Semiparametric robust mean estimations based on the orderliness of quantile averages

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semiparametric | mean-median-mode inequality | asymptotic | unimodal | Hodges—Lehmann estimator

Hodges–Lehmann inequality and γ -U-orderliness

The Hodges-Lehmann estimator stands out as a unique robust location estimator due to its definition being substantially dissimilar from conventional L-estimators, R-estimators, and M-estimators. In their landmark paper, Estimates of location based on rank tests, Hodges and Lehmann (1) proposed two methods for computing the H-L estimator: the Wilcoxon score R-estimator and the median of pairwise means. The Wilcoxon score R-estimator is a location estimator based on signedrank test, or R-estimator, (1) and was later independently discovered by Sen (1963) (2, 3). However, the median of pairwise means is a generalized L-statistic and a trimmed U-statistic, as classified by Serfling in his novel conceptualized study in 1984 (4). Serfling further advanced the understanding by generalizing the H-L kernel as $hl_k(x_1,\ldots,x_k)=\frac{1}{k}\sum_{i=1}^k x_i$, where $k\in\mathbb{N}$ (4). Here, the weighted H-L kernel is defined as $whl_k(x_1,...,x_k) = \frac{\sum_{i=1}^k x_i \mathbf{w}_i}{\sum_{i=1}^k \mathbf{w}_i}$, where \mathbf{w}_i s are the weights applied to each element

By using the weighted H-L kernel and the L-estimator, it is now clear that the Hodges-Lehmann estimator is an LL-statistic, the definition of which is provided as follows:

$$LL_{k,\epsilon,\gamma,n} \coloneqq L_{\epsilon_0,\gamma,n}\left(\operatorname{sort}\left(\left(whl_k\left(X_{N_1},\cdots,X_{N_k}\right)\right)_{N=1}^{\binom{n}{k}}\right)\right),$$

where $L_{\epsilon_0,\gamma,n}(Y)$ represents the ϵ_0,γ -L-estimator that uses the sorted sequence, sort $(whl_k(X_{N_1}, \dots, X_{N_k}))_{N=1}^{\binom{n}{k}}$, as input. The upper asymptotic breakdown point of $LL_{k,\epsilon,\gamma}$ is $\epsilon =$ $1-(1-\epsilon_0)^{\frac{1}{k}}$, as proven in DSSM II. There are two ways to adjust the breakdown point: either by setting k as a constant and adjusting ϵ_0 , or by setting ϵ_0 as a constant and adjusting k. In the above definition, k is discrete, but the bootstrap method can be applied to ensure the continuity of k, also making the breakdown point continuous. Specifically, if $k \in \mathbb{R}$, let the bootstrap size be denoted by b, then first sampling the original sample (1 - k + |k|)b times with each sample size of |k|, and then subsequently sampling $(1-\lceil k \rceil + k)b$ times with each sample size of $\lceil k \rceil$, $(1-k+|k|)b \in \mathbb{N}$, $(1-\lceil k \rceil+k)b \in$ \mathbb{N} . The corresponding kernels are computed separately, and the pooled sorted sequence is used as the input for the Lestimator. Let \mathbf{S}_k represent the sorted sequence. Indeed, for any finite sample, X, when k = n, S_k becomes a single point, $whl_{k=n}(X_1,\ldots,X_n)$. When $\mathbf{w}_i=1$, the minimum of \mathbf{S}_k is $\frac{1}{k} \sum_{i=1}^k X_i$, due to the property of order statistics. The maximum of \mathbf{S}_k is $\frac{1}{k} \sum_{i=1}^k X_{n-i+1}$. The monotonicity of the order statistics implies the monotonicity of the extrema with respect to k, i.e., the support of \mathbf{S}_k shrinks monotonically.

Data Availability. Data for Figure ?? are given in SI Dataset S1. All codes have been deposited in GitHub.

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- J Hodges Jr, E Lehmann, Estimates of location based on rank tests. The Annals Math. Stat. 34, 598–611 (1963).
- PK Sen, On the estimation of relative potency in dilution (-direct) assays by distribution-free methods. *Biometrics* pp. 532–552 (1963).
- 3. M Ghosh, MJ Schell, PK Sen, A conversation with pranab kumar sen. *Stat. Sci.* pp. 548–564
- 4. RJ Serfling, Generalized I-, m-, and r-statistics. The Annals Stat. 12, 76–86 (1984)

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