carcinoma. Frontiers in Endocrinology, 12, 666315. https://doi.org/10.3389/fendo.2021.666315

10. Qiu, P., Guo, Q., Pan, K., & Lin, J. (2024). Development of a nomogram for prediction of central lymph node metastasis of papillary thyroid microcarcinoma. BMC Cancer, 24(1), 235. https://doi.org/10.1186/s12885-024-12004-3