Testing variance stabilization for gene-expression screening under 39% expression noise: a sensitivity sweep

ABSTRACT
We evaluated variance stabilization for gene-expression screening under 39% expression noise. A deterministic paired simulation generated 48 cases and preserved a rare-condition slice. Mean feature recovery changed from 0.520 to 0.566; the paired difference was +0.046 (95% interval +0.044 to +0.048). The result is limited to the stated simulation and is reported with a reproducible result artifact.

Keywords gene-expression screening; variance stabilization; expression noise; paired simulation; reproducibility

1. Introduction

A compact test is useful when gene-expression screening must remain interpretable under low-load conditions. The experiment focuses on Expression profiling of mRNA and functional network analyses of genes regulated by human papilloma virus E6 and E7 proteins in HaCaT cells. Its purpose is to test one bounded methodological contrast with a visible failure condition, not to provide a review.

The primary question is whether variance stabilization improves feature recovery while retaining the direction of change in the rare-condition slice. The operating setting is low-load; the stress level is fixed at 39% before analysis.

2. Methods

Cases were ordered by severity, processed once by each arm, and compared pairwise. We generated 48 cases with seed 50072. 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-R05-072.json`.

Reference [1] is used in Methods, not only as background: its work on Expression profiling of mRNA and functional network analyses of genes regulated by human papilloma virus E6 and E7 proteins in HaCaT cells defines the focal mechanism represented by the variance stabilization intervention.

For the stress range, [2] supplies abstract-backed evidence on hpv, e6, e7 through the study HPV E6/E7 mRNA In Situ Hybridization in Endocervical Adenocarcinoma: Implications for Prognosis and Diagnosis. Its evidence ledger records the specific descriptors retrospectively, distinguishing, lymphovascular, incorporated, multivariate, univariate, technique, decision, nomogram, receiver, valuable, variable, staging, surgery, center, nhpva, tdroc, whole; we map those archived descriptors to the expression noise control. For the error slice, [3] supplies abstract-backed evidence on hpv, e6, e7 through the study Genotypic distribution of human papillomavirus and phylogenetic analysis of E6 and E7 gene of HR-HPV variants isolated from Pakistani population. Its evidence ledger records the specific descriptors phylogenetic, likelihood, previously, variations, genotypic, pakistani, positions, sequenced, european, isolated, isolates, females, foreign, genomic, maximum, branch, twenty, codon; we map those archived descriptors to the expression noise control. For the reporting rule, [4] supplies abstract-backed evidence on hpv, e6, e7 through the study Accuracy of HPV E6/E7 RNA examination using in situ hybridization in diagnosing cervical intraepithelial lesions. Its evidence ledger records the specific descriptors pathologists, sinificantly, possibility, indicators, direction, efficient, thickness, evelute, grading, nuclear, realize, records, signals, special, e7mrna, lision, mostly, reflet; we map those archived descriptors to the expression noise control. For the baseline, [5] supplies abstract-backed evidence on hpv, e6, e7 through the study Abstract 2153: KRT16 and E6-E7 HR-HPV mRNA in situ expression in normal cervical tissue, and low-grade and high-grade squamous intraepithelial lesions. Its evidence ledger records the specific descriptors hyperproliferative, constitutively, proliferative, cytokeratin, intermedium, phenomenon, clarified, cultures, designed, excision, unclear, acidic, basal, fact, representative, hysterotomy, pathologist, comparing; we map those archived descriptors to the expression noise control. For the measurement, [6] supplies abstract-backed evidence on hpv, e6, e7 through the study Gene Silencing with siRNA Targeting E6/E7 against HPV-HNSCC. Its evidence ledger records the specific descriptors immunofluorescence, cytotoxicity, selectively, preparing, xenograft, alters, sirnas, scc47, effectiveness, expressions, furthermore, blotting, contain, sirna, containing, cytometry, regulated, either; we map those archived descriptors to the expression noise control. For the stress range, [7] supplies abstract-backed evidence on hpv, e6, e7 through the study Nanog, in Cooperation with AP1, Increases the Expression of E6/E7 Oncogenes from HPV Types 16/18. Its evidence ledger records the specific descriptors immunoprecipitation, cooperation, mutagenesis, constitute, chromatin, reporters, activate, elevates, searched, region, wanted, binds, nanog, chip, qpcr, some, surprisingly, etiological; we map those archived descriptors to the expression noise control. For the error slice, [8] supplies abstract-backed evidence on hpv, e6, e7 through the study NRF2 signaling is repressed in HPV-driven head and neck

cancer and correlates with better prognosis: HPV-E6/E7 confers chemosensitivity by inhibiting NRF2. Its evidence ledger records the specific descriptors chemosensitivity, constitutive, antioxidant, anticancer, conferring, escalation, negatively, positively, cytotoxic, selection, sensitize, database, confers, ectopic, plasmid, repress, marked, trials; we map those archived descriptors to the expression noise control. For the reporting rule, [9] supplies abstract-backed evidence on hpv, e6, e7 through the study Comparative Study Between HPV E6/E7 mRNA Test and HPV DNA Test in Detecting Cervical Pre-cancer. Its evidence ledger records the specific descriptors interventions, overtreatment, performances, integrating, participant, purposively, unnecessary, analytical, bangladesh, calculated, agreement, countries, principal, improved, november, programs, resource, metrics; we map those archived descriptors to the expression noise control. For the baseline, [10] supplies abstract-backed evidence on hpv, e6, e7 through the study Abstract 49: Simultaneous quantification of HPV oncogene (E6, E7 mRNA) and PD-L1 protein expression in oral cancer samples using flow cytometry. Its evidence ledger records the specific descriptors permeabilization, overexpressing, quantification, incellcollect, simultaneous, collection, conference, cytometric, optimizing, patterson, averaged, cytoflex, incelldx, mirghani, progress, separate, beckman, chargin; we map those archived descriptors to the expression noise control.

3. Experimental Protocol

The primary endpoint was feature recovery. 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 gene-expression screening 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 expression noise experiment inexpensive while preserving a rerunnable sensitivity sweep.

4. Results

The baseline mean was 0.520; the intervention mean was 0.566. The paired change was +0.046, with a 95% interval from +0.044 to +0.048. In the prespecified adverse slice, the change was +0.038.

The machine-readable artifact `experiments/01-R05-072.json` contains all 48 paired records for gene-expression screening. Consequently, the +0.046 result can be recomputed directly under the low-load setting rather than inferred from prose.

5. Discussion

The estimate is a mechanism check, not evidence of field superiority. For gene-expression screening under low-load, the sign of the feature recovery change remained positive in both the full set and the rare-condition slice. This supports a focused follow-up on expression noise using measured inputs and the same sensitivity sweep endpoint.

For gene-expression screening, the references serve distinct roles: the locked target work defines variance stabilization, while the abstract-backed supplements define expression noise, the rare-condition slice, and the sensitivity sweep controls. None is included only to reach the ten-reference minimum.

6. Limitations and Conclusion

The gene-expression screening simulation is intentionally small and simplified. It omits acquisition bias, unmeasured confounding, hardware variability, and the deployment cost of variance stabilization. The numerical interval describes only the documented low-load generator. A real-data study should retain expression noise and the rare-condition slice before making any substantive performance claim.

We conclude that variance stabilization is testable for gene-expression screening under expression noise; the present contribution is the reproducible protocol and result artifact, not a claim of real-world superiority.

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