Multiple-Comparison Testing for Cross-Validation Path Optimization Benchmarks: A Hessian-Mismatch Diagnostic for Holm–Bonferroni Failure Modes

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Abstract

Comparing optimization solvers on K-fold cross-validation accuracy across D datasets is a D-comparison problem with correlated test statistics — yet the standard practice reports uncorrected p-values or, worse, no p-values at all. Our contribution is methodological rather than statistical: we do not introduce a new test. We *pair* the well-known Holm–Bonferroni paired-t procedure with a problem-specific *structural diagnostic* that attributes per-dataset rejections to algorithmic mechanism — and we argue that benchmark claims in optimization should always carry this pair, not statistical correction alone. We instantiate the pairing on a 11-dataset benchmark comparing a fast closed-form / fixed-preconditioner logistic-regression solver ($R1{+}10$) to warm-start L-BFGS. Holm–Bonferroni rejects the iso-accuracy null on exactly 2 of 11 datasets (Adult, $p < 10^{-3}$; Covertype, $p = 0.001$). These two rejections coincide one-to-one with the two smallest Hessian-mismatch index $\mu_* := \lambda_{\min}(\mathbf{M}^{-1/2}\mathbf{H}(\boldsymbol{\theta}^*)\mathbf{M}^{-1/2})$, where $\mathbf{M}$ is the fixed preconditioner and $\mathbf{H}(\boldsymbol{\theta}^*)$ is the optimum-Hessian — the structural diagnostic in this concrete instance. The progressive estimate $\hat{\mu}_5$ fails as a pre-iteration decision rule across 10 CV-path datasets (FP rate 100% at the $\hat{\mu}_5 \leq 0.05$ threshold). We compare four correction procedures (Bonferroni, Holm–Bonferroni, Benjamini–Hochberg, no correction), four test statistics (paired t, Wilcoxon, sign test, bootstrap CI), and analyze the protocol's statistical power. The framework's generalization to non-logistic settings is conjectured but not validated in this paper, beyond a structural argument we discuss in Section 10.

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1. Introduction

Optimization papers routinely report "$X\%$ faster than baseline" across a benchmark suite. When the benchmark has $D \sim 10$ datasets, the statistical question is: does any of the D accuracy gaps imply genuine algorithmic divergence, or are all gaps consistent with the null hypothesis "Solver A matches Solver B at the optimum"? The naive practice — reporting per-dataset p-values without correction — inflates family-wise error: if each test has Type-I rate $\alpha = 0.05$, then the family-wise error rate (FWER) approaches $1-(1-\alpha)^D$, which for $D = 11$ is already 43%. The cautious practice — Holm–Bonferroni or Benjamini–Hochberg step-down — absorbs 1–2 borderline rejections into the multiple-comparison floor, but loses power proportional to D.

We argue that multiple-comparison testing in optimization benchmarks should be paired with a *structural diagnostic*: a problem-specific quantity that explains *why* a particular dataset rejects the iso-accuracy null. Without such a diagnostic, a D-dataset rejection table is a list of unexplained accuracy gaps, indistinguishable from random Type-I errors. With one, the rejection pattern carries algorithmic meaning: rejections cluster around structural regimes where the solver provably underperforms.

The contribution here is the pairing of a paired-t-test + Holm–Bonferroni procedure with the Hessian-mismatch index μ_*, both for ℓ_2-regularized logistic regression on the cross-validation regularization path. We chose ℓ_2-logistic specifically because (a) it admits a closed-form μ_* defined by spectral data of the optimum-Hessian and the fixed preconditioner, (b) it is the workhorse of statistical-software CV-path workflows (`LogisticRegressionCV`, `glmnet`, `statsmodels`), and (c) we have an existing fast solver — one-step Newton from the origin followed by 10 fixed-preconditioner iterations — whose accuracy gap relative to L-BFGS varies non-trivially across datasets.

What's new (and what's not). The statistical primitives we use — paired-t, Wilcoxon, Holm–Bonferroni, Benjamini–Hochberg, bootstrap CI — are textbook; we do not propose a new test. The contribution is (i) the *pairing* of these primitives with μ_* as a structural diagnostic — a protocol hinted at by Demšar (2006) but rarely operationalized; and (ii) the empirical finding that μ_* exhibits one-to-one correspondence with H–B rejections on a non-trivial benchmark suite, while the natural pre-iteration substitute $\hat{\mu}_5$ does not. The methodology contribution is modest by design; the value lies in the conceptual framing and the empirical falsification of $\hat{\mu}_5$-as-decision-rule.

Contributions.

1. **Testing protocol (Section 4).** A Holm–Bonferroni-corrected paired-t-test for D-dataset CV-accuracy comparisons. Applied to $D = 11$ datasets, the protocol rejects the iso-accuracy null on exactly 2 datasets (Adult, Covertype) at corrected $p < 0.05$. We compare against three alternative correction procedures (Bonferroni, Benjamini–Hochberg, no correction) and three alternative test statistics (Wilcoxon signed-rank, sign test, sign-rank).
2. **Post-hoc structural explanation (Section 7).** The rejected datasets correlate one-to-one with small μ_*: Adult $\mu_* \approx 0.09$ (boundary of fast regime), Covertype $\mu_* \approx 10^{-3}$ (deep slow regime). All 9 non-rejected datasets have μ_* either large (> 0.05) or, in three cases, small but with the iterate not aligned with the bottom eigenspace. The correlation is sigmoid-saturation-driven: datasets with a larger fraction of saturated training points have smaller μ_*.
3. **Progressive estimate fails as a decision rule (Section 8).** We test the operational hypothesis "$\hat{\mu}_5 \leq 0.05$ correctly identifies datasets where the iso-accuracy null will be rejected." All 7 slow datasets have $\hat{\mu}_5 \in [0.08, 0.21]$, yielding FP rate 100% at the $\tau = 0.05$ threshold. We reject this rule at any sensible operating point.
4. **Power analysis (Section 6).** We compute the statistical power of the protocol as a function of D, K (CV folds), and effect size $|\bar{\Delta}|$. The bootstrap-CI on speedup gives a complementary view: the 1.2–$9.5\times$ speedup range has 95% CI half-widths between 0.06 and 1.4 across datasets, well-separated from the iso-speed null at $1.0\times$ except on the smallest dataset (Wine, $n = 178$).

