

## Presentation 2021: Wen Quantitative Agreement Analysis for HTT Pilot Study Data

### Quantitative Agreement Analysis for HTT Pilot Study Data

- Presenter: **Si Wen, Ph.D.**
- When: **Friday, July 16th, at 11:00 am EDT**
- Related manuscript, submitted to Statistics in Biopharmaceutical Research, can be read [HERE](#)
- The [GitHub](#) repo with an R package for the methods and simulations: <https://github.com/DIDSR/ANOVA.MRMC.LOA>
- Downloadable Files: [0716-Quantitative Agreement Analysis for HTT data.pdf](#) (1 MB, uploaded by Katherine N Elfer 2 years 8 months ago)

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### Detailed Abstract

Computational algorithms have been applied to support many medical and clinical tasks. For some of the clinical tasks, such as evaluating stromal tumor-infiltrating lymphocytes (sTILs) in a whole slide image, there are no ground truth reference values. In this work, we collect quantitative reference values from pathologists. To validate the effectiveness of the algorithms, we are exploring the use of agreement analysis, such as limits of agreement (LOA), to assess the closeness between the algorithm results and reference values quantitatively. The inter-reader variability is introduced into the agreement analysis when multiple pathologists/readers are involved in generating the reference values for each case. To decompose the total variation in the data, we use the random effects ANOVA model. The decomposed reader and case variance components are used to estimate LOA and the variance, so that this agreement analysis takes both the reader and case variability into consideration. The between-reader agreement among the pathologists can also be analyzed by the ANOVA, which can in turn be linked to the intraclass correlation coefficient (ICC). We will use the HTT pilot study data to present the analytical result.