ABSTRACT FORMAT

'Question' view:

Background:
- Provided a brief background that provides the reader with the information that defines the driving force behind this work
- In **the last sentence in this section** state, in unequivocal terms, the problem that is being addressed

80-100 words

Results:
- In succinct terms, state what the most relevant results are
- Include data details only to the extent needed to convey the uniqueness/value of the results

125-150 words

Significance:
- What do you conclude and why is it significant?

50-75 words

'Exemplar' view:

Background: The SARS-CoV-2 pandemic presented a global challenge that, early on, could not be addressed adequately with testing that met demand. Antigen-based assays were rapid, simple, had low skill requirements and were amenable to point-of-need testing, but performed poorly on sensitivity, specificity and accuracy. In contrast, PCR-based tests provided robust performance, but required multi-step sample preparation, complicated detection optics, lengthy turn-around times and lab-based environments. **It is clear that a PCR-based SARS-CoV-2 assay was needed that was portable, required low skill, provided rapid sample-to-result and amenable to point-of-care testing.** (88)

Results: We describe a microfluidic qPCR-based saliva test that detects sequences from both the N- and E-genes of SARS-CoV-2, with parallel analysis of the necessary positive/negative controls. Sample capture and on-board sample preparation involves a collection cup integrated with an RNA extraction tube that, together, exploits particle-based concentration of the virus, followed by enzymatic extraction of viral RNA in <10 min yielding pico- to nano-gram quantities of RNA. Passive microfluidic transfer of the extracted RNA to an 8-plex PCR cartridge with embedded (PCR) reagents utilizes dual Peltier-driven heating/cooling cycles the 10 uL volume between temperatures at 6C/sec (heat and cool). With transition rate, 45 cycles of PCR are completed in ~12 min. Homebuilt software analyzed fluorescent signal after each cycle, and defined the presence or absence of the virus with a detection limit of 1500 copies per ml. (137)

Significance: This represents the first microfluidic system for detection of SARS-CoV-2 in saliva where 'sampling' and 'result' are obtained by an unskilled user. The small volumes with microfluidics allow for sub-200 uL saliva samples to be adequate, with a time-to-result of <25 minutes, and provides a cost-effective assay platform that is easily portable. (52)

Chemometric example

Background: The selection of optimal preprocessing is among the main bottlenecks in chemometric data analysis. The aim is to enhance the relevant information by removing data artifacts, such as a baseline, scatter effects or noise. A multitude of preprocessing methods exists to deliver one or more of these benefits. It is however a burden to select the (combination of)methods that should be used for the specific data being analyzed. Currently, the approach is limited to trial-and-error and is therefore subjective.
There is a great need for an objective method to select an optimal strategy to preprocess the data (98)

Results We present a novel, simple, and effective approach for preprocessing selection. The defining feature of this approach is a design of experiments. On the basis of the design, model performance of a few well-chosen preprocessing methods, and combinations thereof (called strategies) is evaluated. Interpretation of the main effects and interactions subsequently enables the selection of an optimal preprocessing strategy. The presented approach is applied to eight different spectroscopic data sets, covering both calibration and classification challenges. We show that the approach is able to select a preprocessing strategy which improves model performance by at least 50% compared to the raw data; in most cases, it leads to a strategy very close to the true optimum. (115)

Significance: An appropriate preprocessing is crucial for a proper data analysis. Our approach makes preprocessing selection fast, insightful, and objective. The approach is generic and can be applied to data from different analytical platforms. (33)