

# Extending the Traditional Laboratory in Polygenic Analysis (Total Ridge Finger Count) to Teach Data Presentation and Statistical Analyses Using Three Sizes of Data Sets

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Thirty years after Mendenhall, Mertens, and Hendrix (1989) introduced the laboratory “Fingerprint ridge count: a polygenic trait useful for classroom instruction,” it is still a standard in teaching principles of quantitative inheritance, and a number of modifications have appeared in the literature since that time. The advantages of using this lab are obvious since the trait has a high heritability and the time required for obtaining fingerprints and then characterizing their pattern types and determining the ridge counts is short. The remainder of the laboratory time can be devoted to graphing and analyzing the data and to investigating the literature for supportive and related studies. For this lab, I use data from the current class and past class data, and the summary statistics from Holt’s original data (1961). Students use Microsoft Excel to prepare histograms in the same style as Holt, so they learn how to control variables connected with histogram preparation in Microsoft Excel, to use the data analysis package of Excel for the unpaired t-test with similar variances to compare males and females in the two class populations, and to use a web-based t-test for comparing class data to Holt’s data. Students also evaluate their original hypothesis and discover information linked to total ridge count by looking at articles using twin studies, racial group comparisons, and individuals with chromosomal/ gender disorders, and the processes influencing ridge development.

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