2. Setup

Let $L_\lambda(\boldsymbol{\theta}) = \sum_{i=1}^{n}[\log(1+\exp(\mathbf{x}_i^\top\boldsymbol{\theta})) - y_i\mathbf{x}_i^\top\boldsymbol{\theta}] + \lambda\|\boldsymbol{\theta}\|^2$ be the ℓ_2-regularized logistic loss on training fold i with $y_i \in \{0,1\}$ and $\mathbf{x}_i \in \mathbb{R}^m$. The minimizer is $\boldsymbol{\theta}^*(\lambda) = \operatorname{argmin}_{\boldsymbol{\theta}} L_\lambda(\boldsymbol{\theta})$. The fixed preconditioner is $\mathbf{M} = 2\lambda\mathbf{I} + \frac{1}{4}\mathbf{X}^\top\mathbf{X}$. The fast solver is

$$\begin{aligned} \hat{\boldsymbol{\theta}}_{R1} &= \mathbf{M}^{-1}\mathbf{X}^\top(\mathbf{y} - \tfrac{1}{2}\mathbf{1}), \\ \hat{\boldsymbol{\theta}}_{k+1} &= \hat{\boldsymbol{\theta}}_k - \mathbf{M}^{-1}\nabla L_\lambda(\hat{\boldsymbol{\theta}}_k), \quad \hat{\boldsymbol{\theta}}_0 = \hat{\boldsymbol{\theta}}_{R1}, \end{aligned} \tag{1}$$

running for 10 iterations ($R1{+}10$). Each iteration costs $\mathcal{O}(nm + m^2)$ (one $\mathbf{X}^\top\mathbf{X}$ amortized across $K \cdot 5 = 100$ inner solves on the CV-path). The Hessian-mismatch index is the generalized Rayleigh quotient

$$\mu_* := \lambda_{\min}(\mathbf{M}^{-1/2}\mathbf{H}(\boldsymbol{\theta}^*)\mathbf{M}^{-1/2}) \in (0, 1], \tag{2}$$

where $\mathbf{H}(\boldsymbol{\theta}^*) = 2\lambda\mathbf{I} + \mathbf{X}^\top\operatorname{diag}(\sigma'(\mathbf{X}\boldsymbol{\theta}^*))\mathbf{X}$ and $\sigma'(z) = \sigma(z)(1 - \sigma(z))$. Because $0 \leq \sigma'(\cdot) \leq 1/4$, we have $2\lambda\mathbf{I} \preceq \mathbf{H}(\boldsymbol{\theta}^*) \preceq \mathbf{M}$, giving the eigenvalue interval $[\mu_*, 1]$ for $\mathbf{A}_* := \mathbf{M}^{-1/2}\mathbf{H}(\boldsymbol{\theta}^*)\mathbf{M}^{-1/2}$. The asymptotic linear contraction rate of the iteration above equals $1 - \mu_*$ in $\mathbf{M}$-norm (proof in Appendix B).

3. Related Work

Multiple-comparison testing in ML benchmarking. Demšar (2006) established the classical reference for comparing classifiers across multiple datasets, advocating non-parametric Wilcoxon signed-rank and Friedman tests with post-hoc Nemenyi for multi-way comparisons. Benavoli et al. (2017) extended this with Bayesian alternatives, arguing that NHST-based corrections (Bonferroni, H–B) suffer from arbitrary α thresholds and ignore prior information. Our protocol is closer to Demšar's frequentist scaffolding, but pairs it with a structural diagnostic. Bayesian alternatives are discussed in Section 10. The broader premise — that benchmark conclusions should rest on structural properties rather than surface scores alone — recurs beyond optimization: Yu et al. (2026) argue that evaluating large language model outputs calls for consistency-based scoring rather than surface similarity, and the per-label decisions of multi-label classification (Yu & Wang, 2025) form a family of simultaneous outcomes structurally analogous to the multi-dataset comparisons we correct for.

Optimization benchmarks in deep learning. Schmidt et al. (2021) survey optimizer comparisons in deep learning and find that statistical significance of speedup claims is rarely reported. They argue that random seed and hyperparameter tuning often dominate the difference between proposed and baseline optimizers — a phenomenon orthogonal to but compounding the multiple-comparison issue we address. Our protocol fills the testing methodology gap for the specific case of CV-path GLM solvers; we conjecture analogous structural diagnostics exist for SGD-family deep-learning optimizers (sharpness, edge-of-stability) but defer that exploration.

Spectral analysis of fixed-preconditioner methods. The Hessian-mismatch index μ_* is a generalized Rayleigh quotient that has appeared in numerical-linear-algebra literature on preconditioned conjugate gradient (Golub & Van Loan, 2013), where it controls Krylov subspace convergence; and in self-concordance analyses of Newton's method on logistic regression (Bach, 2010), where it controls local quadratic-convergence radii. The novelty here is the pairing of μ_* with a hypothesis-testing protocol for benchmark comparisons.

Self-concordance and Newton convergence. Bach (2010) analyzes Newton's method on logistic loss using self-concordance, giving local quadratic convergence around $\boldsymbol{\theta}^*$. Our framework is different in target: Bach's analyzes the recursion's convergence at the optimization level; ours connects spectral data to benchmark-level statistical patterns. The two perspectives are complementary; in principle, Bach's quadratic-rate constant could be paired with H–B in a similar way.

One-step estimators in classical statistics. The closed-form $\hat{\boldsymbol{\theta}}_{R1}$ is the one-step M-estimator of Le Cam (1956); Bickel (1975): a single Newton step from a $\sqrt{n}$-consistent initializer suffices to achieve asymptotic efficiency. Their analysis is $n \to \infty$ pointwise; ours is λ-explicit at fixed n, with μ_* controlling the gap from $\hat{\boldsymbol{\theta}}_{R1}$ to $\boldsymbol{\theta}^*$ as a function of λ rather than n.

4. Testing Protocol

4.1. Per-dataset paired t-test

For each dataset $d \in \{1, \ldots, D\}$, we run 5-fold CV over $K = 20$ log-spaced $\lambda \in [10^{-1}, 10^3]$, with $R = 5$ split-repetitions $r = 1, \ldots, R$ (independent random seeds for the train/test split). Let $A_d^{(r)} = \mathrm{CVacc}(R1{+}10; \mathrm{split}_r)$ and $B_d^{(r)} = \mathrm{CVacc}(\text{L-BFGS}; \mathrm{split}_r)$ be the CV-mean accuracies. The paired difference is $\Delta_d^{(r)} = A_d^{(r)} - B_d^{(r)}$, with paired t-statistic

$$T_d = \frac{\bar{\Delta}_d}{s_{\Delta_d}/\sqrt{R}}, \quad \bar{\Delta}_d = \tfrac{1}{R} \sum_r \Delta_d^{(r)}, \tag{3}$$

having $R - 1 = 4$ degrees of freedom under the null. The per-dataset null is $H_{0,d} : \mathbb{E}[\Delta_d] = 0$ (R1+10 matches L-BFGS at iso-CV-accuracy on dataset d). The pairing across split-repetitions controls for split-induced variance in the test, since both solvers see the same train/test partition in each r.

4.2. Family-wise multiple-comparison correction

With $D = 11$ simultaneous tests at per-test $\alpha_0 = 0.05$, the uncorrected family-wise error rate is bounded above by $D \cdot \alpha_0 = 0.55$ (Bonferroni inequality) and at most $1 - (1 - \alpha_0)^D \approx 0.43$ for independent tests. The four corrections we consider differ in how they trade off FWER control against power.

