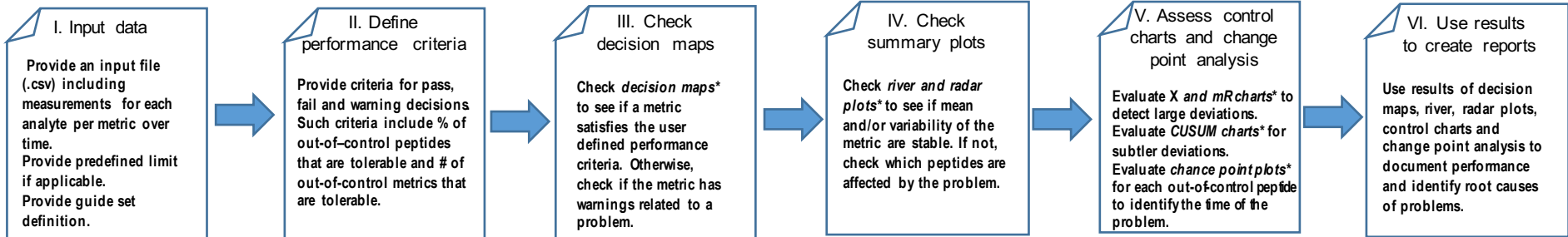# MSstatsQC v 1.0.0

Workflow: `MSstatsQC` is an open-source R-based package and web application for statistical analysis and monitoring of quality control and system suitability testing data produced by spectrometry-based proteomic experiments.
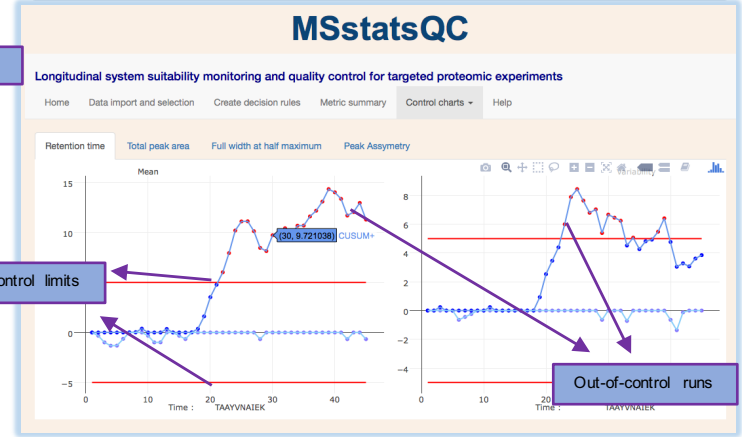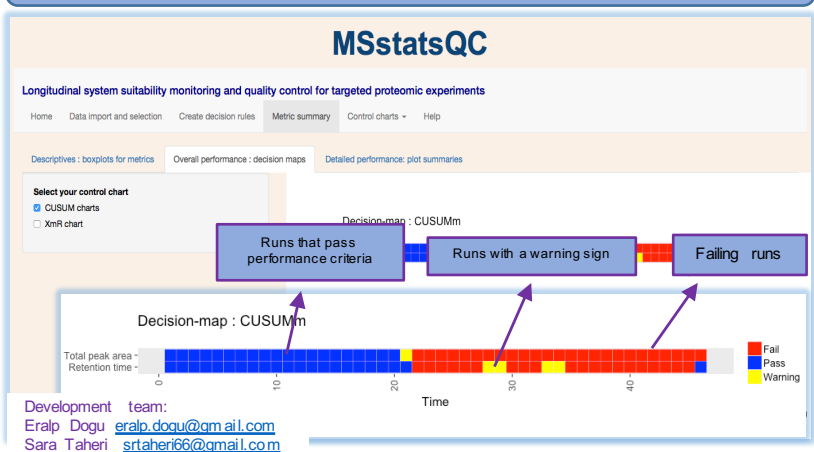
Cheat Sheet
Learn more at
mstats.org/mstatsqc

I. Input data
Provide an input file (.csv) including measurements for each analyte per metric over time.
Provide predefined limit if applicable.
Provide guide set definition.

II. Define performance criteria
Provide criteria for pass, fail and warning decisions. Such criteria include % of out-of–control peptides that are tolerable and # of out-of-control metrics that are tolerable.

III. Check decision maps
Check *decision maps** to see if a metric satisfies the user defined performance criteria. Otherwise, check if the metric has warnings related to a problem.

IV. Check summary plots
Check *river and radar plots** to see if mean and/or variability of the metric are stable. If not, check which peptides are affected by the problem.

V. Assess control charts and change point analysis
Evaluate X *and mR charts** to detect large deviations.
Evaluate *CUSUM charts** for subtler deviations.
Evaluate *chance point plots** for each out-of-control peptide to identify the time of the problem.

VI. Use results to create reports
Use results of decision maps, river, radar plots, control charts and change point analysis to document performance and identify root causes of problems.

I. Input data
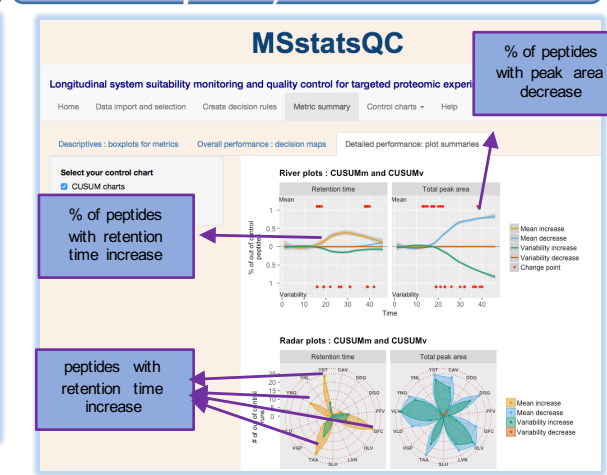

II. Define performance criteria

V. Assess control charts (X and *mR** and *CUSUMm** and *CUSUMv*) and *change point analysis**
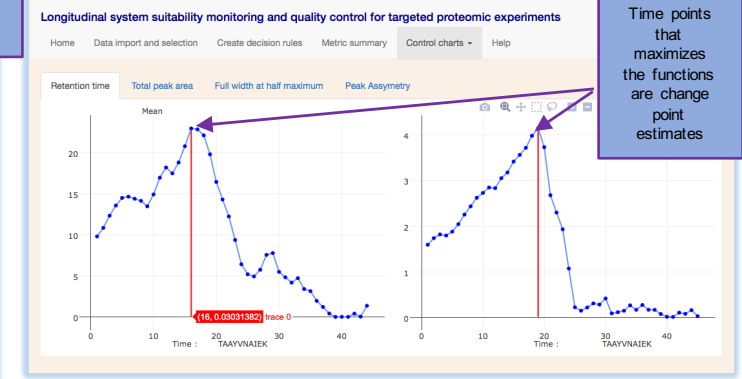

III. Check *decision maps**

IV. Check summary plots (*river plots** and *radar plots**)

Development team:
Eralp Dogu   eralp.dogu@gmail.com
Sara Taheri   srtaheri66@gmail.com
Olga Vitek   o.vitek@neu.edu

*Methods that are available only through MSstatsQC