Claims

1. An in-vitro multi-analyte method of analyzing a micro-volume human serum or plasma specimen, comprising:

   (a) depositing no more than 3 µL of the specimen onto an attenuated total reflection (ATR) crystal and acquiring a mid-infrared spectrum of the specimen;

   (b) restricting the acquired spectrum to at least a first wavelength band of 1750–1300 cm^{-1} and a second wavelength band of 1150–950 cm^{-1} that contain informative biochemical signatures;

   (c) computing a pre-processed spectral vector by (i) subtracting a polynomial baseline from the restricted spectrum, (ii) applying a Savitzky–Golay second-derivative filter to the spectrum, and (iii) performing ℓ_2-normalization on the spectral values within the retained bands;

   (d) selecting, based on an input indicative of the subject's age, one model from a plurality of trained predictive models, each model corresponding to an age range;

   (e) applying the selected model to the pre-processed spectral vector to produce multiple outputs, the outputs comprising:

   (i) predicted concentrations of immunoglobulin G (IgG) and immunoglobulin A (IgA) in the specimen;

   (ii) at least one metabolic biomarker value selected from the group consisting of a glucose-equivalent index and a total cholesterol level;

   (iii) at least one classification result selected from the group consisting of a sepsis risk indicator and a metabolic syndrome indicator;

   (f) computing quality-control statistics including a Hotelling's T^2 score and a Q-residual for the pre-processed spectral vector, and suppressing or invalidating the outputs if the quality-control statistics fall outside predefined acceptable ranges;

   (g) generating a report comprising one or more flags or indicators for primary immunodeficiency and non-communicable disease risk, wherein the flags are determined by comparing the outputs to age-specific reference intervals.

2. The computer-implemented method of claim 1, wherein a processor receives the spectral data as wavenumber–intensity pairs, executes steps (b)–(g) of claim 1, and returns a set of outputs including quantitative values for IgG, IgA, albumin, a glucose-equivalent, and total cholesterol, as well as classification labels for sepsis risk

and metabolic syndrome, wherein parameters of the selected model are specific to an age band and are updated over time by federated learning using summary statistics from remote instruments.

3. A system for multi-analyte spectroscopic analysis, comprising: a mid-infrared Fourier-transform spectrometer; a micro-volume sampling tile configured to spread a blood serum sample of approximately 3 µL into a thin film for ATR measurement; and one or more processors configured to execute the method of claim 2; the system further comprising a quality control module that enforces insertion of control samples at regular intervals and checks two levels of control limits every N patient runs to ensure analytical accuracy.

4. A kit for field sample collection and preparation for use with the method of claim 1, the kit comprising: a capillary tube sized to collect approximately 5 µL of blood from a finger-stick; a micro-patterned ATR sampling tile packaged in a desiccated, barcoded foil pouch; a portable battery-powered micro-centrifuge configured to separate about 3 µL of serum from the collected blood within 60 seconds; and written instructions detailing a procedure to obtain a serum film on the ATR tile for spectroscopic analysis.

5. The method of claim 1, wherein in step (c) the Savitzky–Golay second-derivative uses a window of 9 points and a polynomial order of 2 on spectral data with a digital resolution of approximately 2 cm^{-1} per point.

6. The method of claim 1, wherein the at least one metabolic biomarker value includes a lipid-related feature and the step (b) further comprises retaining an absorbance shoulder between 1745 cm^{-1} and 1730 cm^{-1} corresponding to a cholesterol or triglyceride band.

7. The method of claim 1, wherein the glucose-equivalent index is predicted using only spectral information from the 1150–950 cm^{-1} band.

8. The method of claim 1, wherein the one or more processors are further configured to output an indicator of potential malnutrition when a predicted albumin concentration is below a threshold (3.5 g/dL for example).

9. The method of claim 1, further comprising computing a Bayesian posterior probability that fuses a primary immunodeficiency risk inferred from the spectral analysis with an independent T-cell receptor excision circle (TREC) assay result to produce a combined immunodeficiency risk score.

10. The system of claim 3, wherein the micro-volume sampling tile comprises a hydrophobic perimeter surrounding a hydrophilic center such that, when the sample is applied, the liquid spreads to a uniform film thickness of about 2–5 µm at a volume of 3 µL.

11. The computer-implemented method of claim 2, wherein the prediction of sepsis risk and the prediction of metabolic syndrome are produced by classifier heads that share a common feature extraction trunk in a multi-task learning model trained with a combined loss function.

12. The method of claim 1, wherein the outputs generated in step (g) are formatted and transmitted as a single message conforming to a health data exchange standard, such as an HL7 or FHIR message, for integration into an electronic health record system.

13. The kit of claim 4, wherein the foil pouch containing the ATR sampling tile is configured to maintain a baseline absorbance drift of not more than 0.005 AU after 30 days of storage at 35 °C, thereby preserving the calibration stability of the tile.

14. The method of claim 1, wherein the specimen is obtained by utilizing an existing testing encounter such that the micro-volume blood sample is collected during an HIV rapid diagnostic test or a dried blood spot collection for infant HIV diagnosis, and the additional sample collection and spectroscopic analysis add less than 60 seconds to the overall workflow and do not consume reagents from the existing test.