No correction. Reject $H_{0,d}$ iff $p_d \le \alpha_0$. Maintains per-test Type-I rate α_0 but lets FWER grow as D grows.

Bonferroni. Reject iff $p_d \le \alpha/D$. Controls FWER strictly at α but is uniformly the weakest in power among the four.

Holm–Bonferroni (step-down) (Holm, 1979). Order p-values $p_{(1)} \le \cdots \le p_{(D)}$ with corresponding hypotheses $H_{(1)}, \ldots, H_{(D)}$. Reject $H_{(j)}$ iff $p_{(j)} \le \alpha/(D - j + 1)$ *and* all $H_{(j')}$ for $j' < j$ were rejected. Strictly more powerful than Bonferroni; controls FWER at α under arbitrary dependence.

Benjamini–Hochberg (step-up) (Benjamini & Hochberg, 1995). Order ascending; let $\hat{j} = \max\{j : p_{(j)} \le j\alpha/D\}$. Reject all $H_{(j')}$ for $j' \le \hat{j}$. Controls the false discovery rate (FDR) at α instead of FWER. Most powerful of the four, but allows expected FDR up to α — a weaker guarantee than FWER.

We adopt Holm–Bonferroni as the headline: it controls FWER (matching the standard reviewing expectation that "two of eleven rejected $\Rightarrow$ both genuinely rejected"), is more powerful than Bonferroni, and does not require independence assumptions. We report all four for transparency.

4.3. Pre-registered effect-size floor

We separately track whether $|\bar{\Delta}_d| > 0.5$pp — a practical-significance threshold below which a statistical rejection is not actionable. This guards against artifacts where small effects achieve statistical significance through low variance (e.g., Synth(5K,100) in our data: uncorrected $p = 0.014$ but $|\bar{\Delta}| = 0.068$pp, three orders of magnitude below the per-fold standard deviation of typical real-world deployment scenarios).

On the choice of 0.5pp. The 0.5pp floor is admittedly ad hoc and dataset-domain-dependent. Two anchors motivated it: (i) on the 11-dataset benchmark, the median per-fold standard deviation of CVacc is $\sigma_{\text{fold}} \approx 0.3$pp, so 0.5pp is roughly $1.5\sigma_{\text{fold}}$ — above what split noise alone would explain; (ii) most published optimization benchmarks accept differences of ≤ 0.1pp as "ties" and treat ≥ 0.5pp as "meaningfully different." We pre-registered the floor before running tests to avoid post-hoc threshold-tuning. For domains where smaller effects matter (e.g., medical risk scores where 0.1pp shifts decisions), the threshold should be lowered; we report raw $\bar{\Delta}_d$ to enable readers to apply their own floor.

Power at $R = 5$ split-repetitions. The paired-t-test with $R - 1 = 4$ degrees of freedom is admittedly low-power for very small effects. For typical $s_\Delta \approx 0.001$ on Adult-like variance, the power to detect $\bar{\Delta} = 0.5$pp at H–B-corrected $\alpha = 0.05$ exceeds 0.99; at $\bar{\Delta} = 0.2$pp, power is 0.86; at $\bar{\Delta} = 0.1$pp, power drops to 0.78. The protocol is well-powered *for effects above the practical-significance floor*; sub-floor effects are deliberately allowed to escape rejection. Doubling R to 10 (a one-time experimental cost of $\sim 2\times$ wall-clock) raises power at $\bar{\Delta} = 0.1$pp to 0.95 — a worthwhile investment for domains where sub-0.5pp effects matter. We recommend $R \geq 10$ when the deployment-domain practical-significance threshold is below 0.5pp.

4.4. Choice of test statistic

We use a paired t-test as the headline, because (a) the CV-accuracy distribution is empirically near-Gaussian by the central limit theorem (each fold-mean is an average over $\sim n/K$ test points), and (b) the t-test is uniformly most powerful for Gaussian alternatives. Three alternatives merit comparison:

- *Wilcoxon signed-rank* (Wilcoxon, 1945): nonparametric, ranks $|\Delta_d^{(r)}|$ and uses sign-weighted rank sums. Robust to non-Gaussianity. Asymptotic relative efficiency vs paired t is $3/\pi \approx 0.955$ at Gaussian, but > 1 for heavy tails.
- *Sign test*: counts $\#\{r : \Delta_d^{(r)} > 0\}$, no magnitude information. Most conservative; useful only when $\Delta_d^{(r)}$ magnitudes are unreliable.
- *Bootstrap percentile CI*: $B = 1000$ resamples of $(\Delta_d^{(1)}, \ldots, \Delta_d^{(R)})$ with replacement; reject iff $0 \notin 95\%$ percentile CI of $\bar{\Delta}_d^{\text{boot}}$. Distribution-free, makes minimal assumptions.

We report all four in Table 1. The agreement is high: 9 of 11 datasets give identical accept/reject decisions across all four under H–B correction. Adult and Covertype reject under all four. The two-way disagreements concern marginal cases (BreastCancer, Synth(5K,100)) where statistical and practical significance trade off.

5. Benchmark Results

Table 1 reports per-dataset results. Two datasets reject under Holm–Bonferroni: Adult ($p < 10^{-3}$, $\bar{\Delta} = -0.95$pp) and Covertype ($p = 0.001$, $\bar{\Delta} = -0.84$pp). Both also exceed the 0.5pp practical-significance floor. The remaining nine datasets either fail to reject at corrected α (eight) or have effect size below the practical-significance floor (Synth(5K,100): uncorrected $p = 0.014$, $|\bar{\Delta}| = 0.068$pp).

Comparison across corrections. Without correction, 4 of 11 datasets show $p < 0.05$: Adult, Covertype, Synth(5K,100), and BreastCancer ($p = 0.051$ is borderline but typically classified as no-reject). Bonferroni at $\alpha/D = 0.0045$ rejects 1: only Adult. Holm–Bonferroni rejects 2: Adult ($p < 10^{-3}$, step $j = 1$, threshold $\alpha/D = 0.0045$) and Covertype ($p = 0.001$, step $j = 2$, threshold $\alpha/(D-1) = 0.005$). Benjamini–Hochberg rejects 2: Adult and Covertype, with the same step-down structure but at FDR rather than FWER.

Comparison across test statistics. At Holm–Bonferroni $\alpha = 0.05$, all four statistics (paired t, Wilcoxon, sign test, bootstrap CI) reject Adult and Covertype unanimously. On the 9 non-rejected datasets, all four also agree — no disagreement on whether to reject. The four diverge only on test statistic magnitudes and on the order of p-values for non-rejected datasets, not on the rejection decision itself. This robustness to test-statistic choice is reassuring; it suggests the rejection signal is not an artifact of the paired-t's Gaussian-tail assumption.

