

TraIT WP4: Proteomics QC Tool

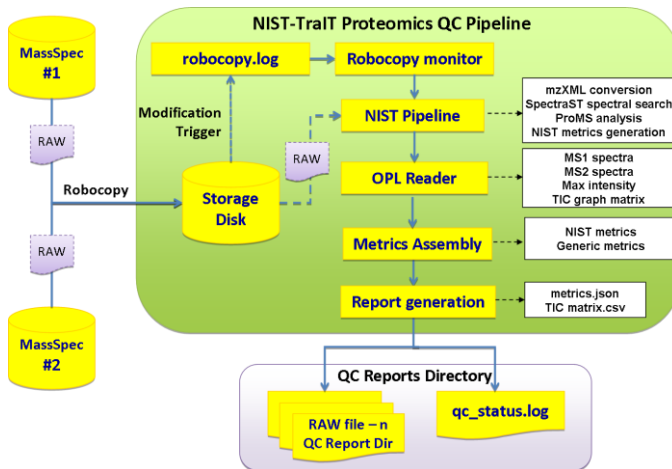
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Background: Monitoring analytical performance of a liquid chromatography mass spectrometry (LC-MS/MS) system is important in a common discovery-based proteomics workflow. The National Institute of Standards and Technology (NIST) has developed a Mass Spectrometry Quality Control (MSQC) pipeline for this purpose. We have adapted this pipeline to automatically trigger the processing on the availability of a newly acquired data file and subsequently create a report of 42 quality control (QC) metrics. These metrics are divided into following categories: *MS*, *MS/MS*, *generic parameters*, *chromatography*, *ion source*, *peptide identification* and *dynamic sampling*.

Illustration: A diagram of the NIST-TraIT Proteomics QC pipeline processing raw files followed by a screenshot of the QC report viewer.



A custom-made report viewer aggregates and shows all available QC reports from the reports directory. It includes functionality of sorting, filtering, zooming, comparing and publishing these reports. The report viewer has been designed to accommodate output of other potential quality control tools.

