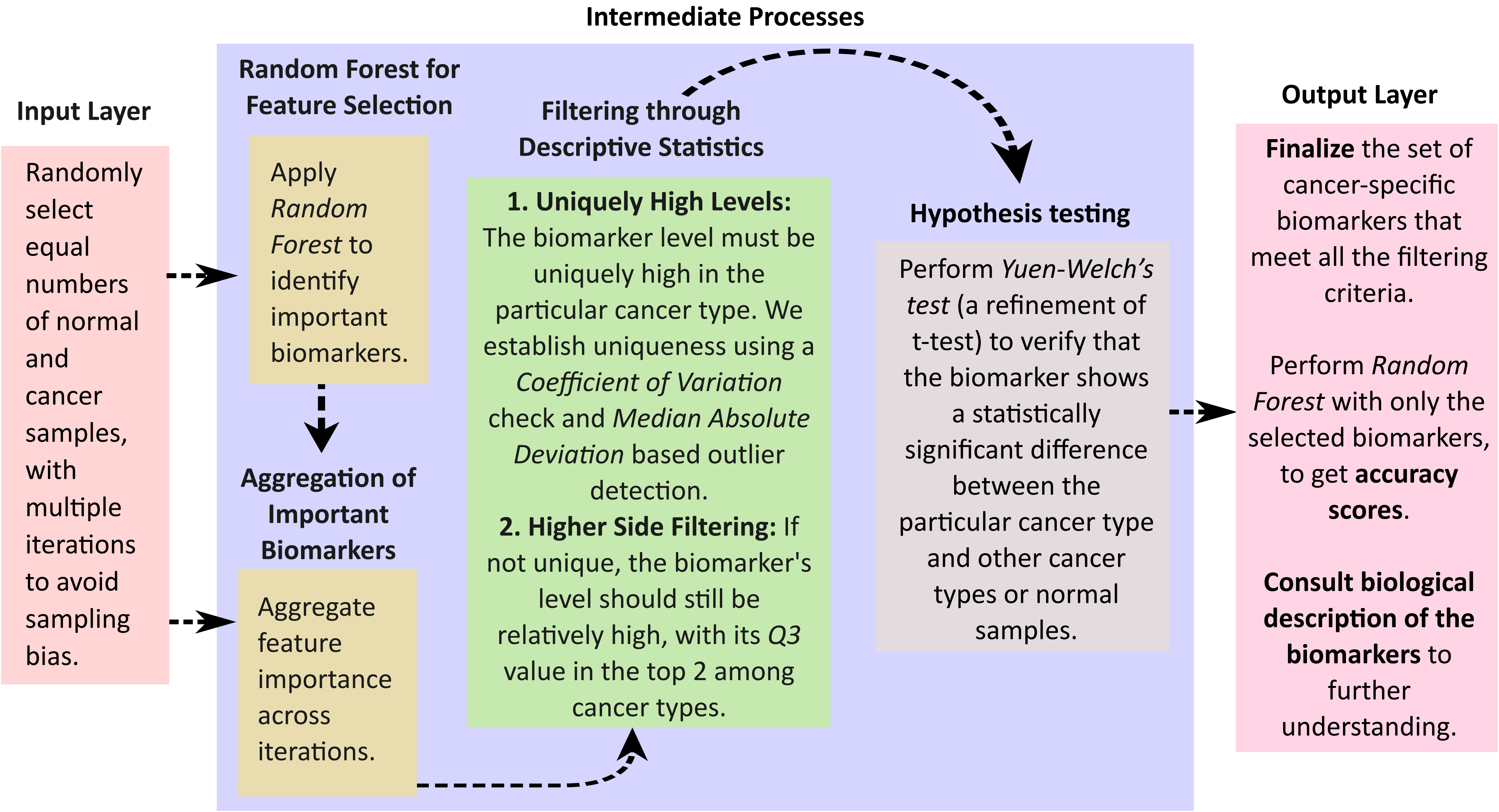
Schema for Biomarker Discovery from Clinical Cancer Data



Input Layer

Randomly select equal numbers of normal and cancer samples, with multiple iterations to avoid sampling bias.

Intermediate Processes

Random Forest for Feature Selection

Apply *Random Forest* to identify important biomarkers.

Aggregation of Important Biomarkers

Aggregate feature importance across iterations.

Filtering through Descriptive Statistics

1. Uniquely High Levels: The biomarker level must be uniquely high in the particular cancer type. We establish uniqueness using a *Coefficient of Variation* check and *Median Absolute Deviation* based outlier detection.

2. Higher Side Filtering: If not unique, the biomarker's level should still be relatively high, with its *Q3* value in the top 2 among cancer types.

Hypothesis testing

Perform *Yuen-Welch's test* (a refinement of t-test) to verify that the biomarker shows a statistically significant difference between the particular cancer type and other cancer types or normal samples.

Output Layer

Finalize the set of cancer-specific biomarkers that meet all the filtering criteria.

Perform *Random Forest* with only the selected biomarkers, to get **accuracy scores**.

Consult biological description of the biomarkers to further understanding.