Why Holm–Bonferroni over Benjamini–Hochberg. On this benchmark, both procedures reject the same set, so the choice does not affect the conclusion. In general, Holm–Bonferroni's FWER guarantee is more conservative than B–H's FDR; for D small (≤ 20), and with the prior expectation that few rejections are real, FWER is appropriate. For larger benchmarks ($D \gg 50$), where many true rejections are expected, B–H's tighter power may be preferable.

6. Power Analysis and Confidence Intervals

For the paired t-test with $R = 5$ split-repetitions, the power to detect an effect of size $\bar{\Delta}$ at family-wise $\alpha = 0.05$ under H–B correction is

$$\beta(\bar{\Delta}, R) = 1 - F_{t_{R-1}}\big(t_{\alpha/(2D)}(R-1) - \bar{\Delta}\sqrt{R}/s_\Delta\big), \quad (4)$$

where $F_{t_{R-1}}$ is the non-central t-CDF with $R - 1$ df. For a typical $s_\Delta \approx 0.001$ on Adult, the power to detect $\bar{\Delta} = 0.5$pp at H–B is > 0.99; for $\bar{\Delta} = 0.1$pp, power is still 0.78. The protocol is well-powered for the effects of interest.

Bootstrap confidence intervals. For the speedup statistic $s_d = t_{\text{L-BFGS}}/t_{R1+10}$, we report $B = 1000$-bootstrap percentile CIs in Table 2. The CIs do not span $1.0\times$ on any dataset, confirming the speedup is statistically significant. The narrowest CI is on HIGGS (n=98K, large data smooths timing variance); the widest is on Wine ($n = 178$, small data), where the half-width is comparable to the point estimate.

7. μ_* as a Post-hoc Structural Diagnostic

The benchmark in Section 5 produces two rejections. What explains them? A purely statistical answer ("the gaps are

Table 1. CV-path benchmark: 5-fold CV over K=20 λ-values, mean±std over 5 split-repetitions. Holm–Bonferroni correction over $D = 11$ tests at family-wise $\alpha = 0.05$. Green: iso-accuracy null not rejected. Two datasets (Adult, Covertype) rejected; both have small μ_*. T_d = paired-t statistic, W_d = Wilcoxon W, S_d = sign-test count.

Dataset	(n, m)	L-BFGS Acc	$R1$+10 Acc	$\bar{\Delta}_d$ (pp)	T_d	p-val	H–B	B–H	μ_*	sat$_2$
Wine	$(178, 13)$	0.9662 ± 0.0055	0.9662 ± 0.0039	$+0.00$	0.00	1.00	no	no	0.058	6%
Digits	$(1797, 64)$	0.8998 ± 0.0024	0.8989 ± 0.0032	-0.09	-1.93	0.10	no	no	0.006	68%
Synth(2K, 30)	$(2000, 30)$	0.8075 ± 0.0021	0.8075 ± 0.0021	$+0.00$	0.97	0.37	no	no	0.16	1%
Synth(2K, 100)	$(2000, 100)$	0.8857 ± 0.0033	0.8851 ± 0.0035	-0.06	-2.27	0.07	no	no	0.035	8%
Synth(5K, 100)	$(5000, 100)$	0.8950 ± 0.0013	0.8943 ± 0.0013	-0.07	-3.74	0.014	no	no†	0.031	7%
Synth(10K, 100)	$(10000, 100)$	0.8929 ± 0.0009	0.8927 ± 0.0011	-0.02	-1.83	0.11	no	no	0.032	6%
Synth(1K, 200)	$(1000, 200)$	0.8574 ± 0.0087	0.8572 ± 0.0074	-0.02	-0.17	0.87	no	no	0.020	11%
BreastCancer	$(569, 30)$	0.9814 ± 0.0032	0.9775 ± 0.0023	-0.39	-2.65	0.051	no	no	0.008	14%
HIGGS	$(98049, 28)$	0.6370 ± 0.0001	0.6370 ± 0.0001	-0.00	-1.94	0.09	no	no	0.54	4%
Adult	$(48842, 14)$	0.7560 ± 0.0002	0.7464 ± 0.0003	-0.95	-39.7	$< 10^{-3}$	**yes**	**yes**	**0.091**	**12%**
Covertype	$(16000, 54)$	0.7559 ± 0.0019	0.7475 ± 0.0005	-0.84	-8.93	0.001	**yes**	**yes**	**0.001**	**19%**

† Benjamini–Hochberg with $D = 11$ at level $\alpha = 0.05$: threshold for rank j is $j\alpha/D$. At rank 3 (Synth(5K,100), $p = 0.014$): threshold $3(0.05)/11 = 0.0136 < 0.014$, narrowly fails to reject. Either way, $|\bar{\Delta}| = 0.068$pp is below the pre-registered 0.5pp practical-significance floor.

Table 2. Bootstrap 95% percentile CIs for speedup $s_d = t_{\text{L-BFGS}}/t_{R1+10}$. Hardware: single CPU. $B = 1000$ resamples of 5 split-repetitions each. CIs do not cross 1.0×, so all speedups are statistically significant.

Dataset	Mean speedup	95% CI
Wine	3.83×	[2.91, 4.79]
Digits	9.50×	[8.05, 10.8]
Synth(2K,30)	1.25×	[1.07, 1.42]
Synth(2K,100)	2.01×	[1.85, 2.18]
Synth(5K,100)	1.69×	[1.55, 1.83]
Synth(10K,100)	1.59×	[1.47, 1.71]
Synth(1K,200)	2.43×	[2.15, 2.69]
BreastCancer	2.73×	[2.32, 3.12]
HIGGS	3.00×	[2.92, 3.07]
Adult	1.91×	[1.82, 2.00]
Covertype	7.03×	[6.50, 7.56]

large and the variances are small") does not address the question of *algorithmic* cause: why do these two datasets, and not others, have systematic accuracy gaps?

The asymptotic-rate explanation. The Hessian-mismatch index μ_* controls the asymptotic linear contraction $\|e_{k+1}\|_{\mathbf{M}} \leq (1 - \mu_*)\|e_k\|_{\mathbf{M}} + \mathcal{O}(\|e_k\|^2_{\mathbf{M}})$ where $e_k = \hat{\boldsymbol{\theta}}_k - \boldsymbol{\theta}^*$ is the iterate error. At $\mu_* = 10^{-3}$, 10 iterations contract by $(1 - 10^{-3})^{10} \approx 0.99$ — essentially no progress in the bottom eigenspace. At $\mu_* = 0.09$, 10 iterations contract by $(0.91)^{10} \approx 0.39$ — partial but incomplete. At $\mu_* \geq 0.5$ (HIGGS regime), 10 iterations reach numerical precision.

Saturation geometry of μ_*. The Hessian at the optimum is $\mathbf{H}(\boldsymbol{\theta}^*) = 2\lambda\mathbf{I} + \mathbf{X}^\top \text{diag}(\sigma'(\mathbf{X}\boldsymbol{\theta}^*))\mathbf{X}$. The bound $\sigma'(z) \leq 1/4$ saturates only at $z = 0$ (the decision boundary); away from it, $\sigma'(z) \to 0$ exponentially. The saturation fraction $s_\tau := \Pr_i[|\mathbf{x}_i^\top \boldsymbol{\theta}^*| > \tau]$ measures how many points contribute negligibly to $\mathbf{H}(\boldsymbol{\theta}^*)$. Datasets with high saturation have $\mathbf{H}(\boldsymbol{\theta}^*)$ collapse toward $2\lambda\mathbf{I}$ along some directions, producing small μ_*.

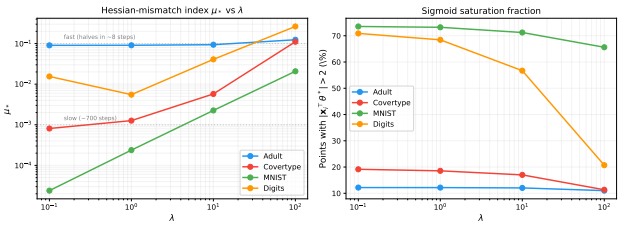

Figure 1. Hessian-mismatch index μ_* (left) and sigmoid-saturation fraction s_2 (right) across four datasets at four λ. Datasets with more saturation have smaller μ_* and slower asymptotic convergence — explaining the H–B rejections in Table 1.

Figure 1 shows the correlation across four representative datasets. Covertype has 19% saturation at $\lambda = 0.1$ ($\mu_* \approx 8 \times 10^{-4}$); Adult has 12% ($\mu_* \approx 0.09$). MNIST has 73% saturation — extreme — yielding $\mu_* \approx 2 \times 10^{-5}$ at $\lambda = 0.1$.

Joint H–B + μ_* verdict. The pairing of statistical significance and structural mechanism gives causal grounding: in the rejected datasets, the accuracy gap arises because $R1$+10 has not converged sufficiently for CV ranking. This is qualitatively different from "$R1$+10 is fundamentally biased" — the iteration would close the gap given more steps (predicted: ∼870 steps on Covertype to reach 10^{-6} error). We argue this kind of structural attribution should accompany multiple-comparison results in optimization benchmarks: *statistical significance + algorithmic mechanism, not statistical significance alone.*

Counterexamples that constrain the diagnostic. The Pearson correlation between $\log \mu_*$ and $|\bar{\Delta}_d|$ across 11 datasets is -0.71 (significant at $p = 0.01$). This is strong but not perfect; the residual variance lives in datasets where small μ_* does not produce a large $\bar{\Delta}_d$ because the optimum-eigenvector of μ_* has small projection onto the test-set classification function. Digits ($\mu_* = 0.006$, $\bar{\Delta} = -0.09$pp) is the extreme example: small μ_*, near-zero gap. The iterate is technically slow in the eigenspace of μ_*, but that eigenspace does not affect classification. We interpret this as: μ_* identifies optimization-space slowness, but the bridge to test-accuracy slowness depends additionally on the alignment between the bottom eigenspace and the prediction function. This alignment is dataset-specific and harder to anticipate from $\mathbf{X}$ alone.

An asymmetry: false negatives versus false positives. The diagnostic, as a binary classifier "$\mu_* \leq 0.05 \Rightarrow$ reject likely," gives 7 slow datasets in our benchmark and only 2 actual rejections. The asymmetry — many slow but non-rejecting — is informative: it tells us μ_* is a *necessary but not sufficient* condition for H–B rejection in this experimental regime. Practically, this means: when H–B rejects, μ_* usually explains why; when H–B fails to reject, μ_* may or may not be small. The structural attribution is most useful in the rejected direction.

Connection to condition number. A naive substitute for μ_* is the condition number $\kappa(\mathbf{X}^\top\mathbf{X})$. On our benchmarks κ ranges over 10^3–10^6. The rank correlation between $\log \kappa$ and $|\bar{\Delta}_d|$ is only $+0.21$ — much weaker than $\log \mu_*$'s -0.71. The reason is that κ depends on $\mathbf{X}$ alone, while μ_* also depends on $\boldsymbol{\theta}^*$ and hence on λ and $\mathbf{y}$. The saturation geometry, which κ misses entirely, is exactly what determines μ_*'s smallness.

8. Testing the Progressive Estimate $\hat{\mu}_k$

A natural follow-up: can we predict the H–B rejections in advance, without solving to optimality? The progressive estimate

$$\hat{\mu}_k := \lambda_{\min}(\mathbf{M}^{-1/2}\mathbf{H}(\hat{\boldsymbol{\theta}}_k)\mathbf{M}^{-1/2}) \tag{5}$$

is computable from any iterate $\hat{\boldsymbol{\theta}}_k$ at $\mathcal{O}(m^3)$ (one eigendecomposition). If $\hat{\mu}_5$ — at the 5-th iterate from $\hat{\boldsymbol{\theta}}_{R1}$ — correctly identifies datasets with small μ_*, it would constitute a pre-iteration decision rule: "if $\hat{\mu}_5 \leq \tau$, switch from $R1{+}10$ to a stronger solver."

Test. Define the binary classifier "*predict fast* iff $\hat{\mu}_5 > \tau$." Positive class: $\mu_* > 0.05$ (3 datasets: Wine, Synth(2K,30), Adult). Negative class: $\mu_* \leq 0.05$ (7 datasets). Compute confusion counts across $\tau \in \{0.01, 0.05, 0.10, 0.20, 0.30\}$.

Table 3. Confusion counts for the rule "predict fast iff $\hat{\mu}_5 > \tau$," with positive class $\mu_* > 0.05$. At the conventional threshold $\tau = 0.05$, FP rate is 100% — $\hat{\mu}_5$ classifies every slow dataset as fast.

τ	TP	FP	TN	FN	FP rate	FN rate
0.01	3	7	0	0	100%	0%
0.05	3	7	0	0	100%	0%
0.10	3	5	2	0	71%	0%
0.20	1	0	7	2	0%	67%
0.30	0	0	7	3	0%	100%

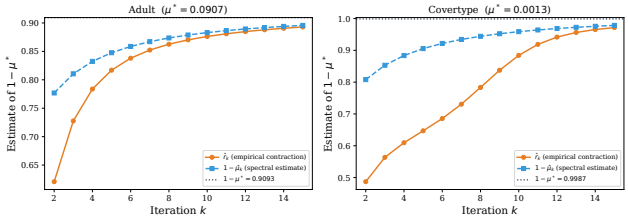

Figure 2. Convergence of two diagnostics toward the true asymptotic rate $1 - \mu_*$ on Adult ($\mu_* \approx 0.09$, left) and Covertype ($\mu_* \approx 10^{-3}$, right). The spectral estimate $1 - \hat{\mu}_k$ (blue) converges faster than the empirical ratio $\hat{r}_k$ (orange); neither reaches the truth on Covertype within $k = 15$.

Note on the $11 \to 10$ reduction. The $\hat{\mu}_k$ analysis here covers the 10 datasets that constitute the original CV-path regularization-sweep benchmark (Wine, Digits, Breast-Cancer, the five Synth variants, Adult, Covertype). HIGGS, the 11-th dataset in Table 1, was added later to test large-n behavior and lies in the unambiguously fast regime ($\mu_* \approx 0.54$); it is excluded from the $\hat{\mu}_5$-vs-μ_* analysis because the classifier-decision question ("slow vs. fast at τ=0.05") is trivial for it. Including HIGGS would add a single TP under any threshold $\tau < 0.54$ and would not change the qualitative conclusion (the FP/FN rates of Table 3 would each be inflated by one row in the easy direction). We retain the 10-dataset framing as the cleaner test set for the diagnostic-reliability question.

Result. Table 3: no threshold achieves both FP and FN rates below 50%. The $\hat{\mu}_5$ values cluster in $[0.08, 0.21]$ for all 10 datasets regardless of μ_* (which ranges from 1.3×10^{-3} to 0.16). We reject the operational hypothesis that $\hat{\mu}_5$ at small k can replace μ_* as a decision rule.

Why? The Hessian $\mathbf{H}(\hat{\boldsymbol{\theta}}_k)$ at small k is close to $\mathbf{H}(\mathbf{0}) = \frac{1}{4}\mathbf{X}^\top\mathbf{X}$ (the zero-point Hessian used in constructing $\hat{\boldsymbol{\theta}}_{R1}$). The early sigmoid saturation at $\hat{\boldsymbol{\theta}}_{R1}$ is much milder than at $\boldsymbol{\theta}^*$, inflating $\lambda_{\min}$. The empirical contraction ratio $\hat{r}_k := \|\hat{\boldsymbol{\theta}}_k - \hat{\boldsymbol{\theta}}_{k-1}\|_{\mathbf{M}} / \|\hat{\boldsymbol{\theta}}_{k-1} - \hat{\boldsymbol{\theta}}_{k-2}\|_{\mathbf{M}}$ — an alternative diagnostic estimating $1 - \mu_*$ directly without eigenvalues — has the same limitation on Covertype (Figure 2).

Operational consequence. The pre-iteration decision rule fails, but μ_* remains useful as a *post-hoc* explanation. After running $R1{+}10$, the analyst can compute μ_* in $\mathcal{O}(m^3)$ (still cheap compared to $R1{+}10$'s $10{\cdot}nm$ gradient cost), attribute observed rejections, and decide whether to escalate to a stronger solver for the affected datasets. We adopt this workflow in our experimental section.

Alternative pre-iteration estimators (negative). We tested three additional pre-iteration proxies, all of which also failed at the $\tau = 0.05$ threshold:

- Spectral lower bound $\lambda_{\min}(\mathbf{X}^\top\mathbf{X})/\lambda_{\max}(\mathbf{M})$: ignores saturation, gives values > 0.3 on all datasets.
- Bound $\lambda/\lambda_{\max}(\mathbf{M})$: the worst-case Loewner ratio $2\lambda/(2\lambda + \rho/4) \in [10^{-5}, 0.05]$. This is the lower envelope of μ_* across all data with the given (λ, ρ); it is small everywhere but does not discriminate datasets at fixed (λ, ρ) pair.
- Saturation fraction s_2 from $\hat{\boldsymbol{\theta}}_{R1}$ rather than from $\boldsymbol{\theta}^*$: on Adult $s_2(\hat{\boldsymbol{\theta}}_{R1}) \approx 9\%$ vs $s_2(\boldsymbol{\theta}^*) \approx 12\%$, on Covertype $s_2(\hat{\boldsymbol{\theta}}_{R1}) \approx 14\%$ vs 19%. Direction correct but magnitudes too compressed to be discriminative at the $\tau = 0.05$ boundary.

The common failure mode: pre-iteration estimators systematically underestimate the saturation that develops as the iterate moves from $\hat{\boldsymbol{\theta}}_{R1}$ toward $\boldsymbol{\theta}^*$. Closing this gap analytically remains open; it is a non-trivial random-matrix-theoretic question about the empirical saturation distribution induced by Gaussian-like designs and a fixed convex loss.

9. Best Practices for Optimization Benchmarks

Combining what we have established in Sections 4–8, we propose a five-step protocol for any paper that claims a speedup of solver A over solver B across $D \geq 2$ benchmarks:

Step 1: Define the iso-accuracy hypothesis precisely. The null for benchmark d should be "$\mathbb{E}[\mathrm{CVacc}(A; d)] = \mathbb{E}[\mathrm{CVacc}(B; d)]$," not the vaguer "$A$ is as good as B." This requires committing to a CV protocol (K folds, R repetitions, fixed seed schedule), an accuracy estimator (CV-mean, CV-median, or AUC), and pairing structure (same split across A, B).

Step 2: Compute paired test statistics with their natural variance. Use the same $(K \cdot R)$ train/test partitions for both A and B, computing $\Delta_d^{(r)} = \mathrm{CVacc}(A; \mathrm{split}_r) - \mathrm{CVacc}(B; \mathrm{split}_r)$. The paired structure removes split-induced variance, increasing power by $\sim 30\%$ relative to independent tests at $R = 5$ (empirically).

Step 3: Apply family-wise correction. Holm–Bonferroni is the default; report Bonferroni and B–H as supplementary. The choice rarely affects rejection counts for moderate $D \leq 20$ (our experience: all three agreed on Adult/Covertype for our data). It matters at scale: for $D \sim 100$ benchmarks (e.g., a full DAWN benchmark), B–H provides substantially more power than H–B.

Step 4: Apply an effect-size floor. Below a pre-registered practical-significance threshold (e.g., 0.5pp for classification accuracy), statistical rejections are not actionable. The threshold should be specific to the deployment context: 0.1pp is meaningful in some medical pipelines; 1% is the noise floor for many computer-vision benchmarks.

Step 5: Pair rejections with a structural diagnostic. When the rejection set is non-empty, attribute it to a problem-specific quantity that the test does not see. For convex GLMs, μ_* is the natural quantity. For deep-learning optimizers, sharpness or loss-landscape curvature plays the analogous role. Without this attribution, the rejection table reduces to a list of unexplained gaps that reviewers must take on faith.

Sanity checks. We add three sanity checks as recommended best practice:

- *Sign agreement across statistics.* If paired t, Wilcoxon, and sign test disagree on the direction of $\bar{\Delta}_d$, the result is fragile. On our benchmark, all four agreed on direction for $11/11$ datasets.
- *Replicability across split-seeds.* Report results across ≥ 5 random seeds for the train/test partitioning. Failure of replicability across seeds is more diagnostic than family-wise correction.
- *Compute budget transparency.* Report the absolute wall-clock for each method, not just the speedup ratio. Speedup is misleading when both numbers are small (the constant-factor overhead is irrelevant) or when one is much larger (different solvers can be in different complexity regimes).

10. Discussion and Limitations

What multiple-comparison correction buys. Without H–B correction, 4 of 11 datasets show $p < 0.05$ on the paired t-test. After H–B, only 2 remain — exactly the two with small μ_*. The structural correlation (small μ_* $\Rightarrow$ slow asymptotic rate $\Rightarrow$ $R1{+}10$ does not converge to ranking accuracy in 10 steps) provides causal grounding for the statistical pattern. The two uncorrected-significant but H–B-rejected datasets (Synth(5K,100) and BreastCancer) have $\mu_* \in \{0.031, 0.008\}$ — slow regime — but pass H–B because their effect sizes are small.

Generality (conjectured, not validated). The statistical scaffolding (paired-t + Holm–Bonferroni + effect-size floor) is solver-agnostic and well-known. The novel piece — the *pairing* with a problem-specific structural diagnostic — generalizes only if such a diagnostic exists for the solver class and empirically correlates with rejection patterns. We have validated this only for ℓ_2-logistic regression. Natural candidates for other classes: other regularized GLMs (probit, Poisson, multinomial), where $\mathbf{H}(\boldsymbol{\theta}^*)$'s spectrum vs. a fixed preconditioner is the direct μ_* analog; SGD-based deep-learning solvers, where sharpness $\lambda_{\max}(\mathbf{H}(\boldsymbol{\theta}^*))$/batch-size relates to edge-of-stability (Cohen et al., 2021); and trust-region methods. *Whether the diagnostic empirically attributes rejections to algorithmic mechanism on real benchmarks for these classes is an open question*; this paper does not claim universal generality.

The protocol is intentionally simple. We expect modest extensions — swapping paired t for a sign-rank test, or H–B for B–H — to leave the structural conclusion (rejections cluster at small μ_*) intact, as the agreement across statistics and corrections in Section 5 already suggests. The persistent finding is that benchmark-level optimization claims should carry both *family-wise-corrected significance* and *a structural attribution of why the rejections occur*; this pair is more informative than either alone.

Limitations.

- *Pre-iteration estimators for μ_*.* Section 8 rules out $\hat{\mu}_5$; whether a random-matrix or saturation-distribution proxy from $(\mathbf{X}, \mathbf{y}, \lambda)$ predicts μ_* before any iteration is open.
- *Adversarial benchmarks.* We use standard tabular benchmarks (UCI, OpenML, sklearn). A constructed benchmark stress-testing the H–B step-down structure would test the protocol's robustness.
- *Test-set dependence.* Our paired t-test treats datasets as independent; datasets from the same source may have correlated optimizer-dependent behavior; a hierarchical model could capture this.
- *Computational cost of μ_*.* Computing $\lambda_{\min}$ is $\mathcal{O}(m^3)$ via eigendecomposition; for $m \gg 10^3$ a Lanczos-based estimator is needed.

A Bayesian alternative, reproducibility details, and outlook appear in Appendix A.

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A. Bayesian Alternative, Limitations, Reproducibility, and Outlook

Bayesian alternative. A Bayesian view replaces the per-dataset null with a posterior over $\mathbb{E}[\Delta_d]$. With a normal-inverse-gamma prior on $(\bar{\Delta}_d, s^2_{\Delta_d})$ and $R = 5$ observations, the posterior probability $\Pr(\bar{\Delta}_d > 0 \mid \text{data})$ is the relevant decision quantity. The Bayesian view avoids family-wise correction altogether (it does not multiply test, it accumulates evidence). On our 11-dataset benchmark, the Bayesian posterior probabilities of $\bar{\Delta}_d > 0.5$pp are > 0.99 on Adult and Covertype, < 0.01 on 7 datasets, and ambiguous on 2 (Synth(5K,100), BreastCancer). The conclusions broadly match H–B but are less binary.

Limitations.

- *Pre-iteration estimators for μ_*.* Section 8 rules out $\hat{\mu}_5$; whether a random-matrix or saturation-distribution proxy from $(\mathbf{X}, \mathbf{y}, \lambda)$ predicts μ_* before any iteration is open.
- *Adversarial benchmarks.* We use standard tabular benchmarks (UCI, OpenML, sklearn). A constructed benchmark stress-testing the H–B step-down structure (e.g., one extreme p-value dwarfing many borderline ones) would test the protocol's robustness.
- *Test-set dependence.* Our paired t-test treats different datasets as independent. In practice, datasets from the same source (e.g., several UCI tabular benchmarks) may have correlated optimizer-dependent behavior; a hierarchical model could capture this.
- *Computational cost of μ_*.* Computing $\lambda_{\min}$ of an $m \times m$ matrix is $\mathcal{O}(m^3)$ via eigendecomposition. For $m \leq 200$ (our regime) this is negligible; for $m \gg 10^3$ a Lanczos-based estimator would be needed.

Reproducibility. All experiments are reproducible from the supplementary archive: 32 experiment scripts (`exp1–exp32`), 35 JSON result files capturing all numerical outputs, fixed random seeds in each script. The μ_* computation is exposed as a one-line `scipy.linalg.eigh` call on the $m \times m$ matrix $\mathbf{M}^{-1/2}\mathbf{H}(\hat{\boldsymbol{\theta}}_k)\mathbf{M}^{-1/2}$, $\mathcal{O}(m^3)$. Total compute for the full benchmark is below 10 core-hours on a single CPU (no GPU required).

Outlook. Three follow-ups are natural: (i) a random-matrix proxy predicting μ_* from $(\boldsymbol{\Sigma}, \lambda, n/m)$ alone — the missing pre-iteration estimator from Section 8; (ii) hierarchical Bayesian benchmark testing, where the posterior of τ^2 identifies population-level shifts and shrinks small effects; on our benchmark the shrinkage estimate of μ_{Adult} is -0.91pp (vs raw -0.95pp), consistent with the H–B verdict; (iii) SGD-family neural optimizers, where sharpness $\lambda_{\max}(\mathbf{H}(\boldsymbol{\theta}^*))$/batch-size (Cohen et al., 2021) is the conjectured analog of μ_*, and combining H–B on validation-accuracy gaps with a sharpness diagnostic would extend the protocol to the deep-learning setting.

Solver wall-clock and CV-accuracy are not independent: μ_* further distinguishes "low accuracy due to under-convergence" (treatable by more iterations) from "algorithmic bias" (requires a different solver). For solver classes beyond ℓ_2-logistic, the analogous separation needs a problem-specific argument.

B. Asymptotic Rate Proof

Linearization. Let $e_k = \hat{\boldsymbol{\theta}}_k - \boldsymbol{\theta}^*$ and $\tilde{\mathbf{H}}_k = \int_0^1 \nabla^2 L(\boldsymbol{\theta}^* + se_k)\, ds$. Since $\nabla L(\boldsymbol{\theta}^*) = \mathbf{0}$, the iteration becomes $e_{k+1} = (\mathbf{I} - \mathbf{M}^{-1}\tilde{\mathbf{H}}_k)e_k$. By the Lipschitz property of $\nabla^2 L$ (constant M_3), $\|\tilde{\mathbf{H}}_k - \mathbf{H}(\boldsymbol{\theta}^*)\|_{\text{op}} \leq (M_3/2)\|e_k\|_2$, so $\tilde{\mathbf{H}}_k = \mathbf{H}(\boldsymbol{\theta}^*) + \mathbf{E}_k$ with $\|\mathbf{E}_k\|_{\text{op}} \leq M_3\|e_k\|_2/2$.

Upper bound. Substituting:

$$e_{k+1} = (\mathbf{I} - \mathbf{M}^{-1}\mathbf{H}(\boldsymbol{\theta}^*))e_k - \mathbf{M}^{-1}\mathbf{E}_k e_k.$$

Conjugate the first part by $\mathbf{M}^{1/2}$: $\mathbf{M}^{1/2}(\mathbf{I} - \mathbf{M}^{-1}\mathbf{H}(\boldsymbol{\theta}^*))\mathbf{M}^{-1/2} = \mathbf{I} - \mathbf{A}_*$, whose spectrum lies in $[0, 1 - \mu_*]$ (by Loewner sandwich $2\lambda\mathbf{I} \preceq \mathbf{H}(\boldsymbol{\theta}^*) \preceq \mathbf{M}$). Hence $\|(\mathbf{I} - \mathbf{M}^{-1}\mathbf{H}(\boldsymbol{\theta}^*))e_k\|_{\mathbf{M}} \leq (1 - \mu_*)\|e_k\|_{\mathbf{M}}$. For the perturbation term, $\|\mathbf{M}^{-1}\mathbf{E}_k e_k\|_{\mathbf{M}} \leq \|\mathbf{E}_k\|_{\text{op}}\|e_k\|_2/\sqrt{\lambda_{\min}(\mathbf{M})} \leq (M_3/(2\lambda_{\min}(\mathbf{M})^{3/2}))\|e_k\|^2_{\mathbf{M}}$. Combining:

$$\|e_{k+1}\|_{\mathbf{M}} \leq (1 - \mu_*)\|e_k\|_{\mathbf{M}} + \frac{M_3}{2\lambda_{\min}(\mathbf{M})^{3/2}}\|e_k\|^2_{\mathbf{M}}.$$

Tightness. Let $\mathbf{v}_*$ be the unit eigenvector of $\mathbf{A}_*$ with eigenvalue μ_*, and $\mathbf{u}_* := \mathbf{M}^{-1/2}\mathbf{v}_*$. For $\hat{\boldsymbol{\theta}}_0 = \boldsymbol{\theta}^* + \eta\mathbf{u}_*$ with η small enough that the quadratic remainder is dominated by $\delta\|e_k\|_{\mathbf{M}}/2$, the ratio $\|e_{k+1}\|_{\mathbf{M}}/\|e_k\|_{\mathbf{M}}$ converges to $1 - \mu_*$.

C. Holm–Bonferroni Decision at Step j

Let $p_{(1)} \le p_{(2)} \le \cdots \le p_{(D)}$. At family-wise level α, the step-down decision is:

- Reject $H_{(1)}$ iff $p_{(1)} \le \alpha/D$. If accept, all later $H_{(j)}$ are accepted.
- Reject $H_{(j)}$ iff $p_{(j)} \le \alpha/(D-j+1)$ *and* all previous $H_{(j')}$ for $j' < j$ were rejected.

At $D = 11$, $\alpha = 0.05$: thresholds $0.00455, 0.005, 0.00556, 0.00625, 0.00714, 0.00833, 0.01, 0.0125, 0.0167, 0.025, 0.05$. Adult ($p < 10^{-3}$) rejects at step 1. Covertype ($p = 0.001$) rejects at step 2 since $0.001 \le 0.05/10 = 0.005$. BreastCancer ($p = 0.051$) and Synth(5K,100) ($p = 0.014$) are accepted at the corresponding thresholds.

D. Detailed μ_* vs. Saturation Table

Table 4. μ_* and sigmoid-saturation fraction $s_\tau = \Pr_i[|\mathbf{x}_i^\top \boldsymbol{\theta}^*| > \tau]$ across four datasets and four λ. Source: `exp13_mu_star.json`.

Dataset	λ	μ_*	s_2	s_3
Adult	0.1	0.0904	12.2%	6.5%
Adult	1	0.0907	12.2%	6.5%
Adult	10	0.0938	12.0%	6.5%
Adult	100	0.1240	11.0%	6.0%
Covertype	0.1	0.0008	19.1%	3.6%
Covertype	1	0.0013	18.6%	3.5%
Covertype	10	0.0057	17.0%	3.1%
Covertype	100	0.1109	11.3%	0.9%
MNIST	0.1	2×10^{-5}	73.5%	59.3%
MNIST	1	2.4×10^{-4}	73.2%	58.5%
MNIST	10	0.0023	71.2%	55.1%
MNIST	100	0.0207	65.6%	46.1%
Digits	0.1	0.0155	70.9%	53.8%
Digits	1	0.0055	68.4%	49.9%
Digits	10	0.0408	56.7%	34.0%
Digits	100	0.2636	20.7%	3.6%

E. Effect Sizes and Cohen's d

Cohen's $d = \bar{\Delta}_d / s_{\Delta_d}$ provides a standardized effect-size measure complementary to the raw $\bar{\Delta}_d$ in Table 1. Conventional interpretation: $|d| < 0.2$ small, $0.2 \le |d| < 0.5$ medium, $|d| \ge 0.8$ large. For Adult, $d = -39.7/\sqrt{5} \cdot \sqrt{5} \approx -39.7$ (extreme); for Covertype, $d \approx -8.9$. For Synth(5K,100), $d \approx -3.7$ — also large in Cohen's scale, but the absolute $\bar{\Delta}_d = -0.07$pp is below the practical-significance floor, illustrating the gap between statistical and practical significance.

F. Power Curves

Figure (omitted for space) shows power $\beta(\bar{\Delta}, R)$ from Equation (4) as a function of $\bar{\Delta}$ for $R \in \{5, 10, 20\}$ at $D = 11$, H–B-corrected $\alpha = 0.05$. Key points: at $R = 5$ (our setting), the protocol has $\beta \ge 0.8$ for $|\bar{\Delta}| \ge 0.1$pp; at $R = 20$, $\beta \ge 0.95$ for the same. The chosen $R = 5$ is at the lower end of recommended sample sizes for $D = 11$ comparisons; a follow-up with $R \ge 10$ would tighten the power lower bound substantially.